STIC-Biotech/ChemLib 150060

From: Bunner, Bridget
Sent: Wednesday, April 06, 2005 2:00 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like to request a sequence search for case 09/810,796:

1. the nucleic acid sequence of SEQ ID NO: 2
2. the nucleic acid sequence of SEQ ID NO: 3

CRTF

Thanks!

Bridget Bunner

Art Unit 1647
Rem 4C65
(571) 272-0881
mailbox 4C70

****
STAFF USE ONLY

Searcher:_____
Searcher Phone: 2-
Date Searcher Picked up:____
Date Completed:_____
Searcher Prep/Rev. Time:___
Online Time:_____

****
Type of Search

NA#:_____ AA#:_____
Interference:____ SPDI:___
S/L:_____ Oligomer:____
Encode/Transl:_____
Structure#:_____ Text:___
Inventor:____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other(Specify):_____

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 09:27:56 ; Search time 426.638 Seconds
(without alignments)
10332.249 Million cell updates/sec

Title: US-09-810-796-2
Perfect score: 2694
Sequence: 1 atgaaggatgtggagtcggg.....ctcatgtcaaactgaaataa 2694

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2689.2	99.8	3137	4	US-09-590-304-1	Sequence 1, Appli
2	2681.2	99.5	3074	4	US-09-813-148-1	Sequence 1, Appli
3	2625.2	97.4	2772	4	US-09-825-147-1	Sequence 1, Appli
4	2625.2	97.4	3111	4	US-09-825-147-3	Sequence 3, Appli
5	518.4	19.2	2196	4	US-09-949-016-1823	Sequence 1823, Ap
6	518.4	19.2	2335	4	US-09-492-361-1	Sequence 1, Appli
7	516	19.2	2273	3	US-09-177-650-88	Sequence 88, Appl
8	510	18.9	2169	3	US-09-105-058C-22	Sequence 22, Appl
9	509.8	18.9	582	4	US-09-495-050A-303	Sequence 303, App
10	465.4	17.3	896	3	US-09-105-058C-1	Sequence 1, Appli
11	464	17.2	2814	3	US-09-177-650-90	Sequence 90, Appl
12	460.8	17.1	2565	3	US-09-105-058C-26	Sequence 26, Appl
13	460.8	17.1	2914	3	US-09-177-650-6	Sequence 6, Appli
14	452	16.8	575	4	US-09-495-050A-305	Sequence 305, App
15	425	15.8	3287	3	US-09-105-058C-19	Sequence 19, Appl
16	423.4	15.7	3232	3	US-09-177-650-1	Sequence 1, Appli
17	423.4	15.7	3237	3	US-09-177-650-95	Sequence 95, Appl
18	421.4	15.6	900	3	US-09-105-058C-3	Sequence 3, Appli
19	420.6	15.6	900	3	US-09-105-058C-5	Sequence 5, Appli
20	363.8	13.5	930	3	US-09-105-058C-17	Sequence 17, Appl
21	334.2	12.4	735	3	US-09-105-058C-7	Sequence 7, Appli
22	276.4	10.3	284	4	US-09-495-050A-304	Sequence 304, App
23	267.8	9.9	2028	3	US-09-634-920-1	Sequence 1, Appli
24	267.8	9.9	2028	4	US-09-840-125-1	Sequence 1, Appli
25	267.8	9.9	3181	3	US-09-135-021-1	Sequence 1, Appli
26	267.8	9.9	3181	3	US-09-135-020-1	Sequence 1, Appli
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33	266.6	9.9	2734	3	US-09-135-021-79	Sequence 79, Appl
34	266.6	9.9	2821	3	US-09-135-010A-115	Sequence 115, App
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41	134.6	5.0	251	4	US-09-495-050A-296	Sequence 296, App
42	95.8	3.6	171	3	US-09-177-650-102	Sequence 102, App
43	95.8	3.6	58543	4	US-09-949-016-13565	Sequence 13565, A
44	95.2	3.5	1481	4	US-09-949-016-4101	Sequence 4101, Ap
45	84.8	3.1	649	3	US-09-177-650-118	Sequence 118, App

ALIGNMENTS

RESULT 1
US-09-590-304-1
; Sequence 1, Application US/09590304
; Patent No. 6649371
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHAN
; FILE REFERENCE: 2815-0136P
; CURRENT APPLICATION NUMBER: US/09/590,304
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2691)
US-09-590-304-1

Query Match 99.8%; Score 2689.2; DB 4; Length 3137;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2691; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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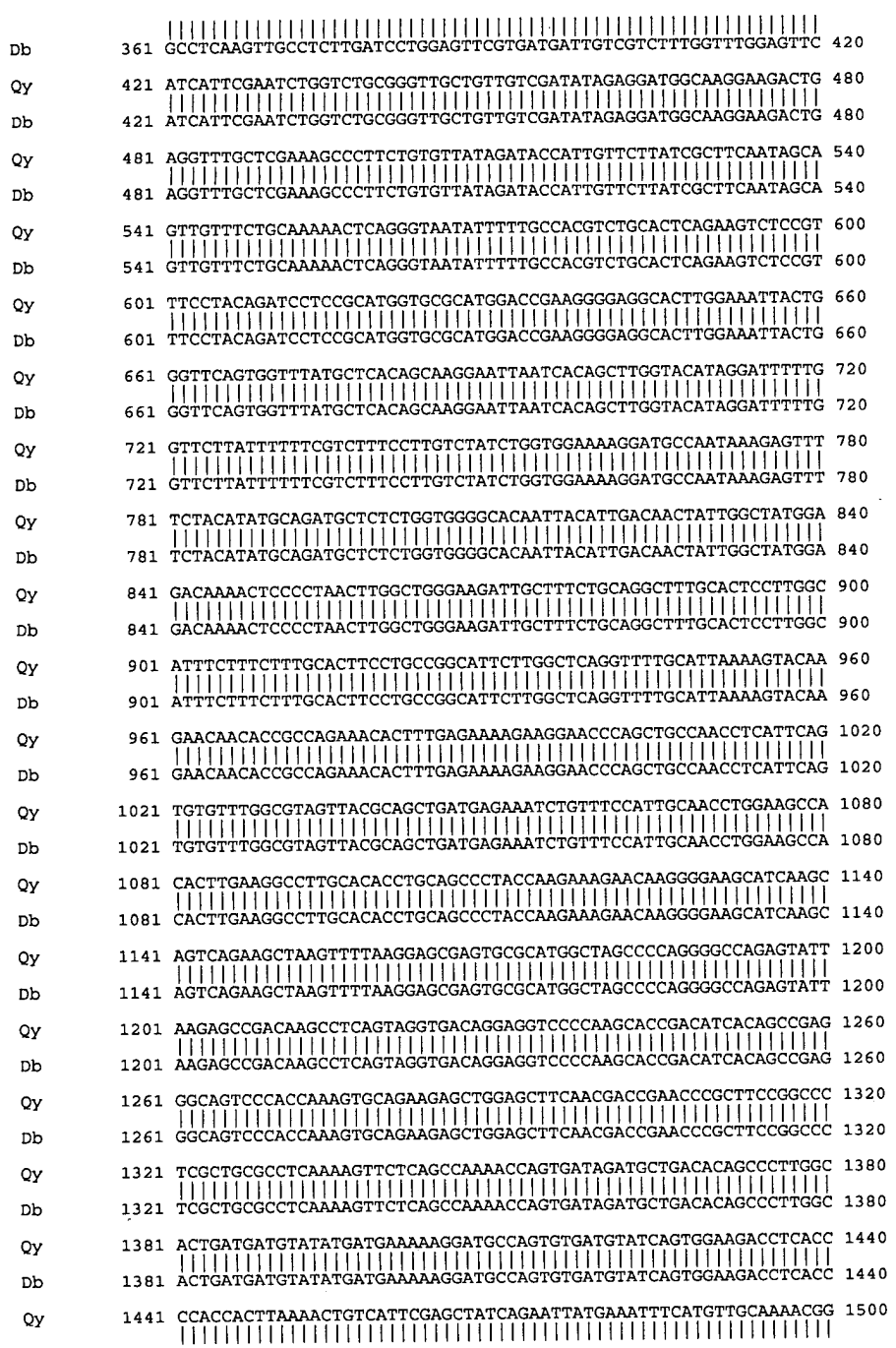
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RESULT 2
US-09-813-148-1
; Sequence 1, Application US/09813148
; Patent No. 6617131
; GENERAL INFORMATION:
;  APPLICANT: STEINMEYER, Klaus
;  APPLICANT:  LERCHE, Christian
;  APPLICANT:  SCHERER, Constanze
;  APPLICANT:  SEEBOHM, Guiscard
;  APPLICANT:  BUSCH, Andreas E.
;  TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN
;  TITLE OF INVENTION:  NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
;  FILE REFERENCE: 38005-119
;  CURRENT APPLICATION NUMBER: US/09/813,148
;  CURRENT FILING DATE:  2001-03-21
;  PRIOR APPLICATION NUMBER: DE 100 13 732.6
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: US 60/194,041
;  PRIOR FILING DATE: 2000-04-03
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 3074
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-813-148-1

  Query Match             99.5%;  Score 2681.2;  DB 4;  Length 3074;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 2686;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

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Qy         121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
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Qy         961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1175 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1234

Qy        1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1235 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1294

Qy        1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1295 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1354

Qy        1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1355 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1414

Qy        1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1415 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1474

Qy        1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1475 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1534

Qy        1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1535 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1594

Qy        1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1595 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1654

Qy        1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1655 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1714

Qy        1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560
               |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        1715 AAGTTTAAGGAAACATTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1774

Qy        1561 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1775 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1834

Qy       1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1835 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1894

Qy       1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1895 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1954

Qy       1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
                ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1955 ATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 2014

Qy       1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2015 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 2074

Qy       1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2075 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 2134

Qy       1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2135 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 2194

Qy       1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2195 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2254

Qy       2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2255 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2314

Qy       2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2315 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2374

Qy       2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2375 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2434

Qy       2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2435 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2494

Qy       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2495 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2554

Qy       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2555 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2614

Qy       2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2615 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2674

Qy       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2675 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2734

Qy       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2735 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2794

Qy       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2795 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2854

Qy       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       2855 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2908


RESULT 3
US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
;  APPLICANT: Hu, Yi
;  APPLICANT:  Kieke, James Alvin
;  APPLICANT:  Turner, C. Alexander Jr.
;  APPLICANT:  Nehls, Michael C.
;  APPLICANT:  Friedrich, Glenn
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and
;  TITLE OF INVENTION:  Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0160-USA
;  CURRENT APPLICATION NUMBER: US/09/825,147
;  CURRENT FILING DATE:  2001-04-03
;  PRIOR APPLICATION NUMBER: US 60/194,255
;  PRIOR FILING DATE: 2000-04-03
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 2772
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-825-147-1

  Query Match             97.4%;  Score 2625.2;  DB 4;  Length 2772;
  Best Local Similarity   98.9%;  Pred. No. 0;
  Matches 2664;  Conservative    0;  Mismatches    3;  Indels   27;  Gaps    1;

Qy         1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       106 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 165

Qy        61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       166 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTCGGTGGCGGCGGCGGTGGCCTG 225

Qy       121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       226 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 285

Qy       181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       286 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 345

Qy       241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       346 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 405

Qy       301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       406 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 465

Qy       361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       466 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 525

Qy       421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       526 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 585

Qy       481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       586 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 645

Qy       541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       646 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 705
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Qy       601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
Db       706 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 765

Qy       661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
Db       766 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 825

Qy       721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
Db       826 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 885

Qy       781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
Db       886 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 945

Qy       841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
Db       946 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 1005

Qy       901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
Db      1006 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 1065

Qy       961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
Db      1066 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1125

Qy      1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Db      1126 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1185

Qy      1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
Db      1186 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAA---------------------------- 1220

Qy      1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
Db      1221 --TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1278

Qy      1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
Db      1279 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1338

Qy      1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320
Db      1339 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1398

Qy      1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380
Db      1399 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1458

Qy      1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440
Db      1459 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1518

Qy      1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500
Db      1519 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1578

Qy      1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560
Db      1579 AAGTTTAAGGAAACATTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1638

Qy      1561 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620
Db      1639 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1698

Qy      1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680
Db      1699 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1758

Qy      1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
Db      1759 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1818

Qy      1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
Db      1819 ATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1878

Qy      1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
Db      1879 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1938

Qy      1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
Db      1939 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1998

Qy      1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
Db      1999 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 2058

Qy      1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
Db      2059 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2118

Qy      2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
Db      2119 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2178

Qy      2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
Db      2179 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2238

Qy      2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
Db      2239 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2298

Qy      2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280
Db      2299 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2358

Qy      2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
Db      2359 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2418

Qy      2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400
Db      2419 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2478

Qy      2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460
Db      2479 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2538

Qy      2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
Db      2539 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2598

Qy      2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
Db      2599 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2658

Qy      2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
Db      2659 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2718

Qy      2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
Db      2719 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2772
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RESULT 4
US-09-825-147-3
; Sequence 3, Application US/09825147
; Patent No. 6767736

; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-3

Query Match 97.4%; Score 2625.2; DB 4; Length 3111;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

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Qy        1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
Db      165 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 224
Qy       61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
Db      225 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTCGGTGGCGGCGGCGGTGGCCTG 284
Qy      121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
Db      285 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 344
Qy      181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
Db      345 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 404
Qy      241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
Db      405 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 464
Qy      301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
Db      465 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 524
Qy      361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
Db      525 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 584
Qy      421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
Db      585 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 644
Qy      481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
Db      645 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 704
Qy      541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
Db      705 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 764
Qy      601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
Db      765 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 824
Qy      661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
Db      825 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 884
Qy      721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
Db      885 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 944
Qy      781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
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Qy      841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
Db     1005 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 1064
Qy      901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
Db     1065 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 1124
Qy      961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
Db     1125 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1184
Qy     1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Db     1185 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1244
Qy     1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
Db     1245 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAA---------- 1279
Qy     1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
Db     1280 --TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1337
Qy     1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
Db     1338 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1397
Qy     1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320
Db     1398 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1457
Qy     1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380
Db     1458 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1517
Qy     1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440
Db     1518 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1577
Qy     1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500
Db     1578 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1637
Qy     1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560
Db     1638 AAGTTTAAGGAAACATTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1697
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Qy     1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680
Db     1758 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1817
Qy     1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
Db     1818 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1877
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Qy       1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
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Qy       1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
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Db       1998 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 2057

Qy       1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
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Db       2058 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 2117

Qy       1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
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Db       2118 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2177

Qy       2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
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Db       2178 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2237

Qy       2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
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Db       2238 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2297

Qy       2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
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Db       2298 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2357

Qy       2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280
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Db       2358 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2417

Qy       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
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Db       2418 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2477

Qy       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400
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Db       2478 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2537

Qy       2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460
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Db       2538 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2597

Qy       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
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Db       2598 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2657

Qy       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
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Db       2658 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2717

Qy       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
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Db       2718 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2777

Qy       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
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Db       2778 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2831
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RESULT 5
US-09-949-016-1823
; Sequence 1823, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1823
;   LENGTH: 2196
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-1823

  Query Match             19.2%;  Score 518.4;  DB 4;  Length 2196;
  Best Local Similarity   60.1%;  Pred. No. 1.2e-143;
  Matches 1103;  Conservative    0;  Mismatches  566;  Indels  165;  Gaps    8;

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Qy        337 ACCATCCCTGAGCACACAAAATTGGCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATG 396
              || ||||  ||||||    || | |||      || ||| | ||| |||| |||||||||
Db        301 ACTATCCAGGAGCACCAGGAACTTGCCAACGAGTGTCTCCTCATCTTGGAATTCGTGATG 360

Qy        397 ATTGTCGTCTTTGGTTTGGAGTTCATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGA 456
              || || || || || |||||||| |||| | ||  ||||||| || || ||||| || ||
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Qy        457 TATAGAGGATGGCAAGGAAGACTGAGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACC 516
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Db        421 TACCGAGGATGGCAGGGTCGCTTCCGCTTTGCCAGAAAGCCCTTCTGTGTCATCGACTTC 480

Qy        517 ATTGTTCTTATCGCTTCAATAGCAGTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCC 576
              || ||  |  | || ||  | || ||  |  | ||   || ||||| || || || |||
Db        481 ATCGTGTTCGTGGCCTCGGTGGCCGTCATCGCCGCGGGTACCCAGGGCAACATCTTCGCC 540

Qy        577 ACGTCTGCACTCAGAAGTCTCCGTTTCCTACAGATCCTCCGCATGGTGCGCATGGACCGA 636
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Qy        637 AGGGGAGGCACTTGGAAATTACTGGGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATC 696
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Db        601 CGCGGCGGCACCTGGAAGCTGCTGGGCTCAGTGGTCTACGCGCATAGCAAGGAGCTGATC 660

Qy        697 ACAGCTTGGTACATAGGATTTTTGGTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTG 756
              || || |||||||| || ||  |||| || || ||  | || ||||| ||||| ||||
Db        661 ACCGCCTGGTACATCGGGTTCCTGGTGCTCATCTTCGCCTCCTTCCTGGTCTACCTGGCT 720

Qy        757 GAAAAGGATGCCAATAAAGAGTTTTCTACATATGCAGATGCTCTCTGGTGGGGCACAATT 816
              || ||||| ||||    || || ||  | || || ||  | ||||||||||| || |||
Db        721 GAGAAGGACGCCAACTCCGACTTCTCCTCCTACGCCGACTCGCTCTGGTGGGGGACGATT 780

Qy        817 ACATTGACAACTATTGGCTATGGAGACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTT 876
              |||||||||| || |||||||| ||||| || || |  || |||||||| ||  | ||
Db        781 ACATTGACAACCATCGGCTATGGTGACAAGACACCGCACACATGGCTGGGCAGGGTCCTG 840

Qy        877 TCTGCAGGCTTTGCACTCCTTGGCATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGC 936
              |||| ||||| ||  | || ||||| |||||||||| || |||||||||| || |||
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Qy        937 TCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAGAAACACTTTGAGAAAAGAAGG 996
              || || ||||  | || || || || ||||| ||||| ||||| |  |||
Db        901 TCCGGCTTTGCCCTGAAGGTCCAGGAGCAGCACCGGCAGAAGCACTTCGAGAAGCGGAGG 960

Qy        997 AACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCT 1056
              |  || || |||||||||| |||  ||  |||||    ||| |  | |||  ||
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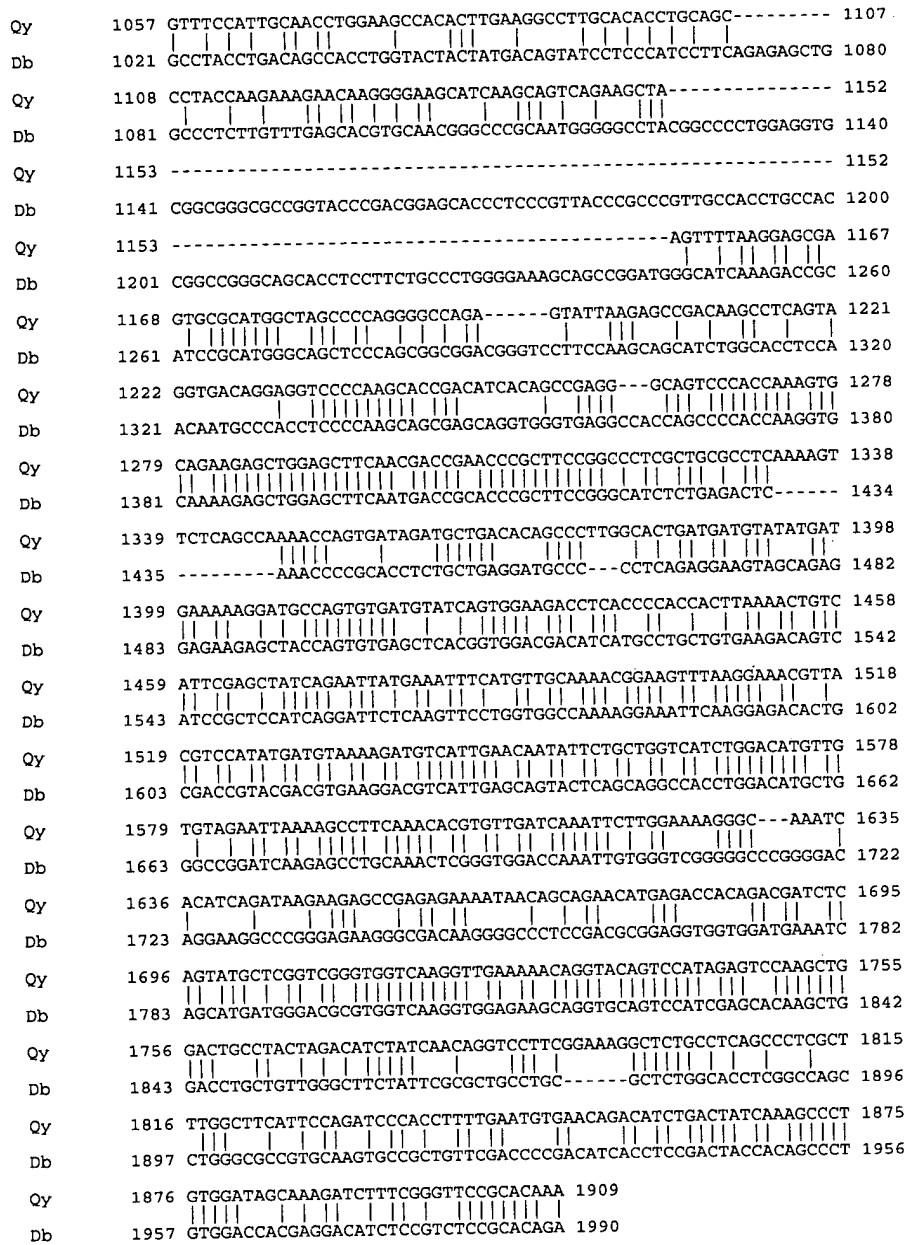
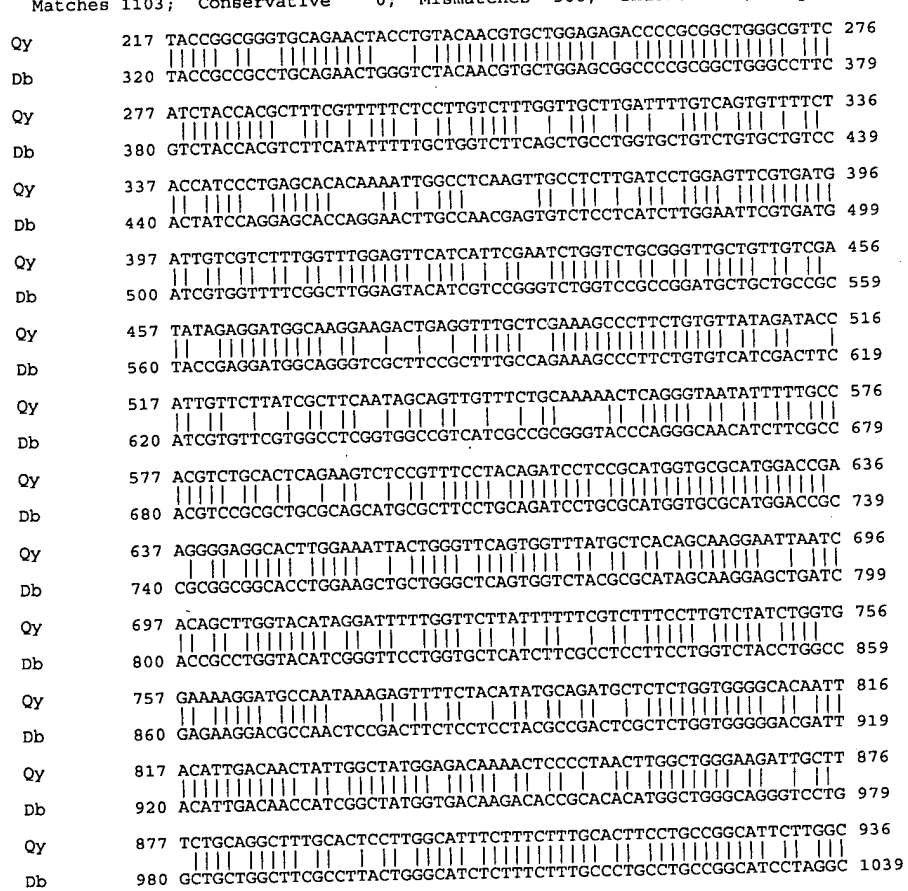


RESULT 6
US-09-492-361-1
; Sequence 1, Application US/09492361

; Patent No. 6794161
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
; TITLE OF INVENTION: POTASSIUM CHANNELS
; FILE REFERENCE: 2815-127P
; CURRENT APPLICATION NUMBER: US/09/492,361
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(2335)
; NAME/KEY: CDS
; LOCATION: (83)..(2170)
US-09-492-361-1

Query Match 19.2%; Score 518.4; DB 4; Length 2335;
Best Local Similarity 60.1%; Pred. No. 1.3e-143;
Matches 1103; Conservative 0; Mismatches 566; Indels 165; Gaps 8;



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Qy    997 AACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCT 1056
Db   1100 ATGCCGGCAGCCAACCTCATCCAGGCTGCCTGGCGCCTGTACTCCACCGATATGAGCCGG 1159

Qy   1057 GTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGCACACCTGCAGC--------- 1107
Db   1160 GCCTACCTGACAGCCACCTGGTACTACTATGACAGTATCCTCCCATCCTTCAGAGAGCTG 1219

Qy   1108 CCTACCAAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGCTA--------------- 1152
Db   1220 GCCCTCTTGTTTGAGCACGTGCAACGGGCCCGCAATGGGGGCCTACGGCCCCTGGAGGTG 1279

Qy   1153 ------------------------------------------------------------ 1152
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Qy   1153 ---------------------------------------------AGTTTTAAGGAGCGA 1167
Db   1340 CGGCCGGGCAGCACCTCCTTCTGCCCTGGGGAAAGCAGCCGGATGGGCATCAAAGACCGC 1399

Qy   1168 GTGCGCATGGCTAGCCCCAGGGGCCAGA------GTATTAAGAGCCGACAAGCCTCAGTA 1221
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Qy   1222 GGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAGG---GCAGTCCCACCAAAGTG 1278
Db   1460 ACAATGCCCACCTCCCCAAGCAGCGAGCAGGTGGGTGAGGCCACCAGCCCCACCAAGGTG 1519

Qy   1279 CAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGT 1338
Db   1520 CAAAAGAGCTGGAGCTTCAATGACCGCACCCGCTTCCGGGCATCTCTGAGACTC------ 1573

Qy   1339 TCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGAT 1398
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Qy   1399 GAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTC 1458
Db   1622 GAGAAGAGCTACCAGTGTGAGCTCACGGTGGACGACATCATGCCTGCTGTGAAGACAGTC 1681

Qy   1459 ATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTA 1518
Db   1682 ATCCGCTCCATCAGGATTCTCAAGTTCCTGGTGGCCAAAAGGAAATTCAAGGAGACACTG 1741

Qy   1519 CGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTG 1578
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Qy   1579 TGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGC---AAATC 1635
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Qy   1636 ACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTC 1695
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Qy   1816 TTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCT 1875
Db   2036 CTGGGCGCCGTGCAAGTGCCGCTGTTCGACCCCGACATCACCTCCGACTACCACAGCCCT 2095

Qy   1876 GTGGATAGCAAAGATCTTTCGGGTTCCGCACAAA 1909
Db   2096 GTGGACCACGAGGACATCTCCGTCTCCGCACAGA 2129
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RESULT 7
US-09-177-650-88
; Sequence 88, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; TITLE OF INVENTION: AND OTHER EPILEPSIES
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
;   LENGTH: 2273
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2271)
US-09-177-650-88

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  Query Match             19.2%;  Score 516;  DB 3;  Length 2273;
  Best Local Similarity   57.6%;  Pred. No. 6.4e-143;
  Matches 1030;  Conservative    2;  Mismatches  684;  Indels   72;  Gaps    4;

Qy     64 GGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTGAGG 123
Db     67 GGCTTCGTGGGGCTGGACCCCGGCGNGCCCGANTCCACACGCGACGGCNCNCTACTCATC 126

Qy    124 GAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCTTAC 183
Db    127 GCGGGCTCCGAGGCCCCCAAGCGCGGCANCNTNTTGAGCAAGCCGCGGACGGGCGGCGCG 186

Qy    184 ACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTGTAC 243
Db    187 GGANCCGGGAAGCCCCCNAANCGCAACGCCTTCTACCGCAAGCTGCAGAATTTCCTCTAC 246

Qy    244 AACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTCCTT 303
Db    247 AACGTGCTAGAGCGGCCCCGCGGCTNGGCGTTCATCTACCACGCCTACGTGTTCCTCCTG 306

Qy    304 GTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTGGCC 363
Db    307 GTTTTCTCCTGCCTTGTGCTTTCTGTGTTTTCCACCATCAAGGAGTACGAGAAGAGCTCT 366

Qy    364 TCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTCATC 423
Db    367 GAGGGGGCCCTCTACATCTTGGAAATCGTGACTATCGTGGTATTCGGTGTTGAGTACTTT 426

Qy    424 ATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTGAGG 483
Db    427 GTGAGGATCTGGGCTGCAGGCTGCTGTTGCCGGTATCGAGGCTGGAGGGGCAGGCTCAAG 486

Qy    484 TTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCAGTT 543
Db    487 TTTGCCAGGAAGCCGTTCTGTGTGATTGATATCATGGTGCTGATTGCCTCCATTGCTGTG 546

Qy    544 GTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGTTTC 603
Db    547 CTGGCTGCTGGTTCCCAGGGCAATGTCTTTGCCACATCTGCGCTTCGGAGCTTGCGGTTC 606

Qy    604 CTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTGGGT 663
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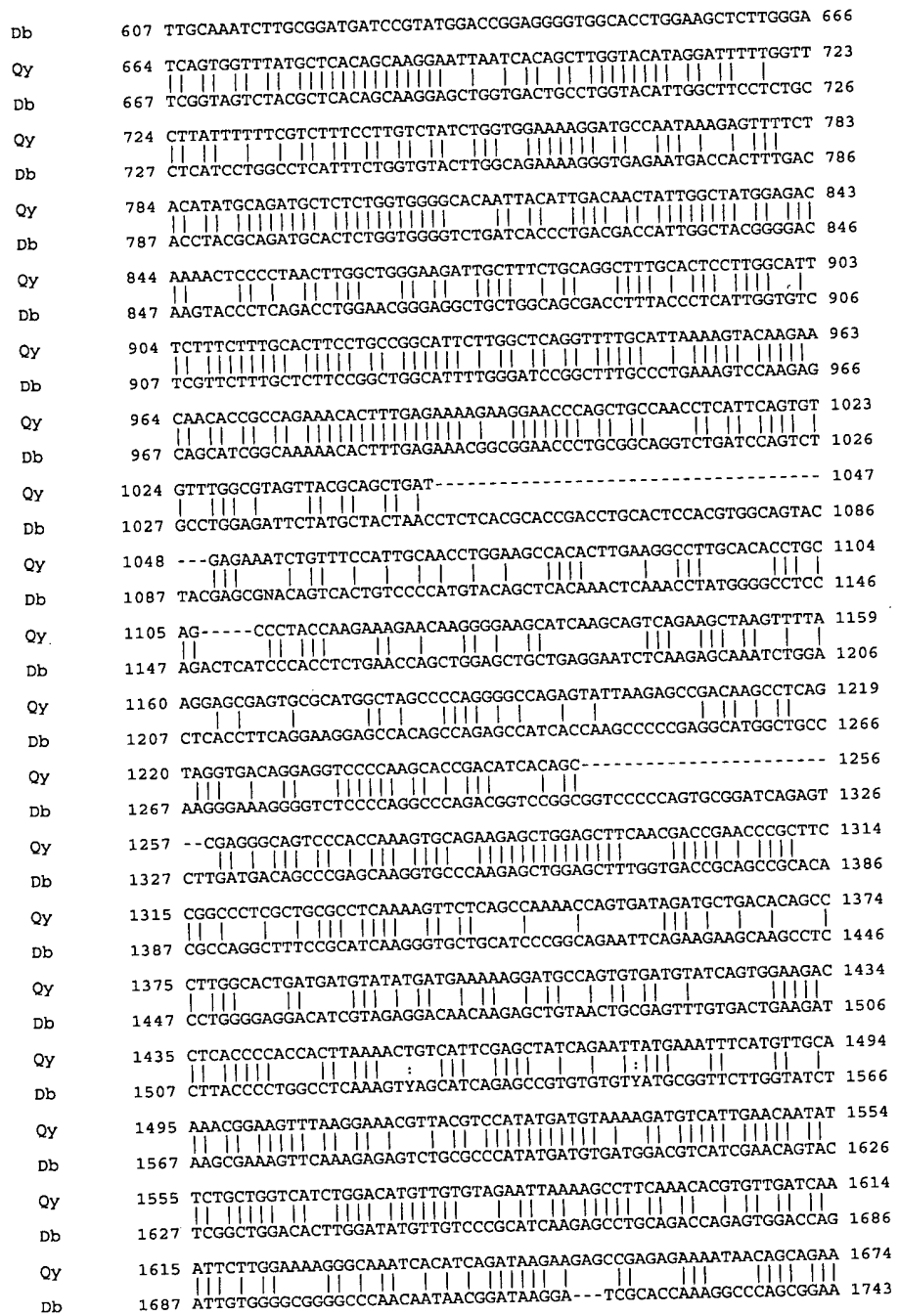
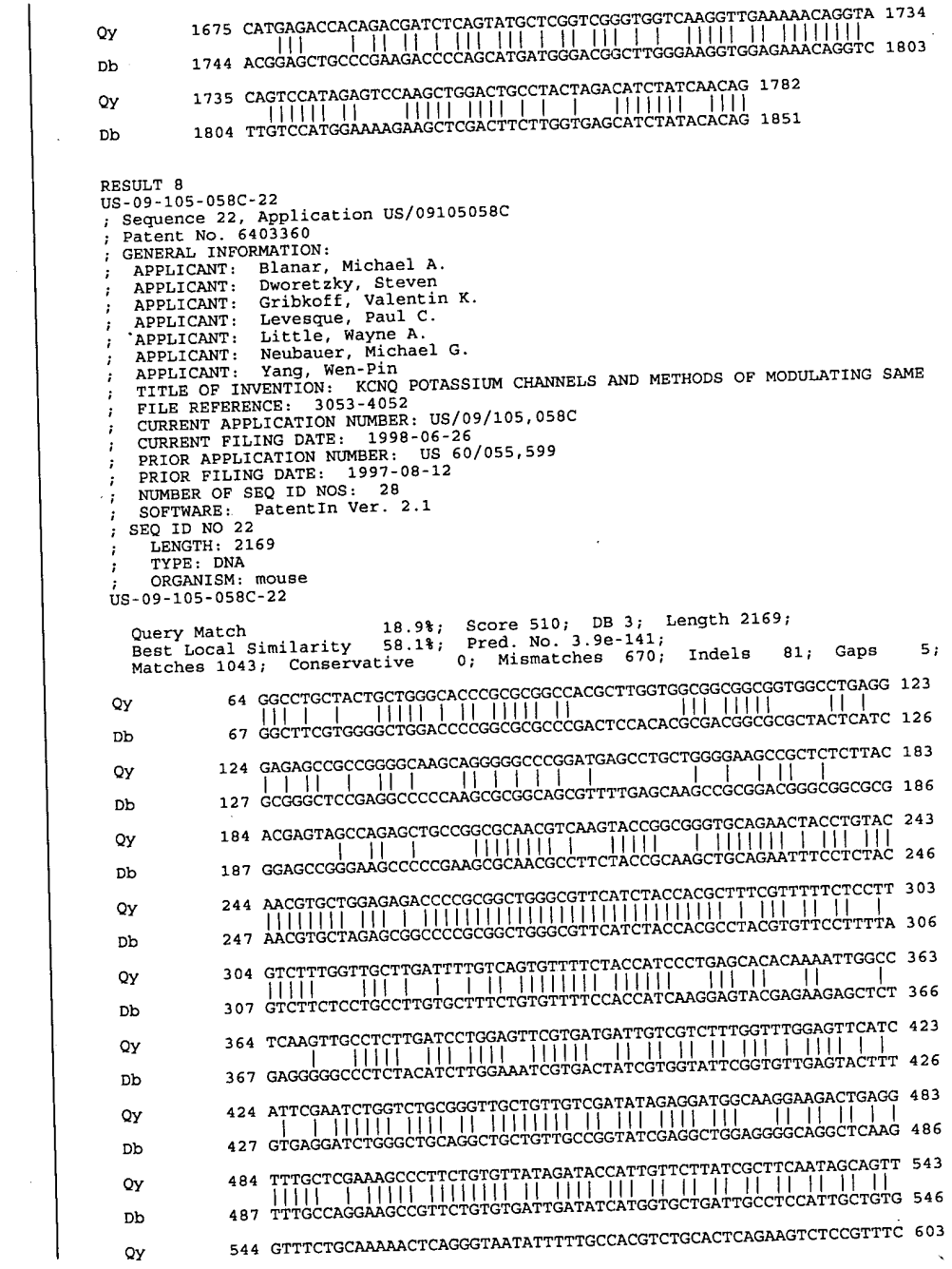
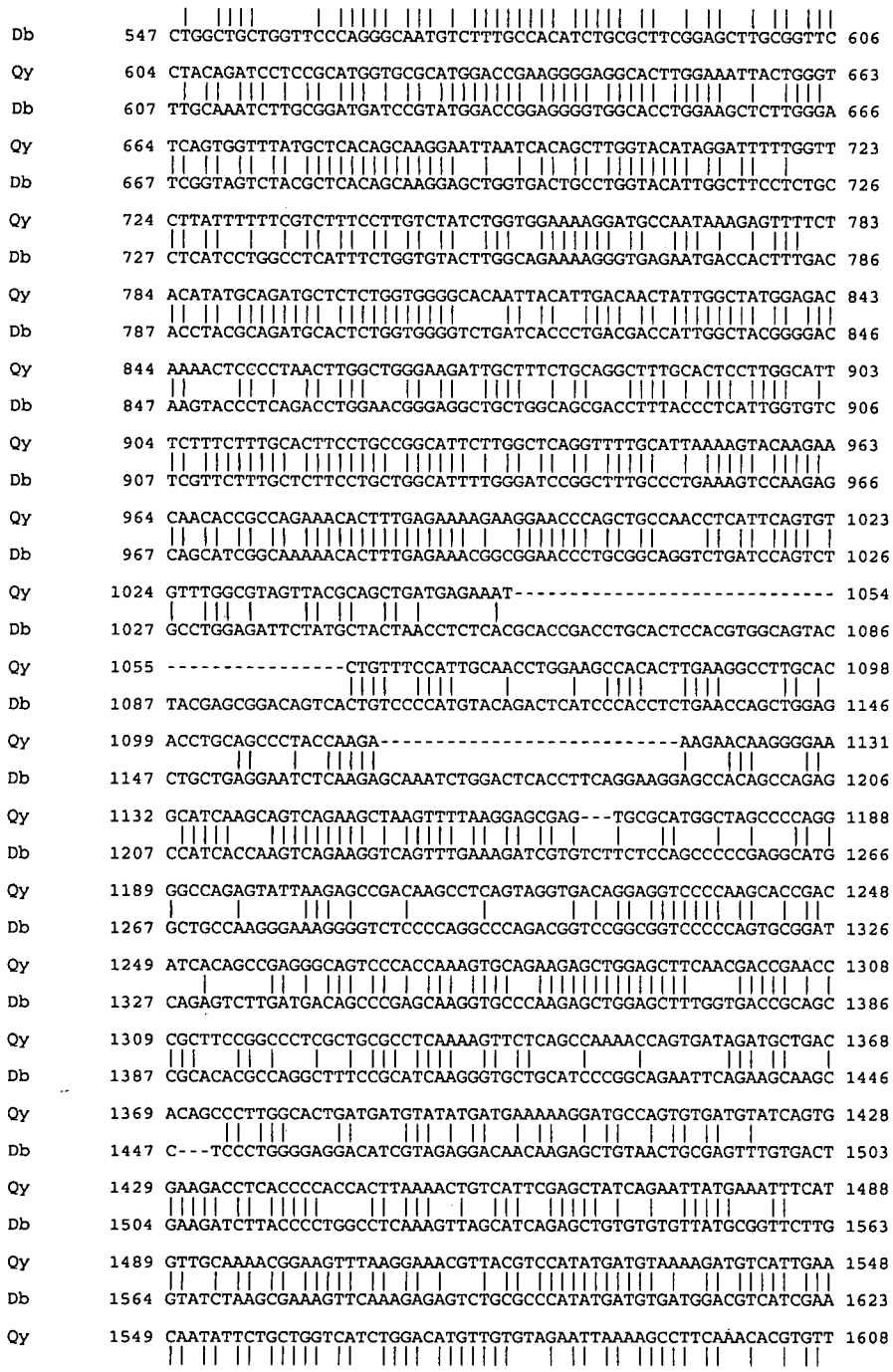
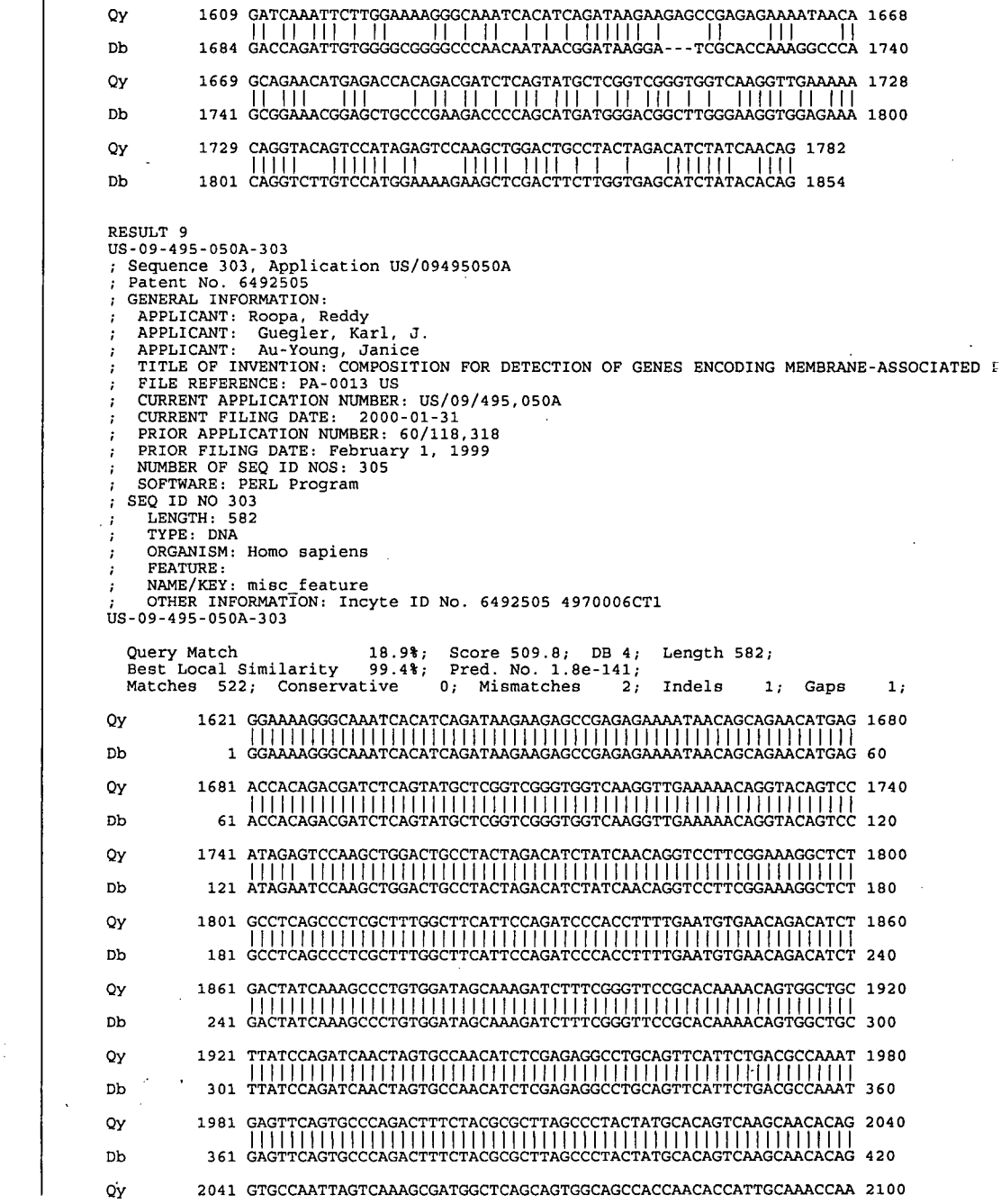




RESULT 8
US-09-105-058C-22
; Sequence 22, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blanar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: mouse
US-09-105-058C-22

Query Match 18.9%; Score 510; DB 3; Length 2169;
Best Local Similarity 58.1%; Pred. No. 3.9e-141;
Matches 1043; Conservative 0; Mismatches 670; Indels 81; Gaps 5;





RESULT 9
US-09-495-050A-303
; Sequence 303, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 303
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6492505 4970006CT1
US-09-495-050A-303

Query Match 18.9%; Score 509.8; DB 4; Length 582;
Best Local Similarity 99.4%; Pred. No. 1.8e-141;
Matches 522; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 480

Qy       2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATC 2145
              ||||||||||||| ||||||||| ||||||||||||||||||
Db        481 ATAAATACGGCACCAAAGCCAGCAG-CCCAACAACTTTACAGATC 524
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RESULT 10
US-09-105-058C-1
; Sequence 1, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blanar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 896
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Consensus
; OTHER INFORMATION: nucleotide sequence as shown in Fig. 16A-16D
; OTHER INFORMATION: y=c or t; r=a or g; m=a or c; k=g or t; s=g or c;
; OTHER INFORMATION: w=a or t; h=a, c, or t; b=g, t, or c; v=g, c, or a
US-09-105-058C-1

Query Match 17.3%; Score 465.4; DB 3; Length 896;
Best Local Similarity 53.7%; Pred. No. 4.4e-128;
Matches 460; Conservative 231; Mismatches 162; Indels 4; Gaps 2;

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Qy        190 AGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTGTACAACGTG 249
              :|::::  :  :  |:|:||||  |:::|||||::::  |:||:|:  |  ::|  |||:||:||::
Db         13 RGSMRSCCMSYSAAGMGMAACGCCWWSTACCGSMRSMTSCARAMTTTSMTCTACRACGYS 72

Qy        250 CTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTCCTTGTCTTT 309
              ||:|||:|:||:||:|||||||||||:::|:||||||||  |::||  ||  ||::|:|||:|
Db         73 CTRGAGMGRCCSCGSGGCTGGGCGYTSMTYTACCACGCSTWSGTGTTCCTBHTDGTYYTS 132

Qy        310 GGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTGGCCTCAAGT 369
              ::  |||:|::|:  ||:|  ||:  :::|  ||::||    |||  |:    |:  :    |:  :  :
Db        133 KSSTGCYTBRTKCTGKCTGTS-YKWCCACMWTCAAGGAGTAYGAGAMKRKYTCBGRRGRS 191

Qy        370 TGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTCATCATTCGA 429
              :::||:::::|::||||:  :::|::    ||:|::|:||:||:  ::||||::  ::  |  :|:
Db        192 KSSCTYYWSWTMYTGGARAYMKTKRCYATYKTSRTVTTYGGHGYBGAGTWYKYYKTGMGR 251

Qy        430 ATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTGAGGTTTGCT 489
              ||||||  |:||  ||  ||:|::||  ||:|  :::||  |||:    ||  :|:||:|  ||||||
Db        252 ATCTGGGCYGCWGGMTGYTSYTGCCGRTACMRWGGCTGGMGGGGSMGRCTSAAGTTTGCC 311

Qy        490 CGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCAGTTGTTTCT 549
              :|  ||:||:  |:||::|  :|  ||:|  |:|:||  ||  ||:||  ||  :|  :|:||  :|:  |:
Db        312 MGGAARCCVCTSTGYRTGWTBGAYATCWTKGTGCTSATYGCCTCYRTKSCDGTGSTKGCY 371

Qy        550 GCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGTTTCCTACAG 609
              |:    :::  ||:||  ||:  |::|:||:||:    ||:  |:||  :|  ||  |||:|:||:
Db        372 GYBGGHWMCCARGGCAAYGTYYTKGCYACVTCY---CTBCGRAGCYTGCGSTTCYTRCAR 428

Qy        610 ATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTGGGTTCAGTG 669
              ||::|  ||:|||  |:||:||||||||  :|:||:|||||  |||||    |  :||||  ||:|::
Db        429 ATYYTRCGSATGMTSCGBATGGACCGGMGRGGHGGCACCTGGAAGCTBYTGGGMTCDGYV 488

Qy        670 GTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTGGTTCTTATT 729
              :|  |::||:||||||||:||:  |  :|:||  ||  ||||||||  ||  ||    |:    :||  ||
Db        489 RTCTRYGCYCACAGCAARGARCTSRTSACKGCSTGGTACATYGGYTTCCTBWSHCTCATC 548

Qy        730 TTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTTTCTACATAT 789
              |::|  ||  ||:||:||:||  :|||:  ||:||::  :|    :::  |  ::  ||:    ||  ||:
Db        549 CTKKCYTCRTTYCTKGTSTACYTGGYWGARAARSSDGAGRWBGAYSMMTTYGASACCTAY 608

Qy        790 GCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGAGACAAAACT 849
              ||:|||||  ||:||||||||:    ||  ||:  ||:|:||  ||||||||:||:|||||  ::
Db        609 GCRGATGCMCTSTGGTGGGGYCTGATCACVCTGRCVACCATTGGCTAYGGRGACAAGWMM 668

Qy        850 CCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGCATTTCTTTC 909
              ||::  :||  |||    ||  :|    |::|:  |  ||:    :||:  |  :|:  |:||:  |  ||  ||:
Db        669 CCYMARACSTGGRAMGGSMGKCTSHTDGCVGCVACSTTYWCCYTMATYGGYGTCTCVTTY 728

Qy        910 TTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAAGAACAACAC 969
              ||:||  ||:||:||  |||||::|  ||  ||  ||  :|:||    |  ||:||  ||:||  ||:||:
Db        729 TTYGCBCTKCCWGCDGGCATYYTGGGRTCYGGSYTKGCCCTSAARGTBCARGAGCARCAY 788

Qy        970 CGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGG 1029
              :|  ||:||:|||||||||||::|  :||||:||:||:|    ::||:|:|||:  :|  |||
Db        789 MGKCARAARCACTTTGAGAARMGGMGGAABCCDGCDGCWGRBCTSATYCAGKCKGCCTGG 848

Qy       1030 CGTAGTTACGCAGCTGA 1046
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Db        849 AGRTWYTAYGCYACYAA 865
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RESULT 11
US-09-177-650-90
; Sequence 90, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; TITLE OF INVENTION: AND OTHER EPILEPSIES
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 2814
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (202)..(2811)
US-09-177-650-90

Query Match 17.2%; Score 464; DB 3; Length 2814;
Best Local Similarity 57.9%; Pred. No. 2.5e-127;
Matches 952; Conservative 3; Mismatches 623; Indels 66; Gaps 5;

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Qy         15 GTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGCGACGGCCTGCTACT 74
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Db        294 GGCGGTGGCCGGCGACGAGGAGCGGAAAGTGGGGCTGGCGCCAGGAGACGTGGAGCAAGT 353

Qy         75 GCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTGAGGGAGAGCCGCCG 134
              |  |  ||||        |        |  |||      |||    ||||  ||  |    |
Db        354 CACCTTGGCGCTAGGGGCCGGAGCCGACAAAGACGGGACCCTGCTGCTGGAGGGCGGTGG 413

Qy        135 GGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCTTACACGAGTAGCCA 194
              ||  |    |||||    |||  ||  ||  ||  |||  |        ||||      |  ||    ||
Db        414 CCGCGAAGAGGGGCAGAGGAGGACCCCGCAGGGCATCGGGCTCCTGGCAAAGACCCCCCT 473
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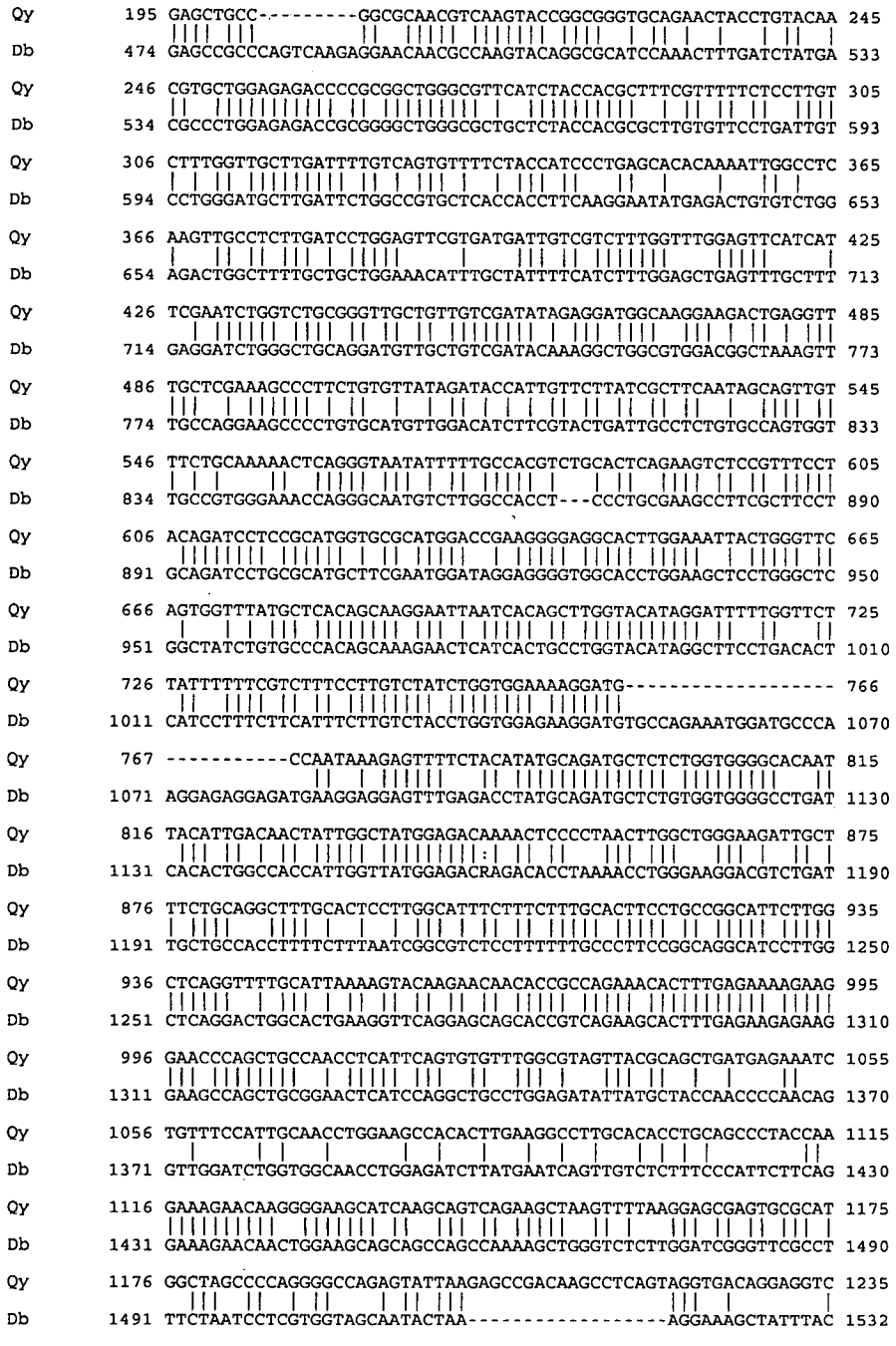
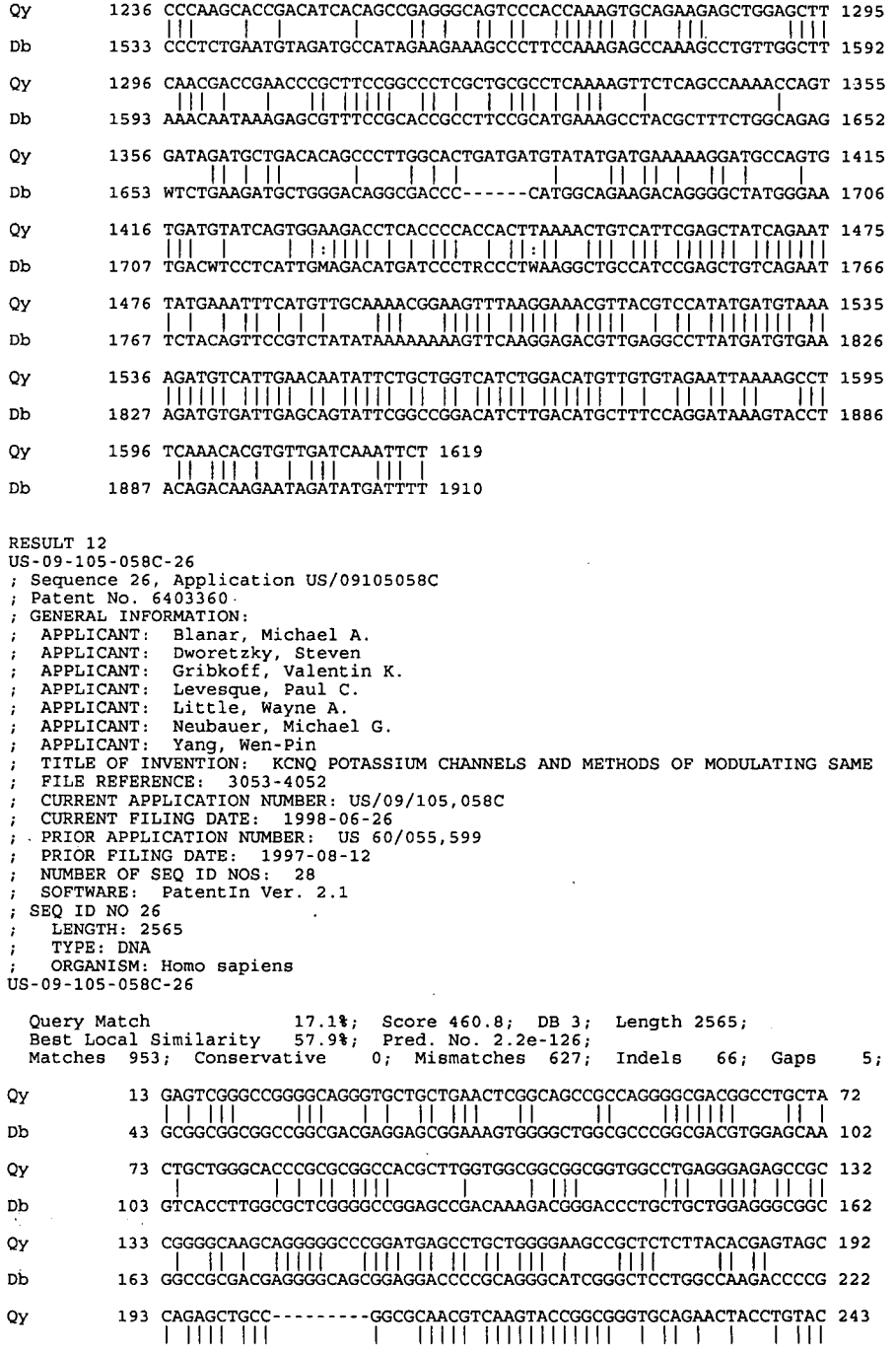
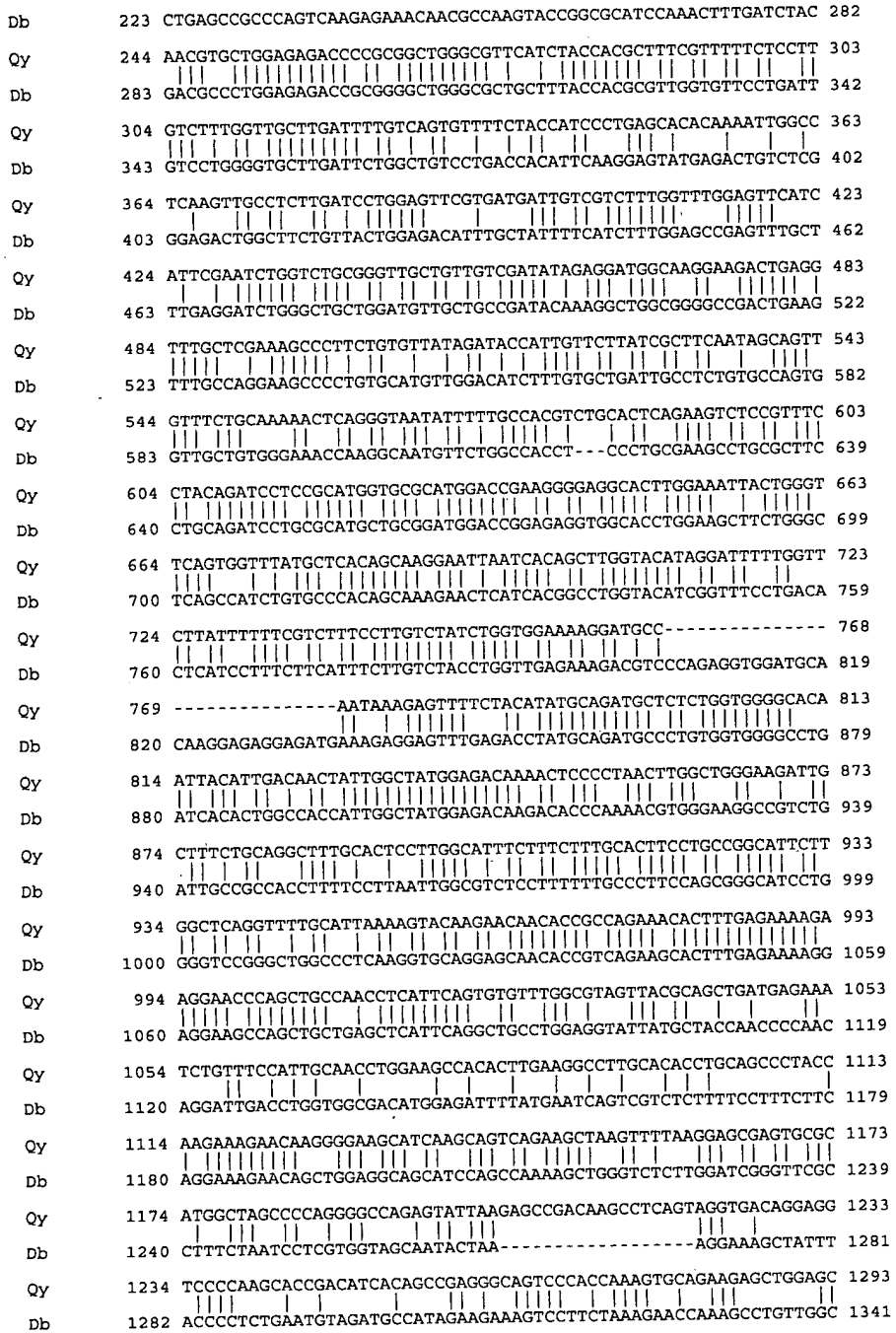
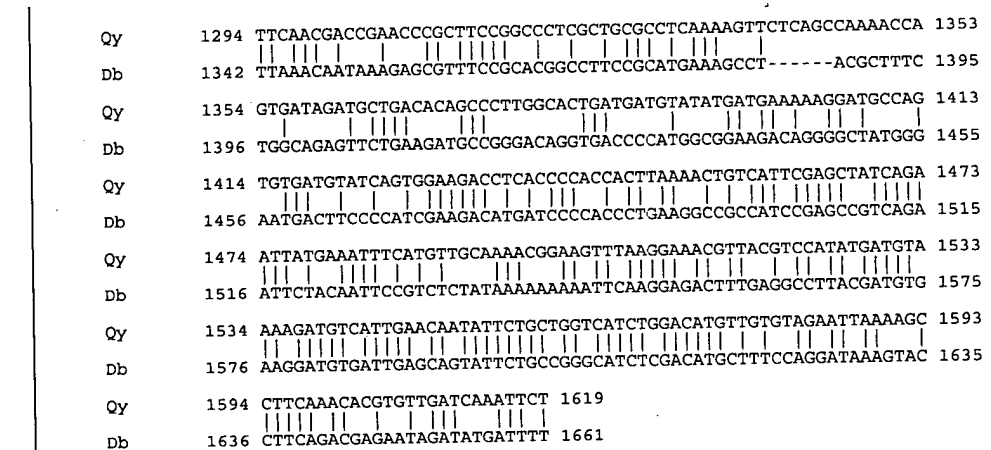




RESULT 12
US-09-105-058C-26
; Sequence 26, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blanar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 2565
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-105-058C-26

Query Match 17.1%; Score 460.8; DB 3; Length 2565;
Best Local Similarity 57.9%; Pred. No. 2.2e-126;
Matches 953; Conservative 0; Mismatches 627; Indels 66; Gaps 5;





RESULT 13
US-09-177-650-6
; Sequence 6, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; TITLE OF INVENTION: AND OTHER EPILEPSIES
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 2914
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(2634)
; FEATURE:
; NAME/KEY: allele
; LOCATION: (840)
; OTHER INFORMATION: The polymorphism of a T to a C at this position
; OTHER INFORMATION: has appeared in one individual.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (947)
; OTHER INFORMATION: The missense mutation from a G to a T occurs at
; OTHER INFORMATION: this position in a BFNC family.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (678)
; OTHER INFORMATION: This position is polymorphic for C or T.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (750)
; OTHER INFORMATION: This position is polymorphic for T or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1089)
; OTHER INFORMATION: This position is polymorphic for G or C.

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;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: (2598)
;   OTHER INFORMATION: This position is polymorphic for T or C.
US-09-177-650-6

  Query Match             17.1%;  Score 460.8;  DB 3;  Length 2914;
  Best Local Similarity   57.9%;  Pred. No. 2.4e-126;
  Matches  953;  Conservative    0;  Mismatches  627;  Indels   66;  Gaps    5;

Qy          13 GAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGCGACGGCCTGCTA  72
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Db         115 GCGGCGGCGGCCGGCGACGAGGAGCGGAAAGTGGGGCTGGCGCCCGGCGACGTGGAGCAA 174

Qy          73 CTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTGAGGGAGAGCCGC 132
                |        | | || ||||       |    | |||          |||   |||| || ||
Db         175 GTCACCTTGGCGCTCGGGGCCGGAGCCGACAAAGACGGGACCCTGCTGCTGGAGGGCGGC 234

Qy         133 CGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCTTACACGAGTAGC 192
                |  || |  |||||   |||| || || || |||  |    ||||     || ||
Db         235 GGCCGCGACGAGGGGCAGCGGAGGACCCCGCAGGGCATCGGGCTCCTGGCCAAGACCCCG 294

Qy         193 CAGAGCTGCC---------GGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTGTAC 243
               | |||| |||         |   ||||| ||||||||||||   | || |   |   | |||
Db         295 CTGAGCCGCCCAGTCAAGAGAAACAACGCCAAGTACCGGCGCATCCAAACTTTGATCTAC 354

Qy         244 AACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTCCTT 303
                |||  |||||||||||  || |||||||||  |   | ||||||||  || || || ||  ||
Db         355 GACGCCCTGGAGAGACCGCGGGGCTGGGCGCTGCTTTACCACGCGTTGGTGTTCCTGATT 414

Qy         304 GTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTGGCC 363
               |||  |  ||  |||||||||  || |  ||   |  ||   ||   |||  |     |   |  |
Db         415 GTCCTGGGGTGCTTGATTCTGGCTGTCCTGACCACATTCAAGGAGTATGAGACTGTCTCG 474

Qy         364 TCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTCATC 423
                  |   || ||   || |  ||||||      |     |||  || |||||||     |||||
Db         475 GGAGACTGGCTTCTGTTACTGGAGACATTTGCTATTTTCATCTTTGGAGCCGAGTTTGCT 534

Qy         424 ATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTGAGG 483
                |  | ||||||  |||| || || ||  || |||||  | |||  ||||   ||  |||||| |
Db         535 TTGAGGATCTGGGCTGCTGGATGTTGCTGCCGATACAAAGGCTGGCGGGGCCGACTGAAG 594

Qy         484 TTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCAGTT 543
               |||||   | ||||||  | ||   |  | || |  | ||||  || ||  ||  |  ||||
Db         595 TTTGCCAGGAAGCCCCTGTGCATGTTGGACATCTTTGTGCTGATTGCCTCTGTGCCAGTG 654

Qy         544 GTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGTTTC 603
               |||  |||     ||  || || ||| || | |||||  |    | ||  |||| || || |||
Db         655 GTTGCTGTGGGAAACCAAGGCAATGTTCTGGCCACCT---CCCTGCGAAGCCTGCGCTTC 711

Qy         604 CTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTGGGT 663
               || |||||||| |||||| |||| |||||||| || || |||||  |||||   | |||||
Db         712 CTGCAGATCCTGCGCATGCTGCGGATGGACCGGAGAGGTGGCACCTGGAAGCTTCTGGGC 771

Qy         664 TCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTGGTT 723
               ||||    | | ||| |||||||| ||| | ||||| || |||||||| || ||   ||
Db         772 TCAGCCATCTGTGCCCACAGCAAAGAACTCATCACGGCCTGGTACATCGGTTTCCTGACA 831

Qy         724 CTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCC--------------- 768
               || ||  |||| || || |||||||| ||||| || || || | |
Db         832 CTCATCCTTTCTTCATTTCTTGTCTACCTGGTTGAGAAAGACGTCCCAGAGGTGGATGCA 891

Qy         769 ---------------AATAAAGAGTTTTCTACATATGCAGATGCTCTCTGGTGGGGCACA 813
                             ||  | ||||||   || ||||||||||| || |||||||||
Db         892 CAAGGAGAGGAGATGAAAGAGGAGTTTGAGACCTATGCAGATGCCCTGTGGTGGGGCCTG 951

Qy         814 ATTACATTGACAACTATTGGCTATGGAGACAAAACTCCCCTAACTTGGCTGGGAAGATTG 873
               || ||| || | || |||||||||||||||||| || |||  ||| |||   ||  |  ||
Db         952 ATCACACTGGCCACCATTGGCTATGGAGACAAGACACCCAAAACGTGGGAAGGCCGTCTG 1011

Qy         874 CTTTCTGCAGGCTTTGCACTCCTTGGCATTTCTTTCTTTGCACTTCCTGCCGGCATTCTT 933
               || | ||   |||| |  |  ||||| | || || |||||  ||||| || ||||| ||
Db        1012 ATTGCCGCCACCTTTTCCTTAATTGGCGTCTCCTTTTTTGCCCTTCCAGCGGGCATCCTG 1071

Qy         934 GGCTCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAGAAACACTTTGAGAAAAGA 993
               || || ||  | ||  | || || || || |||||||| ||||| ||||||||||||||
Db        1072 GGGTCCGGGCTGGCCCTCAAGGTGCAGGAGCAACACCGTCAGAAGCACTTTGAGAAAAGG 1131

Qy         994 AGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGTTACGCAGCTGATGAGAAA 1053
               ||||| ||||||||  | |||||||||  ||  ||| |   ||| ||  |  |    ||
Db        1132 AGGAAGCCAGCTGCTGAGCTCATTCAGGCTGCCTGGAGGTATTATGCTACCAACCCCAAC 1191

Qy        1054 TCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGCACACCTGCAGCCCTACC 1113
                  ||  | | |  |       | |  |  | | |  |  | | |           |
Db        1192 AGGATTGACCTGGTGGCGACATGGAGATTTTATGAATCAGTCGTCTCTTTTCCTTTCTTC 1251

Qy        1114 AAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGC 1173
               | |||||||||   ||| ||| ||  ||| || |||||  || |   ||| || || |||
Db        1252 AGGAAAGAACAGCTGGAGGCAGCATCCAGCCAAAAGCTGGGTCTCTTGGATCGGGTTCGC 1311

Qy        1174 ATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGG 1233
               |  |||  ||  | ||    | || |||                   |||  |
Db        1312 CTTTCTAATCCTCGTGGTAGCAATACTAA------------------AGGAAAGCTATTT 1353

Qy        1234 TCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGC 1293
               ||||    | |       |    || |  ||||  | ||||  |  |||        ||
Db        1354 ACCCCTCTGAATGTAGATGCCATAGAAGAAAGTCCTTCTAAAGAACCAAAGCCTGTTGGC 1413

Qy        1294 TTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCA 1353
               || ||| |   |   || |||||  |  |  | ||| | |||   |
Db        1414 TTAAACAATAAAGAGCGTTTCCGCACGGCCTTCCGCATGAAAGCCT------ACGCTTTC 1467

Qy        1354 GTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAG 1413
                  |    | ||||   |||         |||      |   || || |  || |    |
Db        1468 TGGCAGAGTTCTGAAGATGCCGGGACAGGTGACCCCATGGCGGAAGACAGGGGCTATGGG 1527

Qy        1414 TGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGA 1473
               |||  |  |  | |||||| | | |||  | || ||  | | |||  |||||   |||||
Db        1528 AATGACTTCCCCATCGAAGACATGATCCCCACCCTGAAGGCCGCCATCCGAGCCGTCAGA 1587

Qy        1474 ATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATATGATGTA 1533
               ||| |  |||| | | |     |||   || || ||||| || ||  | ||| || |||||
Db        1588 ATTCTACAATTCCGTCTCTATAAAAAAAAAATTCAAGGAGACTTTGAGGCCTTACGATGTG 1647

Qy        1534 AAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGC 1593
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Db        1648 AAGGATGTGATTGAGCAGTATTCTGCCGGGCATCTCGACATGCTTTCCAGGATAAAGTAC 1707

Qy        1594 CTTCAAACACGTGTTGATCAAATTCT 1619
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Db        1708 CTTCAGACGAGAATAGATATGATTTT 1733


RESULT 14
US-09-495-050A-305
; Sequence 305, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
;  APPLICANT: Roopa, Reddy
;  APPLICANT:  Guegler, Karl, J.
;  APPLICANT:  Au-Young, Janice
;  TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
;  FILE REFERENCE: PA-0013 US
;  CURRENT APPLICATION NUMBER: US/09/495,050A
;  CURRENT FILING DATE:  2000-01-31
;  PRIOR APPLICATION NUMBER: 60/118,318
;  PRIOR FILING DATE: February 1, 1999
;  NUMBER OF SEQ ID NOS: 305
;  SOFTWARE: PERL Program
; SEQ ID NO 305
;   LENGTH: 575
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6492505 4970006F6
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;   NAME/KEY: unsure
;   LOCATION: 486, 510, 552, 573
;   OTHER INFORMATION: a, t, c, g, or other
US-09-495-050A-305

  Query Match             16.8%;  Score 452;  DB 4;  Length 575;
  Best Local Similarity   95.0%;  Pred. No. 3.2e-124;
  Matches  509;  Conservative    0;  Mismatches   22;  Indels    5;  Gaps    4;

Qy       1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db             1 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 60

Qy       1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           121 ATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 180

Qy       1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
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Qy       1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           241 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 300

Qy       1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
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Qy       1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
             |||||||||||||||||||||||  ||  |  ||||||||||||||||||||||||||||||
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RESULT 15
US-09-105-058C-19
; Sequence 19, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
;  APPLICANT:  Blanar, Michael A.
;  APPLICANT:  Dworetzky, Steven
;  APPLICANT:  Gribkoff, Valentin K.
;  APPLICANT:  Levesque, Paul C.
;  APPLICANT:  Little, Wayne A.
;  APPLICANT:  Neubauer, Michael G.
;  APPLICANT:  Yang, Wen-Pin
;  TITLE OF INVENTION:  KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
;  FILE REFERENCE:  3053-4052
;  CURRENT APPLICATION NUMBER: US/09/105,058C
;  CURRENT FILING DATE:  1998-06-26
;  PRIOR APPLICATION NUMBER:  US 60/055,599
;  PRIOR FILING DATE:  1997-08-12
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 3287
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-105-058C-19

  Query Match             15.8%;  Score 425;  DB 3;  Length 3287;
  Best Local Similarity   64.7%;  Pred. No. 1.3e-115;
  Matches  632;  Conservative    0;  Mismatches  345;  Indels    0;  Gaps    0;

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Qy        184 ACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTGTAC 243
                 |  ||  |  |||||||| |  |||||  | ||||||| | ||| |||
Db        247 GGCGCCGGGAAGCCCCCCAAGCGCAACGCCTTCTACCGCAAGCTGCAGAATTTCCTCTAC 306

Qy        244 AACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTCCTT 303
              |||||||||||| | || |||||||||||||||||||||||||||| | ||| || |||||
Db        307 AACGTGCTGGAGCGGCCGCGCGGCTGGGCGTTCATCTACCACGCCTACGTGTTCCTCCTG 366

Qy        304 GTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTGGCC 363
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Db        367 GTTTTCTCCTGCCTCGTGCTGTCTGTGTTTTCCACCATCAAGGAGTATGAGAAGAGCTCG 426

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                 |  |||||  ||||||||  ||||||  || || || |||||  |||||| | ||
Db        427 GAGGGGGCCCTCTACATCCTGGAAATCGTGACTATCGTGGTGTTTGGCGTGGAGTACTTC 486

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Qy       1024 GTTTGGCGTAGTTACGC 1040
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GenCore version 5.1.6

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Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2689.2	99.8	3137	6	AR430568	AR430568 Sequence
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5	2681.2	99.5	3074	6	AR393778	AR393778 Sequence
6	2681.2	99.5	3074	6	AX253254	AX253254 Sequence
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9	2625.2	97.4	2772	6	AR565635	AR565635 Sequence
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11	2625.2	97.4	3111	6	AR565636	AR565636 Sequence
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19	963.4	35.8	120846	9	AL365232	AL365232 Human DNA
20	963.4	35.8	125910	6	BD275571	BD275571 Novel Hum
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22	843.4	31.3	200585	2	AC146636	AC146636 Otolemur
23	843.4	31.3	202246	2	AC146646	AC146646 Otolemur
24	841.8	31.2	148254	2	AC151566	AC151566 Dasypus n
c 25	767.6	28.5	161759	10	AC115920	AC115920 Mus muscu
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41	477	17.7	2565	6	BD136514	BD136514 Human bra
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ALIGNMENTS

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DEFINITION Sequence 1 from Patent WO0192526.
ACCESSION AX322509
VERSION AX322509.1 GI:18093555
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Dworetzky,S.I., Ramanathan,C.S., Trojnacki,J.T., Boissard,C.G. and Gribkoff,V.K.
TITLE Human kcnq5 potassium channel, methods and compositions thereof
JOURNAL Patent: WO 0192526-A 1 06-DEC-2001;
Bristol-Myers Squibb Company (US)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
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ORIGIN

Query Match 100.0%; Score 2694; DB 6; Length 2694;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
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Db        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
Db        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
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Db        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
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Db        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
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Qy       2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
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Qy       2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
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Db       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
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Qy       2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460
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Qy       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
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Qy       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
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Qy       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
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Db       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640

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RESULT 2
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LOCUS       AR430568               3137 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1 from patent US 6649371.
ACCESSION   AR430568
VERSION     AR430568.1  GI:40191384
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3137)
  AUTHORS   Jentsch,T.J.
  TITLE     Potassium channel KCNQ5 and sequences encoding the same
  JOURNAL   Patent: US 6649371-A 1 18-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .3137
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ORIGIN

  Query Match             99.8%;  Score 2689.2;  DB 6;  Length 3137;
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  Matches 2691;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
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Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
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Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
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Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
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Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
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Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
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Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
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DEFINITION  Sequence 1 from Patent WO0077035.
ACCESSION   AX056817
VERSION     AX056817.1  GI:12309758
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jentsch,T.J.
  TITLE     Novel potassium channels and genes encoding these potassium
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  JOURNAL   Patent: WO 0077035-A 1 21-DEC-2000;
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ORIGIN

  Query Match           99.8%;  Score 2689.2;  DB 6;  Length 3137;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 2691;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

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ACCESSION   AF202977
VERSION     AF202977.1  GI:7798695
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 3137)
  AUTHORS   Schroeder,B.C., Hechenberger,M., Weinreich,F., Kubisch,C. and
            Jentsch,T.J.
  TITLE     KCNQ5, a novel potassium channel broadly expressed in brain,
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  JOURNAL   J. Biol. Chem. 275 (31), 24089-24095 (2000)
  MEDLINE   20379054
   PUBMED   10816588
REFERENCE   2  (bases 1 to 3137)
  AUTHORS   Schroeder,B.C., Hechenberger,M., Weinreich,F., Kubisch,C. and
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  TITLE     Direct Submission
  JOURNAL   Submitted (09-NOV-1999) ZMNH, Hamburg University, Martinistrasse
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ORIGIN

  Query Match          99.8%;  Score 2689.2;  DB 9;  Length 3137;
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  Matches 2691;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

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Qy        61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
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Qy       301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
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Qy       361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
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Qy       481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
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Qy       721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
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Qy       781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
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VERSION     AR393778.1  GI:40120748
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ORIGIN

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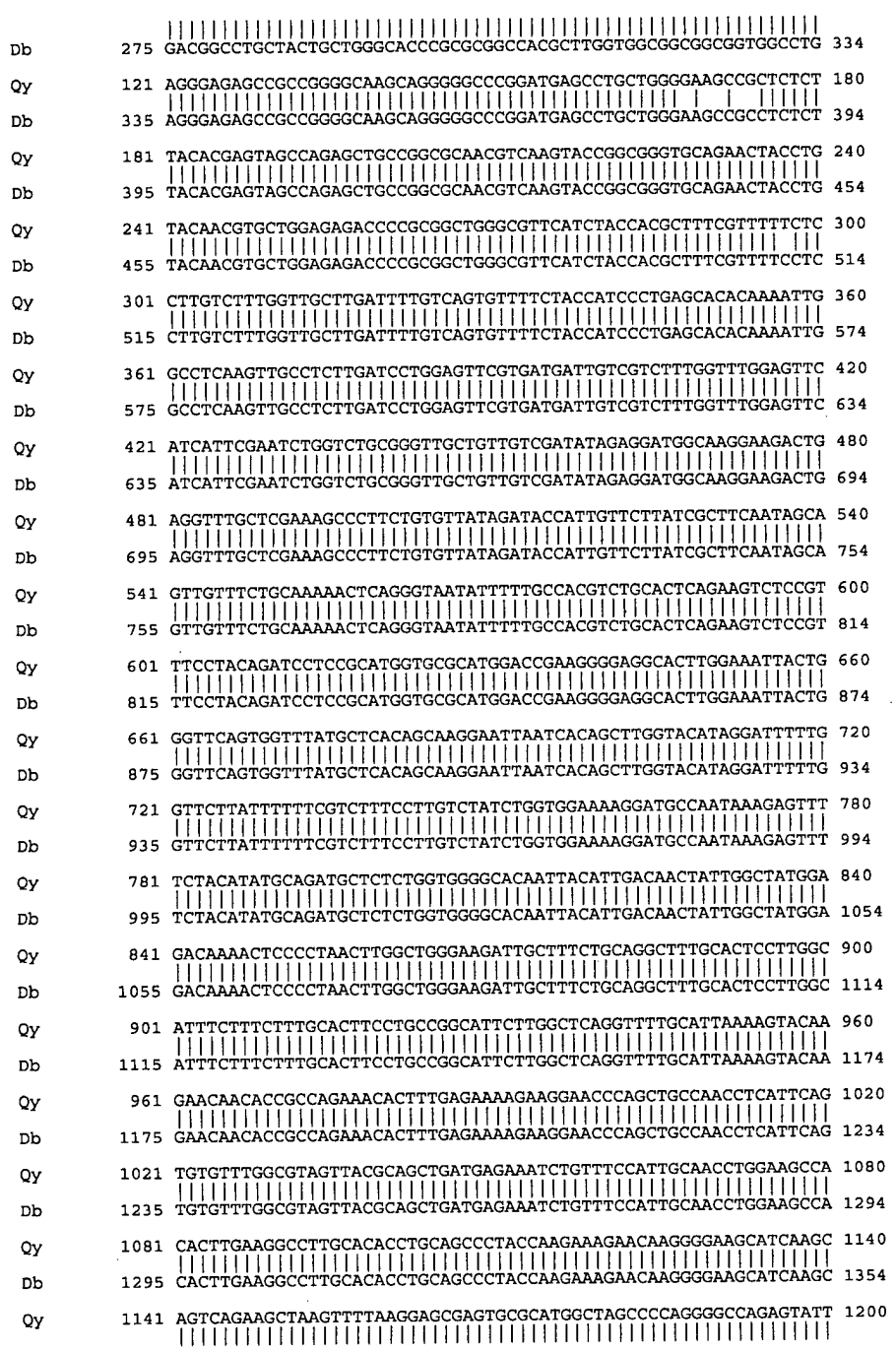
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Qy 1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
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RESULT 6
AX253254
LOCUS       AX253254               3074 bp    DNA     linear   PAT 10-OCT-2001
DEFINITION  Sequence 1 from Patent WO0170811.
ACCESSION   AX253254
VERSION     AX253254.1  GI:16073802
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lerche,C., Scherer,C., Seebohm,G., Busch,A. and Steinmeyer,K.
  TITLE     Potassium channel protein kcnq5, a target for diseases of central
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  JOURNAL   Patent: WO 0170811-A 1 27-SEP-2001;
            Aventis Pharma Deutschland GmbH (DE)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
ORIGIN

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  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 2686;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 274

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        335 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGAAGCCGCCTCTCT 394

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Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
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Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
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RESULT 7
AX456864
LOCUS AX456864 3074 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 5 from Patent WO0232960.
ACCESSION AX456864
VERSION AX456864.1 GI:21715731
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Argentieri,T.M. and Sheldon,J.H.
TITLE Methods of selecting compounds for modulation of bladder function
JOURNAL Patent: WO 0232960-A 5 25-APR-2002;
Wyeth (US)
FEATURES Location/Qualifiers
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ORIGIN

Query Match 99.5%; Score 2681.2; DB 6; Length 3074;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2686; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
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Db        455 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTCCTC 514

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
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Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
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Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
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RESULT 8
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DEFINITION  Homo sapiens voltage-gated potassium channel (KCNQ5) mRNA, complete
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ACCESSION   AF249278
VERSION     AF249278.1  GI:9651966
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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  AUTHORS   Lerche,C., Scherer,C.R., Seebohm,G., Derst,C., Wei,A.D., Busch,A.E.
            and Steinmeyer,K.
  TITLE     Molecular cloning and functional expression of KCNQ5, a potassium
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  JOURNAL   J. Biol. Chem. 275 (29), 22395-22400 (2000)
  MEDLINE   20357367
   PUBMED   10787416
REFERENCE   2  (bases 1 to 3074)
  AUTHORS   Lerche,C., Scherer,C.R., Seebohm,G., Derst,C., Wei,A.D., Busch,A.E.
            and Steinmeyer,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAR-2000) Cardiovascular Diseases, Aventis Pharma
            Deutschland GmbH, Building H824, Frankfurt a. M. 65926, Germany
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ORIGIN

  Query Match          99.5%;  Score 2681.2;  DB 9;  Length 3074;
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DEFINITION  Sequence 1 from patent US 6767736.
ACCESSION   AR565635
VERSION     AR565635.1  GI:53981668
KEYWORDS    .
SOURCE      Unknown.
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REFERENCE   1  (bases 1 to 2772)
  AUTHORS   Hu,Y., Kieke,J.A., Turner,C.A. Jr., Nehls,M.C., Friedrich,G.,
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  TITLE     Human ion channel protein and polynucleotides encoding the same
  JOURNAL   Patent: US 6767736-A 1 27-JUL-2004;
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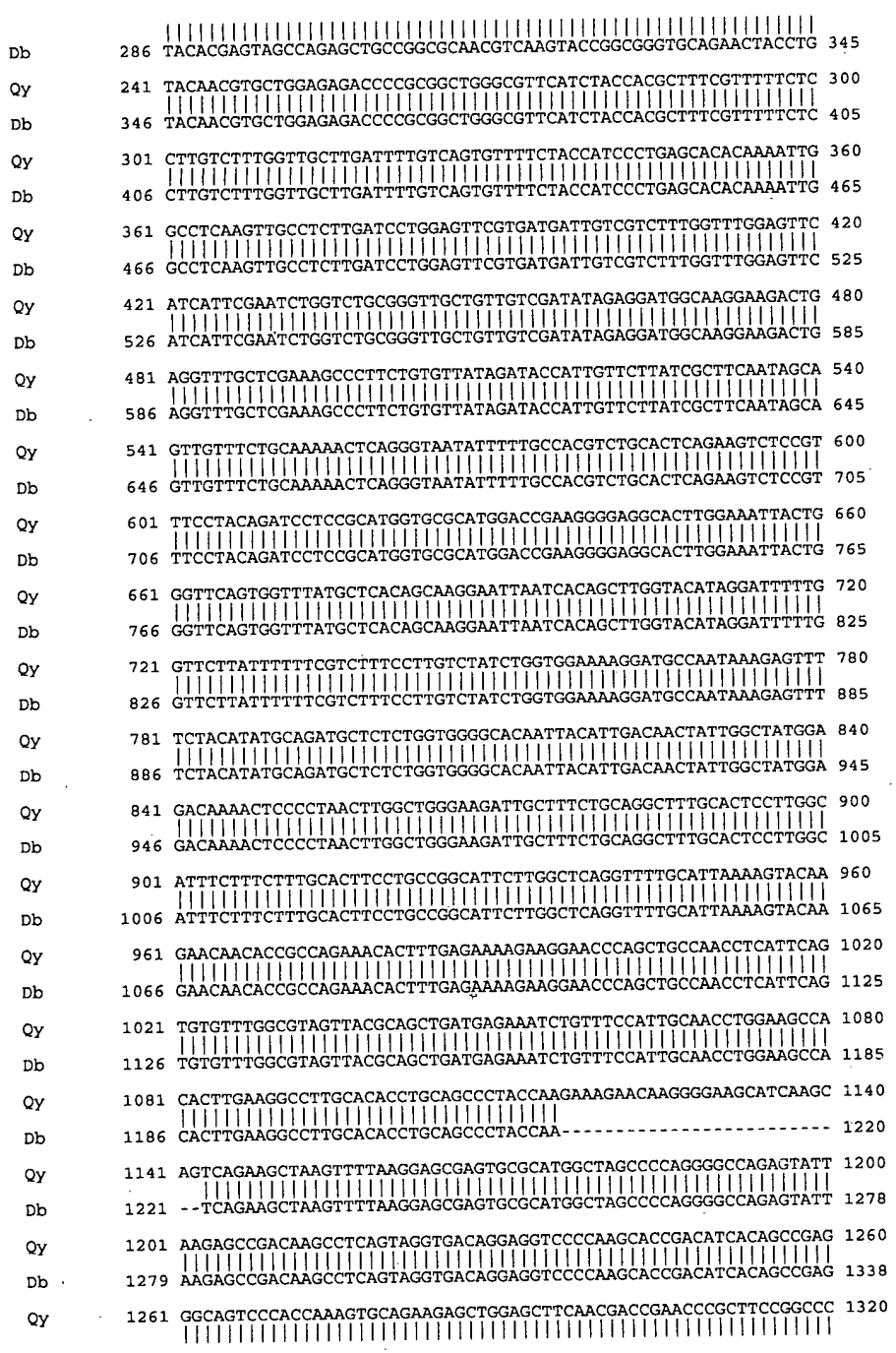
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Qy 301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
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REFERENCE   1
  AUTHORS   Hu,Y., Kieke,J.A., Turner,A.C., Nehls,M.C., Friedrich,G.B.,
            Zambrowicz,B. and Sands,A.T.
  TITLE     Human ion channel protein and polynucleotides encoding the same
  JOURNAL   Patent: WO 0175108-A 1 11-OCT-2001;
            Lexicon Genetics Incorporated (US)
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Qy       1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680
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Qy       1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
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Qy       1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
Db       1819 ATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1878

Qy       1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
Db       1879 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1938

Qy       1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
Db       1939 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1998

Qy       1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
Db       1999 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 2058

Qy       1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
Db       2059 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2118

Qy       2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
Db       2119 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2178

Qy       2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
Db       2179 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2238

Qy       2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
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Db       2299 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2358

Qy       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
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Db       2599 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2658

Qy       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
Db       2659 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2718

Qy       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
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RESULT 11
AR565636
LOCUS AR565636 3111 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 3 from patent US 6767736.
ACCESSION AR565636
VERSION AR565636.1 GI:53981669
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 3111)
AUTHORS Hu,Y., Kieke,J.A., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B. and Sands,A.T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: US 6767736-A 3 27-JUL-2004;
FEATURES Location/Qualifiers
source 1. .3111
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 97.4%; Score 2625.2; DB 6; Length 3111;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

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Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
Db        225 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTCGGTGGCGGCGGCGGTGGCCTG 284

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
Db        285 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 344

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
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Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
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Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
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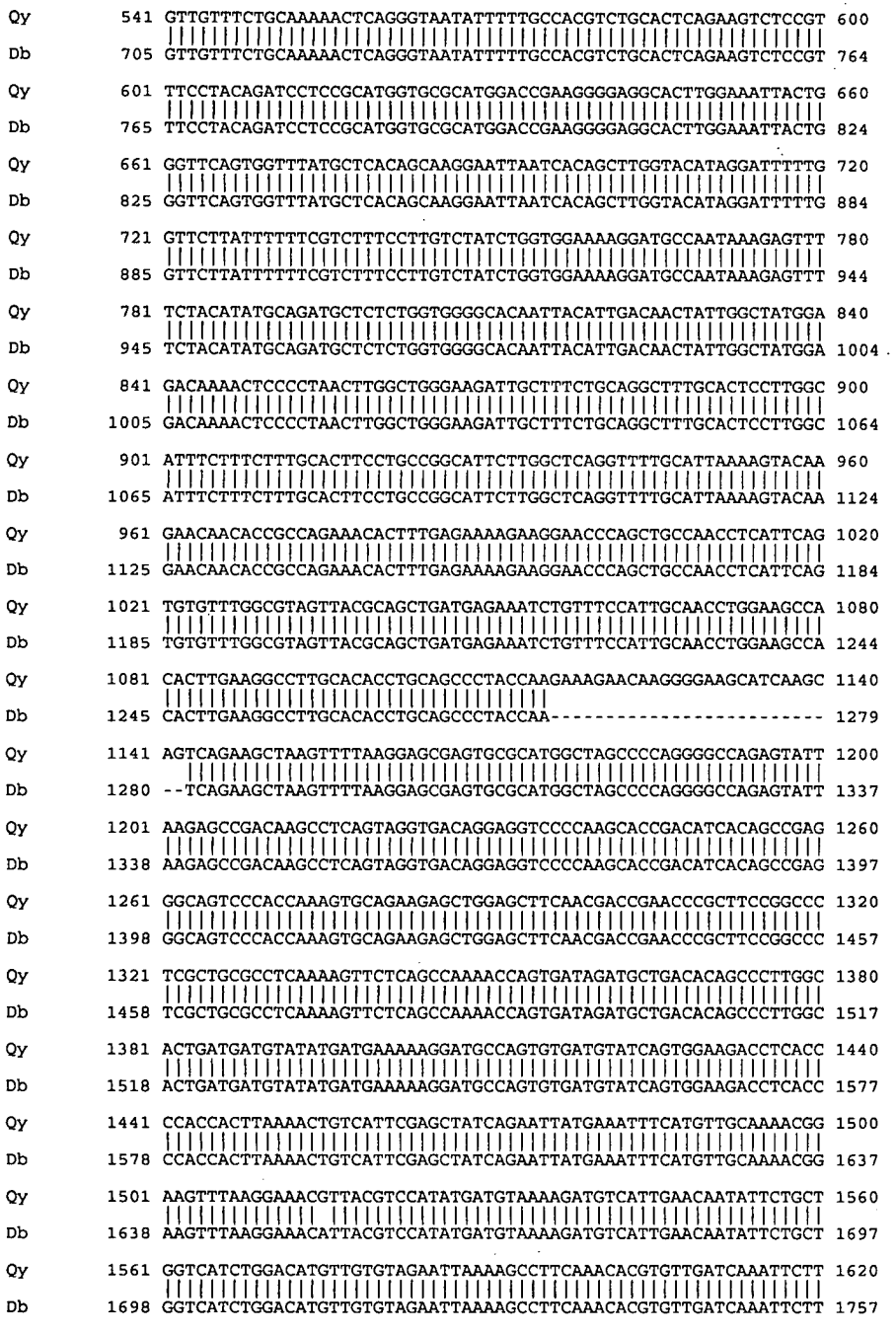

RESULT 12

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AX268476
LOCUS       AX268476               3111 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 3 from Patent WO0175108.
ACCESSION   AX268476
VERSION     AX268476.1  GI:16541653
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hu,Y., Kieke,J.A., Turner,A.C., Nehls,M.C., Friedrich,G.B.,
            Zambrowicz,B. and Sands,A.T.
  TITLE     Human ion channel protein and polynucleotides encoding the same
  JOURNAL   Patent: WO 0175108-A 3 11-OCT-2001;
            Lexicon Genetics Incorporated (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             97.4%;  Score 2625.2;  DB 6;  Length 3111;
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Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
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Db        165 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 224

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
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Db        225 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTCGGTGGCGGCGGCGGTGGCCTG 284

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
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Db        285 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 344

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
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Db        345 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 404

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
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Db        405 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 464

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
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Db        465 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 524

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
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Db        525 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 584

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
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Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
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Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
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Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
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Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
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Db        825 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 884

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Db        885 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 944

Qy        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
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Qy        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
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Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
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Db       1065 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 1124

Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
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Db       1125 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1184

Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
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Qy       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
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Db       1338 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1397

Qy       1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320
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Qy       1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440
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Qy       1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
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Qy       2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
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Qy       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400
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RESULT 13
BD275572
LOCUS       BD275572               3718 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Novel Human Voltage-Gated Potassium Channel.
ACCESSION   BD275572
VERSION     BD275572.1  GI:33085340
KEYWORDS    JP 2002543768-A/2.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3718)
  AUTHORS   Metzker,M.L., Li,W., Petrukhin,K. and Caskey,T.C.
  TITLE     Novel Human Voltage-Gated Potassium Channel
  JOURNAL   Patent: JP 2002543768-A 2 24-DEC-2002;
            Merck and Co Inc
COMMENT     OS   Homo Sapiens
            PN   JP 2002543768-A/2
            PD   24-DEC-2002
            PF   10-APR-2000 JP 2000611548
            PR   14-APR-1999 US    60/129274
            PI   michael l metzker,wen li,konstantin petrukhin,thomas c caskey
            CC
            FH   Key             Location/Qualifiers.
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ORIGIN

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  Best Local Similarity   99.6%;  Pred. No. 0;
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Qy         94 ACGCTTGGTGGCGGCGGCGGTGGCCTGAGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGG 153
              ||   ||   | | ||||||||||||||||||||||||||||||||||||||||||||||
Db         78 ACTGCTGAGGACTGCGGCGGTGGCCTGAGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGG 137

Qy        154 ATGAGCCTGCTGGGGAAGCCGCTCTCTTACACGAGTAGCCAGAGCTGCCGGCGCAACGTC 213
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Qy        334 TCTACCATCCCTGAGCACACAAAATTGGCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTG 393
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RESULT 14
AF263835
LOCUS       AF263835               2832 bp    mRNA    linear   PRI 01-JUN-2000
DEFINITION  Homo sapiens voltage-gated potassium channel KCNQ5 (KCNQ5) mRNA,
            partial cds.
ACCESSION   AF263835
VERSION     AF263835.1  GI:8132996
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2832)
  AUTHORS   Kniazeva,M. and Han,M.
  TITLE     A new gene of the voltage-gated potassium channel KCNQ family,
            KCNQ5, is a candidate gene for retinal disorders
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2832)
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  AUTHORS   Kniazeva,M. and Han,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder,
            Porter Biosciences Bldg., Boulder, CO 80309, USA
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ORIGIN

  Query Match             95.5%;  Score 2571.6;  DB 9;  Length 2832;
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  Matches 2577;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy        109 GGCGGTGGCCTGAGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGG 168
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RESULT 15
AF263836
LOCUS       AF263836               3108 bp    mRNA    linear   ROD 01-JUN-2000
DEFINITION  Mus musculus voltage-gated potassium channel KCNQ5 (Kcnq5) mRNA,
            partial cds.
ACCESSION   AF263836
VERSION     AF263836.1  GI:8132998
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3108)
  AUTHORS   Kniazeva,M. and Han,M.
  TITLE     A new gene of the voltage-gated potassium channel KCNQ family,
            KCNQ5, is a candidate gene for retinal disorders
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3108)
  AUTHORS   Kniazeva,M. and Han,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder,
            Porter Biosciences Bldg., Boulder, CO 80309, USA
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ORIGIN

  Query Match           82.3%;  Score 2217.4;  DB 10;  Length 3108;
  Best Local Similarity   90.0%;  Pred. No. 0;
  Matches 2374;  Conservative    0;  Mismatches  264;  Indels    0;  Gaps    0;

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Qy        117 CCTGAGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCT 176
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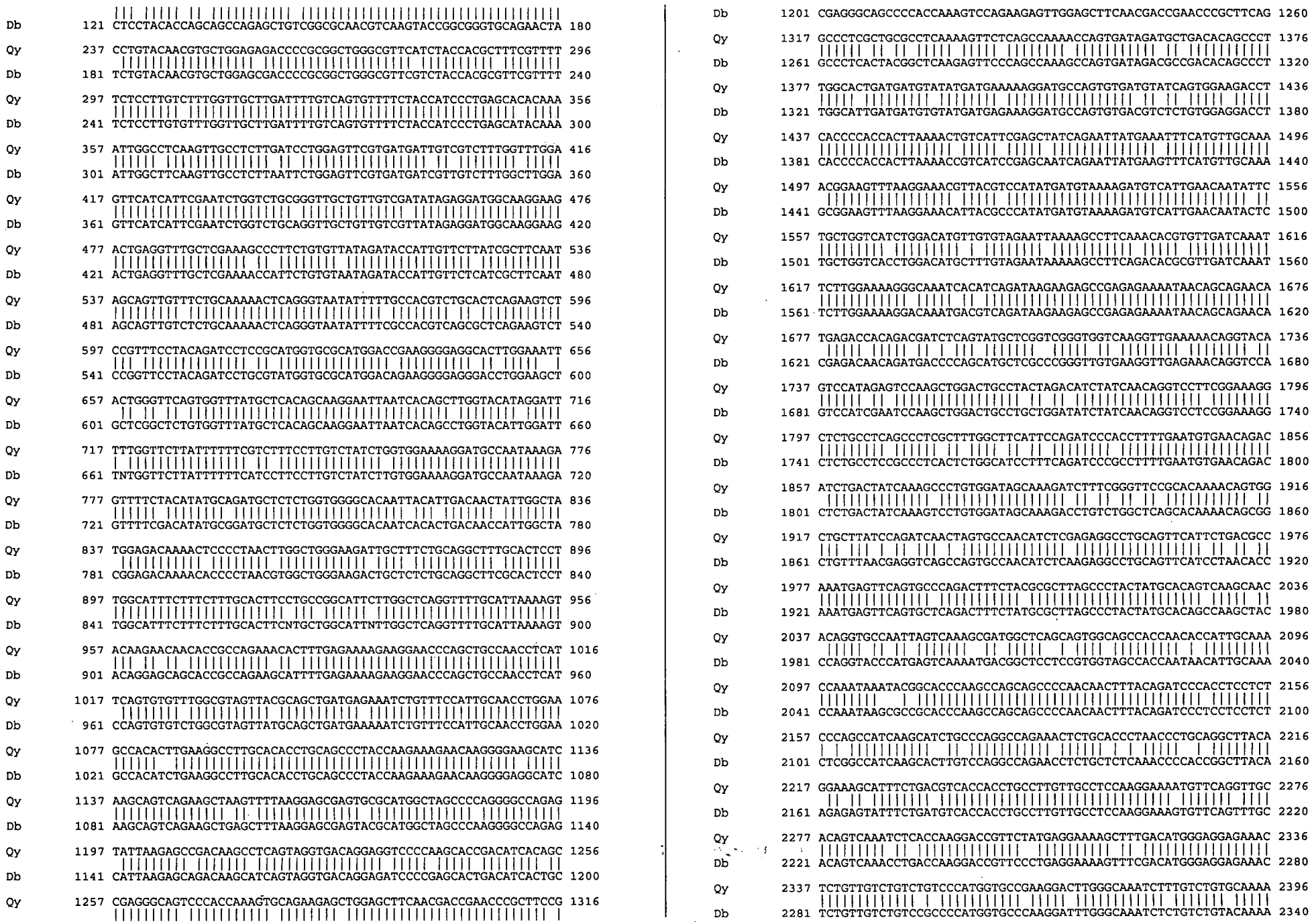
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Db       2581 TTGTAAGACAGGAGACAGTACAGACGCCCTCAGTTTGCCTCACGTCAAACTGAACTAA 2638
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Job time : 13351.3 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 08:07:42 ; Search time 1379.41 Seconds
(without alignments)
11561.287 Million cell updates/sec

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Perfect score: 2694
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2694	100.0	2694	4	AAS14652	Aas14652 Human cDN
2	2694	100.0	2694	6	AAD27192	Aad27192 Human pot
3	2690.4	99.9	3071	4	AAS14651	Aas14651 Human cDN
4	2689.2	99.8	3137	4	AAC85414	Aac85414 Human KCN
5	2681.2	99.5	3074	4	AAH49499	Aah49499 Human KCN
6	2679.6	99.5	3074	10	ADB78684	Adb78684 Human pot
7	2630	97.6	2667	4	AAS14653	Aas14653 Human cDN
8	2625.2	97.4	2772	5	AAH43633	Aah43633 Human ion
9	2625.2	97.4	3111	5	AAH43634	Aah43634 Human ion
10	2585	96.0	3718	3	AAC64371	Aac64371 Human KCN
11	963.4	35.8	125910	3	AAC64370	Aac64370 Human KCN
12	518.4	19.2	2335	3	AAA47618	Aaa47618 KCNQ4 Pot
13	518.4	19.2	2335	10	ADE31698	Ade31698 Human 323
14	516	19.2	2273	2	AAX57140	Aax57140 Mouse KCN
15	510	18.9	2169	2	AAX26588	Aax26588 Nucleotid
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19	500.6	18.6	7407	10	ADB78683	Adb78683 Human pot
20	500.6	18.6	7407	10	ADB78687	Adb78687 Human pot
21	500.6	18.6	7411	10	ADD29557	Add29557 Human tum
22	500.6	18.6	7420	11	ADN38963	Adn38963 Cancer/an
23	500.6	18.6	7420	11	ADP65810	Adp65810 Human mRN
24	500.6	18.6	7420	11	ADP65731	Adp65731 Human pot
25	500.6	18.6	7420	12	ADL06495	Adl06495 Human tum
26	500.6	18.6	7863	10	ADJ56529	Adj56529 Human cDN
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28	480.6	17.8	7413	5	AAS74832	Aas74832 DNA encod
29	478.4	17.8	5595	13	ADS17851	Ads17851 Rattus no
30	477	17.7	2565	2	AAX81548	Aax81548 Human bra
31	477	17.7	3195	5	AAS74831	Aas74831 DNA encod
32	466.6	17.3	3029	2	AAX81547	Aax81547 Human bra
33	465.8	17.3	2766	13	ADS17849	Ads17849 Rattus no
34	465	17.3	548	6	ABA90234	Aba90234 Human ORF
35	464	17.2	2814	2	AAX57141	Aax57141 Mouse KCN
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39	460.8	17.1	2926	10	ADB78682	Adb78682 Human pot
40	460.8	17.1	2926	10	ADB78691	Adb78691 Human pot
41	459.2	17.0	2926	10	ADB78689	Adb78689 Human pot
42	457.4	17.0	2755	13	ADS17847	Ads17847 Human KCN
43	455.8	16.9	1848	12	ADH51119	Adh51119 Potassium
44	455.8	16.9	1848	12	ADM77995	Adm77995 KCNQ2-15b
45	454.2	16.9	4512	10	ADJ56528	Adj56528 Rat cDNA

ALIGNMENTS

RESULT 1
AAS14652
ID AAS14652 standard; cDNA; 2694 BP.
XX
AC AAS14652;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human cDNA encoding a voltage gated potassium channel hKVNQ5-1.
XX
KW Human; ss; voltage-gated potassium channel; hKCNQ5-1; nootropic;
KW cerebroprotective; neurotropic; analgesic; vision disorder;
KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder; stroke;
KW pain; gene therapy; splice variant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .2994
FT /*tag= a
FT /product= "hKCNQ5-1"
XX
PN WO200170759-A1.
XX
PD 27-SEP-2001.
XX
PF 20-MAR-2001; 2001WO-US009328.
XX
PR 21-MAR-2000; 2000US-0190954P.
XX
PA (ICAG-) ICAGEN INC.
XX
PI Jegla TJ;
XX
DR WPI; 2001-611467/70.
DR P-PSDB; AAU09020.
XX
PT Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT identifying a compound modulating ion flux in eukaryotic cell or cell
PT membrane expressing the protein, comprises KCNQ approximatelya- subunits.
XX
PS Claim 5; Page 62-63; 78pp; English.

XX
CC The invention relates to an isolated polypeptide comprising an alpha-
CC subunit of a KCNQ potassium channel, with a subsequence having 65%
CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
CC and forms a KCNQ potassium channel having the characteristic of voltage-
CC gating with at least an additional KCNQ alpha-subunit. Also included in
CC the scope of the invention are the nucleic acids encoding hKCNQ5
CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
CC vectors encoding them, antibodies against them, the use of 3-dimensional
CC computer modelling to identify molecules that bind to a KCNQ containing
CC potassium channel and modulate ion flux through the channel. The KCNQ
CC polypeptide is useful for identifying a compound that increases or
CC decreases ion flux through a potassium channel expressed in an eukaryotic
CC host cell or cell membrane. The compound (and the KCNQ nucleic acid when
CC used in gene therapy)is useful as a pharmaceutical agent for treating
CC diseases involving abnormal ion flux, such as disorders of the central
CC nervous system, such as epilepsy, migraines, hearing and vision problems,
CC psychotic disorders, seizures, learning and memory disorders, stroke and
CC pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
CC human tissue and the use of a nucleotide sequence of KCNQ5 to search
CC computer databases to find variants of the sequence which are associated
CC with disease states, is useful for screening mutations of KCNQ5. The
CC present sequence is a splice variant of hKCNQ5 encoding hKCNQ5-1
XX
SQ Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 U; 0 Other;

Query Match 100.0%; Score 2694; DB 4; Length 2694;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
Db   121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180

Qy   181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
Db   181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240

Qy   241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
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Qy   301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
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Qy   421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
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Qy   481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
Db   481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540

Qy   541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
Db   541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600

Qy   601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
Db   601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660

Qy   661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
Db   661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720

Qy   721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
Db   721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780

Qy   781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
Db   781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840

Qy   841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
Db   841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900

Qy   901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
Db   901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960

Qy   961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
Db   961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020

Qy  1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Db  1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080

Qy  1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
Db  1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140

Qy  1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
Db  1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200

Qy  1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
Db  1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260

Qy  1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320
Db  1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320

Qy  1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380
Db  1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380

Qy  1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440
Db  1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440

Qy  1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500
Db  1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500

Qy  1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560
Db  1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560

Qy  1561 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620
Db  1561 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620

Qy  1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680
Db  1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680

Qy  1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
Db  1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
```

```
Qy       1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800

Qy       1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860

Qy       1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920

Qy       1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980

Qy       1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040

Qy       2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100

Qy       2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160

Qy       2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220

Qy       2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280

Qy       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340

Qy       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400

Qy       2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460

Qy       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520

Qy       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580

Qy       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640

Qy       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
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RESULT 2
AAD27192
ID   AAD27192 standard; cDNA; 2694 BP.
XX
AC   AAD27192;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human potassium channel polypeptide, KCNQ5 cDNA.
XX
KW   Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;
KW   dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis; ALS;
KW   multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
KW   anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
KW   addiction; myokymia; Alzheimer's disease; age-associated memory loss;
KW   learning deficiency; cognitive disorder; motor disease; neuron disease;
KW   neurophysiological disorder; neuropsychological disorder; asthma;
KW   neuron cell death; brain tumour; gene therapy; antisense therapy;
KW   synaptic transmission; electrical excitability; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2694
FT                   /*tag=  a
FT                   /product= "Human KCNQ5 protein"
XX
PN   WO200192526-A1.
XX
PD   06-DEC-2001.
XX
PF   24-MAY-2001; 2001WO-US017314.
XX
PR   26-MAY-2000; 2000US-0207389P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Dworetzky SI,  Ramanathan CS,  Trojnacki JT,  Boissard CG;
PI   Gribkoff VK;
XX
DR   WPI; 2002-122069/16.
DR   P-PSDB; AAE16599.
XX
PT   Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding
PT   it, for diagnosing, treating and identifying modulators useful in
PT   treating neurological, neurophysiological and neuropsychological
PT   diseases.
XX
PS   Claim 3; Fig 1; 128pp; English.
XX
CC   The invention relates to potassium channel polypeptides referred to as
CC   KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5
CC   polypeptides are useful for identifying compounds that modulate their
CC   biological activity. The compounds identified and KCNQ5 polynucleotides
CC   are useful for treating acute and chronic pain, migraine, acute stroke,
CC   dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis (ALS),
CC   multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety disorders,
CC   depression, bipolar disorders, sleep disorders, eating disorders,
CC   addiction, myokymia, Alzheimer's disease, age-associated memory loss,
CC   learning deficiencies, cognitive disorders and motor neuron diseases. The
CC   nucleic acid molecules of the invention are further useful for treating
CC   neurophysiological, neuropsychological disorders, asthma, neuron cell
CC   death and brain tumours. They are also used in gene therapy and antisense
CC   therapy. KCNQ5 polypeptides modulate synaptic transmission and electrical
CC   excitability in the brain and are useful for generating antibodies. They
CC   are also useful to affinity purify biological effectors from biological
CC   materials e.g. disease tissues or cells. The present sequence is human
CC   KCNQ5 cDNA
XX
SQ   Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 U; 0 Other;
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  Query Match            100.0%;  Score 2694;  DB 6;  Length 2694;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2694;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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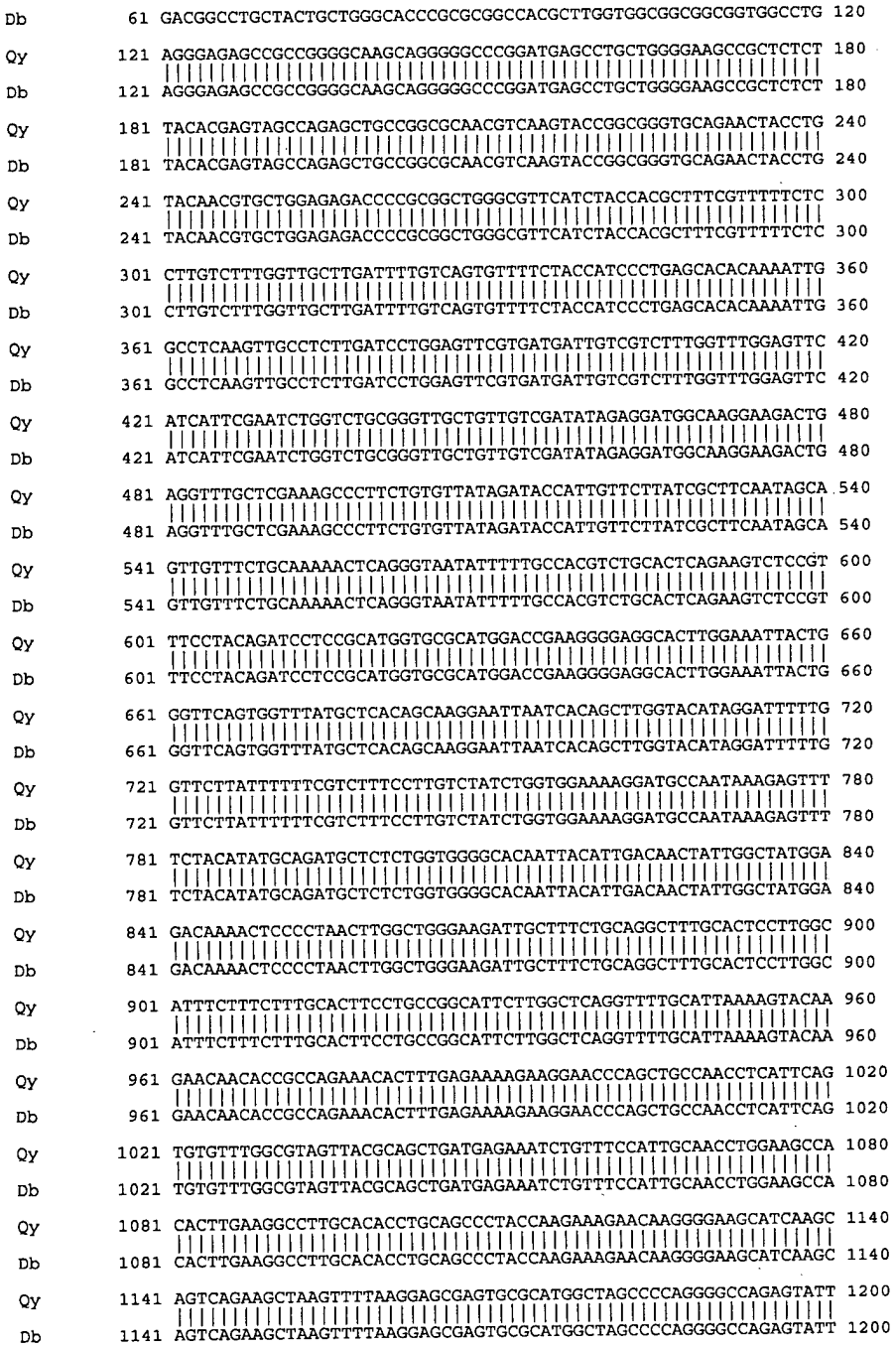
Db 61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
Qy 121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
Db 121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
Qy 181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
Db 181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
Qy 241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
Db 241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
Qy 301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
Db 301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
Qy 361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
Db 361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
Qy 421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
Db 421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
Qy 481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
Db 481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
Qy 541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
Db 541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
Qy 601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
Db 601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
Qy 661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
Db 661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
Qy 721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
Db 721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
Qy 781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
Db 781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
Qy 841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
Db 841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
Qy 901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
Db 901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
Qy 961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
Db 961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
Qy 1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Db 1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Qy 1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
Db 1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
Qy 1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
Db 1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
Qy 1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
Db 1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
Qy 1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320
Db 1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320
Qy 1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380
Db 1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380
Qy 1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440
Db 1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440
Qy 1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500
Db 1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500
Qy 1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560
Db 1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560
Qy 1561 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620
Db 1561 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620
Qy 1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680
Db 1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680
Qy 1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
Db 1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
Qy 1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
Db 1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
Qy 1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
Db 1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
Qy 1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
Db 1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
Qy 1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
Db 1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
Qy 1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
Db 1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
Qy 2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
Db 2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
Qy 2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
Db 2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
Qy 2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
Db 2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
Qy 2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280
Db 2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280

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Qy       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340

Qy       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400

Qy       2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460

Qy       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520

Qy       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580

Qy       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640

Qy       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
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RESULT 3
AAS14651
ID AAS14651 standard; cDNA; 3071 BP.
XX
AC AAS14651;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human cDNA for voltage gated potassium channel hKVNQ5.
XX
KW Human; ss; voltage-gated potassium channel; hKCNQ5; nootropic;
KW cerebroprotective; neurotropic; analgesic; vision disorder;
KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder; stroke;
KW pain; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200170759-A1.
XX
PD 27-SEP-2001.
XX
PF 20-MAR-2001; 2001WO-US009328.
XX
PR 21-MAR-2000; 2000US-0190954P.
XX
PA (ICAG-) ICAGEN INC.
XX
PI Jegla TJ;
XX
DR WPI; 2001-611467/70.
XX
PT Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT identifying a compound modulating ion flux in eukaryotic cell or cell
PT membrane expressing the protein, comprises KCNQ approximatelya- subunits.
XX
PS Claim 5; Page 61-62; 78pp; English.
XX
CC The invention relates to an isolated polypeptide comprising an alpha-
CC subunit of a KCNQ potassium channel, with a subsequence having 65%
CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
CC and forms a KCNQ potassium channel having the characteristic of voltage-
CC gating with at least an additional KCNQ alpha-subunit. Also included in
CC the scope of the invention are the nucleic acids encoding hKCNQ5
CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
CC vectors encoding them, antibodies against them, the use of 3-dimensional
CC computer modelling to identify molecules that bind to a KCNQ containing
CC potassium channel and modulate ion flux through the channel. The KCNQ
CC polypeptide is useful for identifying a compound that increases or
CC decreases ion flux through a potassium channel expressed in an eukaryotic
CC host cell or cell membrane. The compound (and the KCNQ nucleic acid when
CC used in gene therapy)is useful as a pharmaceutical agent for treating
CC diseases involving abnormal ion flux, such as disorders of the central
CC nervous system, such as epilepsy, migraines, hearing and vision problems,
CC psychotic disorders, seizures, learning and memory disorders, stroke and
CC pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
CC human tissue and the use of a nucleotide sequence of KCNQ5 to search
CC computer databases to find variants of the sequence which are associated
CC with disease states, is useful for screening mutations of KCNQ5. The
CC present sequence is a representative cDNA for hKCNQ5
XX
SQ Sequence 3071 BP; 849 A; 734 C; 737 G; 750 T; 0 U; 1 Other;

Query Match 99.9%; Score 2690.4; DB 4; Length 3071;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2691; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 69

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 129

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 189

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 249

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 309

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 369

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 429

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 489

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 549

Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 609

Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 669

Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
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Db        670 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 729

Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
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Db        730 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 789
Qy        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
Db        790 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 849
Qy        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
Db        850 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 909
Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
Db        910 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 969
Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
Db        970 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1029
Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Db       1030 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1089
Qy       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
Db       1090 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1149
Qy       1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
Db       1150 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1209
Qy       1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
Db       1210 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1269
Qy       1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320
Db       1270 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1329
Qy       1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380
Db       1330 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1389
Qy       1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440
Db       1390 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1449
Qy       1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500
Db       1450 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1509
Qy       1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560
Db       1510 AAGTTTAAGGAAACRTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1569
Qy       1561 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620
Db       1570 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1629
Qy       1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680
Db       1630 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1689
Qy       1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
Db       1690 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1749
Qy       1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
Db       1750 ATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1809
Qy       1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
Db       1810 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGTTCCCACCTTTTGAATGTGAACAGACATCT 1869
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Qy       1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
Db       1870 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1929
Qy       1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
Db       1930 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1989
Qy       1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
Db       1990 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2049
Qy       2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
Db       2050 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2109
Qy       2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
Db       2110 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2169
Qy       2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
Db       2170 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2229
Qy       2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280
Db       2230 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2289
Qy       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
Db       2290 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2349
Qy       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400
Db       2350 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2409
Qy       2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460
Db       2410 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2469
Qy       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
Db       2470 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2529
Qy       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
Db       2530 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2589
Qy       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
Db       2590 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2649
Qy       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
Db       2650 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2703
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RESULT 4
AAC85414
ID AAC85414 standard; cDNA; 3137 BP.
XX
AC AAC85414;
XX
DT 20-APR-2001 (first entry)
XX
DE Human KCNQ5 potassium channel subunit coding sequence.
XX
KW Human; KCNQ5; heteromeric channel; chromosome 6; Parkinson's disease;
KW central nervous system; CNS; Alzheimer's disease; anxiety; ataxia;
KW CNS damage; trauma; stroke; neurodegenerative illness; schizophrenia;
KW compulsive behaviour; dementia; depression; Huntington's disease; mania;
KW memory impairment; memory dysfunction; spinal cord damage; phobia;

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KW   pick's disease; psychosis; stroke; tremor; seizure; convulsion; epilepsy;
KW   ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2694
FT                   /*tag=  a
FT                   /product= "KCNQ5 subunit"
XX
PN   WO200077035-A2.
XX
PD   21-DEC-2000.
XX
PF   29-MAY-2000; 2000WO-DK000289.
XX
PR   11-JUN-1999;   99DK-00000828.
XX
PA   (NEUR-) NEUROSEARCH AS.
XX
PI   Jentsch TJ;
XX
DR   WPI; 2001-080678/09.
DR   P-PSDB; AAB47046.
XX
PT   Novel genes encoding KCNQ5 potassium channel subunits, useful for
PT   treating Alzheimer's disease, anxiety, ataxia, stroke, dementia,
PT   depression, Huntington's disease, schizophrenia and Parkinson's disease.
XX
PS   Claim 2; Page 44-48; 50pp; English.
XX
CC   This sequence encodes the human KCNQ5 protein. The KCNQ5 protein forms
CC   heteromeric channels with other KCNQ channel subunits, in particular
CC   KCNQ3 and KCNQ4. The KCNQ5 gene has been localised to the long arm of
CC   chromosome 6 (6q14). Chemicals which have the ability to bind to KCNQ5
CC   are useful for diagnosis, treatment, prevention or alleviation of
CC   diseases related to diseases or adverse conditions of the central nervous
CC   system (CNS), including affective disorders, Alzheimer's disease,
CC   anxiety, ataxia, CNS damage caused by trauma, stroke or neurodegenerative
CC   illness, cognitive deficits, compulsive behavior, dementia, depression,
CC   Huntington's disease, mania, memory impairment, memory disorders, memory
CC   dysfunction, motion disorders, motor disorders, neurodegenerative
CC   diseases, Parkinson's disease and Parkinson-like motor disorders,
CC   phobias, pick's disease, psychosis, schizophrenia, spinal cord damage,
CC   stroke, tremor, seizures, convulsions and epilepsy
XX
SQ   Sequence 3137 BP; 865 A; 749 C; 745 G; 778 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 2689.2;  DB 4;  Length 3137;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2691;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTCGGTGGCGGCGGCGGTGGCCTG 120

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540

Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600

Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660

Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720

Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780

Qy        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840

Qy        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900

Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960

Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020

Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080

Qy       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140

Qy       1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260

Qy       1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320

Qy       1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380

Qy       1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440
Qy      1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500
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Qy      1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560
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Qy      1561 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620
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Db      1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680
Qy      1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
Db      1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
Qy      1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
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Qy      1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
Db      1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
Qy      1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
Db      1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
Qy      1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
Db      1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
Qy      1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
Db      1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
Qy      2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
Db      2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
Qy      2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
Db      2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
Qy      2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
Db      2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
Qy      2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280
Db      2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280
Qy      2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
Db      2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
Qy      2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400
Db      2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400
Qy      2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460
Db      2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460
Qy      2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
Db      2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
Qy      2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
Db      2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
Qy      2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
Db      2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
Qy      2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
Db      2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
```

RESULT 5
AAH49499
ID AAH49499 standard; DNA; 3074 BP.
XX
AC AAH49499;
XX
DT 11-DEC-2001 (first entry)
XX
DE Human KCNQ5 DNA.
XX
KW KCNQ5; potassium channel protein; human; neurological; cardiovascular;
KW anticonvulsant; excitablilty modulator; membrane potential; neuron;
KW voltage-dependent KCNQ5 potassium channel; cardiomyocyte; epilepsy;
KW screening; central nervous system disease; cardiovascular disease; ds.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   110. .2908
FT   /*tag= a
FT   /product= "KCNQ5"
XX
PN DE10013732-A1.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2000; 2000DE-01013732.
XX
PR 21-MAR-2000; 2000DE-01013732.
XX
PA (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI Steinmeyer K, Lerche C, Scherer C, Seebohm G, Busch AE;
XX
DR WPI; 2001-571700/65.
DR P-PSDB; AAB86979.
XX
PT New DNA sequence encoding potassium channel KCNQ5, useful in screening
PT for specific modulators, potential agents for treating central nervous
PT system and cardiovascular diseases.
XX
PS Claim 2a; Page 9-10; 20pp; German.
XX
CC This invention describes a novel DNA sequence (I) encoding: (i) a
CC polypeptide (II) with potassium channel KCNQ5 activity; (ii) a
CC polypeptide with the amino acid (aa) sequence of KCNQ5. The products of
CC the invention have neurological, cardiovascular and anticonvulsant
CC activity and act as modulators of the voltage-dependent KCNQ5 potassium
CC channel, a key regulator of membrane potential and modulator of
CC excitability of electrically activated cells such as neurons and
CC cardiomyocytes. KCNQ5 may be implicated in some forms of epilepsy. (II)
CC are used to screen for compounds that modulate the activity of KCNQ5,
CC potentially useful for treating central nervous system (e.g. epilepsy)
CC and cardiovascular diseases. This sequence encodes the human potassium
CC channel KCNQ5 protein described in the invention
XX
SQ Sequence 3074 BP; 788 A; 784 C; 789 G; 713 T; 0 U; 0 Other;

  Query Match   99.5%; Score 2681.2; DB 4; Length 3074;

Best Local Similarity 99.7%; Pred. No. 0;
Matches 2686; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 274

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 334

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              |||||||||||||||||||||||||||||||||||||||||||| |  |  ||||||
Db        335 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGAAGCCGCCTCTCT 394

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 454

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        455 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTCCTC 514

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 574

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        575 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 634

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        635 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 694

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        695 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 754

Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        755 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 814

Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        815 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 874

Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        875 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 934

Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        935 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 994

Qy        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        995 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 1054

Qy        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1055 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 1114

Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1115 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 1174

Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1175 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1234

Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1235 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1294

Qy       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1295 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1354

Qy       1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1355 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1414

Qy       1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1415 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1474

Qy       1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1475 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1534

Qy       1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1535 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1594

Qy       1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1595 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1654

Qy       1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1655 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1714

Qy       1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1715 AAGTTTAAGGAAACATTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1774

Qy       1561 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1775 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1834

Qy       1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1835 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1894

Qy       1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1895 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1954

Qy       1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1955 ATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 2014

Qy       1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2015 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 2074

Qy       1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2075 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 2134

Qy       1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2135 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 2194

Qy       1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2195 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2254

Qy       2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2255 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2314

Qy       2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2315 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2374
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Qy       2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2375 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2434

Qy       2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2435 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2494

Qy       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2495 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2554

Qy       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2555 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2614

Qy       2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2615 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2674

Qy       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2675 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2734

Qy       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2735 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2794

Qy       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2795 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2854

Qy       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2855 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2908
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RESULT 6
ADB78684
ID   ADB78684 standard; cDNA; 3074 BP.
XX
AC   ADB78684;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human potassium channel subunit mutant cDNA SEQ ID NO:55.
XX
KW   ss; gene; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW   neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW   antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW   nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW   ion channel dysfunction; human.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003008574-A1.
XX
PD   30-JAN-2003.
XX
PF   08-JUL-2002; 2002WO-AU000910.
XX
PR   18-JUL-2001; 2001AU-00006452.
PR   05-MAR-2002; 2002AU-00000910.
PR   13-MAY-2002; 2002AU-00002292.
XX
PA   (BION-) BIONOMICS LTD.
PA   (WALL/) WALLACE R W.
XX
PI   Mulley JC,  Harkin LA,  Dibbens LM,  Phillips HA,  Heron SE;
PI   Berkovic SF,  Scheffer IE;
XX
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DR   WPI; 2003-239332/23.
XX
PT   Identifying predisposition to an ion channel dysfunction, such as
PT   periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT   schizophrenia, anxiety and depression, by detecting encoding-gene
PT   mutation events.
XX
PS   Claim 6; SEQ ID NO 55; 106pp; English.
XX
CC   The invention relates to a novel method for identifying a subject
CC   predisposed to a disorder associated with ion channel dysfunction. The
CC   method comprises ascertaining if at least one of the genes encoding ion
CC   channel subunits (ICS) has undergone a mutation event so that a cDNA
CC   derived from the subject has any of 134 nucleotide sequences. The method
CC   of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC   antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC   neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC   ophthalmological activity. A polynucleotide of the invention acts as an
CC   ion channel agonist, or ion channel antagonist. The methods, isolated
CC   nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC   modulator of an ion channel, cells and genetically modified non-human
CC   animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC   disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC   kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC   myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC   disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC   depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC   pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC   Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC   fibrosis, congenital stationary night blindness and total colour
CC   blindness. The present sequence represents a mutant cDNA of the
CC   invention. The sequence data for this patent is not represented in the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ   Sequence 3074 BP; 787 A; 784 C; 789 G; 714 T; 0 U; 0 Other;
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  Query Match             99.5%;  Score 2679.6;  DB 10;  Length 3074;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 2685;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 274

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 334

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| | | ||||||
Db        335 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGAAGCCGCCTCTCT 394

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 454

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        455 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTCCTC 514

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 574

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        575 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 634

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        635 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 694
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Qy       481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
Db       695 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 754

Qy       541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
Db       755 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 814

Qy       601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
Db       815 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 874

Qy       661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
Db       875 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 934

Qy       721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
Db       935 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 994

Qy       781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
Db       995 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 1054

Qy       841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
Db      1055 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 1114

Qy       901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
Db      1115 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 1174

Qy       961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
Db      1175 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1234

Qy      1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Db      1235 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1294

Qy      1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
Db      1295 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1354

Qy      1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
Db      1355 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1414

Qy      1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
Db      1415 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1474

Qy      1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320
Db      1475 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1534

Qy      1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380
Db      1535 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1594

Qy      1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440
Db      1595 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1654

Qy      1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500
Db      1655 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1714

Qy      1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560
Db      1715 AAGTTTAAGGAAACATTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1774

Qy      1561 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620

Db      1775 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1834

Qy      1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680
Db      1835 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1894

Qy      1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
Db      1895 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1954

Qy      1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
Db      1955 ATAGAATCCAAGCTGGACTGCCTTCTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 2014

Qy      1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
Db      2015 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 2074

Qy      1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
Db      2075 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 2134

Qy      1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
Db      2135 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 2194

Qy      1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
Db      2195 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2254

Qy      2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
Db      2255 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2314

Qy      2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
Db      2315 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2374

Qy      2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
Db      2375 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2434

Qy      2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280
Db      2435 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2494

Qy      2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
Db      2495 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2554

Qy      2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400
Db      2555 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2614

Qy      2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460
Db      2615 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2674

Qy      2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
Db      2675 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2734

Qy      2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
Db      2735 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2794

Qy      2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
Db      2795 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2854

Qy      2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
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Db       2855 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2908

RESULT 7
AAS14653
ID   AAS14653 standard; cDNA; 2667 BP.
XX
AC   AAS14653;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human cDNA encoding a voltage gated potassium channel hKVNQ5-2.
XX
KW   Human; ss; voltage-gated potassium channel; KCNQ5-2; nootropic;
KW   cerebroprotective; neurotropic; analgesic; vision disorder;
KW   central nervous system disorder; epilepsy; migraine; hearing disorder;
KW   psychotic disorder; seizure; learning disorder; memory disorder; stroke;
KW   pain; gene therapy; splice variant.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2967
FT                   /*tag=  a
FT                   /product= "hKCNQ5-2"
XX
PN   WO200170759-A1.
XX
PD   27-SEP-2001.
XX
PF   20-MAR-2001; 2001WO-US009328.
XX
PR   21-MAR-2000; 2000US-0190954P.
XX
PA   (ICAG-) ICAGEN INC.
XX
PI   Jegla TJ;
XX
DR   WPI; 2001-611467/70.
DR   P-PSDB; AAU09021.
XX
PT   Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT   identifying a compound modulating ion flux in eukaryotic cell or cell
PT   membrane expressing the protein, comprises KCNQ approximatelya- subunits.
XX
PS   Claim 5; Page 63-64; 78pp; English.
XX
CC   The invention relates to an isolated polypeptide comprising an alpha-
CC   subunit of a KCNQ potassium channel, with a subsequence having 65%
CC   sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
CC   and forms a KCNQ potassium channel having the characteristic of voltage-
CC   gating with at least an additional KCNQ alpha-subunit. Also included in
CC   the scope of the invention are the nucleic acids encoding hKCNQ5
CC   (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
CC   vectors encoding them, antibodies against them, the use of 3-dimensional
CC   computer modelling to identify molecules that bind to a KCNQ containing
CC   potassium channel and modulate ion flux through the channel. The KCNQ
CC   polypeptide is useful for identifying a compound that increases or
CC   decreases ion flux through a potassium channel expressed in an eukaryotic
CC   host cell or cell membrane. The compound (and the KCNQ nucleic acid when
CC   used in gene therapy)is useful as a pharmaceutical agent for treating
CC   diseases involving abnormal ion flux, such as disorders of the central
CC   nervous system, such as epilepsy, migraines, hearing and vision problems,
CC   psychotic disorders, seizures, learning and memory disorders, stroke and
CC   pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
CC   human tissue and the use of a nucleotide sequence of KCNQ5 to search
CC   computer databases to find variants of the sequence which are associated
CC   with disease states, is useful for screening mutations of KCNQ5. The
CC   present sequence is a splice variant of hKCNQ5 encoding hKCNQ5-2
XX
SQ   Sequence 2667 BP; 701 A; 667 C; 660 G; 639 T; 0 U; 0 Other;

  Query Match             97.6%;  Score 2630;  DB 4;  Length 2667;

  Best Local Similarity   99.0%;  Pred. No. 0;
  Matches 2667;  Conservative    0;  Mismatches    0;  Indels   27;  Gaps    1;

Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540

Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600

Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660

Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720

Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780

Qy        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900

Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960

Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020

Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Qy       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
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Db       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAA---------------------------- 1115
Qy       1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1116 --TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1173
Qy       1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1233
Qy       1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1293
Qy       1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440
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Qy       1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1473
Qy       1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560
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Qy       1561 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1834 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1893
Qy       1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1954 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2013
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Qy       2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
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Qy       2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2134 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2193
Qy       2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2194 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2253
Qy       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2314 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2373
Qy       2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2374 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2433
Qy       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2434 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2493
Qy       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2494 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2553
Qy       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2554 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2613
Qy       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2614 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2667
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RESULT 8
AAH43633
ID   AAH43633 standard; cDNA; 2772 BP.
XX
AC   AAH43633;
XX
DT   21-JAN-2002  (first entry)
XX
DE   Human ion-channel forming protein ORF.
XX
KW   Ion-channel forming protein; voltage-gated potassium channel; fetal;
KW   brain; thymus; prostate; heart; skeletal muscle; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175108-A1.
XX
PD   11-OCT-2001.
XX
PF   03-APR-2001; 2001WO-US010875.
XX
PR   03-APR-2000; 2000US-0194255P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Hu Y,  Kieke JA,  Turner AC,  Nehls MC,  Friedrich G,  Zambrowicz B;
PI   Sands AT;
XX
DR   WPI; 2001-656987/75.
DR   P-PSDB; AAB47678.
XX
PT   New human ion channel protein and polynucleotides encoding the protein,
PT   useful in diagnosing or treating diseases, in drug screening, and in
PT   clinical trial monitoring.
XX
```

PS Claim 1; Page 34-35; 41pp; English.
XX
CC The sequences in AAH43633-34 encode a novel ion-channel forming protein.
CC The protein shares structural similarity with mammalian ion channel
CC proteins, particularly voltage-gated potassium channel proteins. The
CC protein is expressed in many human cell lines including fetal brain,
CC brain, thymus,prostate, heart and skeletal muscle. The novel protein can
CC be used in the diagnosis or treatment of diseases, in drug screening, and
CC in clinical trial monitoring. The oligonucleotides may be used as
CC hybridization probes for screening libraries, and assessing gene
CC expression patterns (particularly using a micro array or high throughput
CC chip format). The nucleic acids and novel protein can also be used in the
CC identification, selection and validation of novel molecular targets for
CC drug discovery, to screen collections of genetic material from patients
CC who have a particular medical condition, to identify mutations associated
CC with a particular disease, as a diagnostic or prognostic assay, and to
CC screen for drugs which can be used to treat symptomatic or phenotypic
CC manifestations of perturbing the normal function of novel human protein.
CC The polypeptides are further used in generating antibodies
XX
SQ Sequence 2772 BP; 715 A; 700 C; 713 G; 644 T; 0 U; 0 Other;

Query Match 97.4%; Score 2625.2; DB 5; Length 2772;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

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Qy     1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
Db   106 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 165

Qy    61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
Db   166 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTCGGTGGCGGCGGCGGTGGCCTG 225

Qy   121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
Db   226 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 285

Qy   181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
Db   286 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 345

Qy   241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
Db   346 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 405

Qy   301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
Db   406 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 465

Qy   361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
Db   466 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 525

Qy   421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
Db   526 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 585

Qy   481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
Db   586 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 645

Qy   541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
Db   646 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 705

Qy   601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
Db   706 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 765

Qy   661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
Db   766 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 825

Qy   721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
Db   826 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 885

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Qy   841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
Db   946 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 1005

Qy   901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
Db  1006 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 1065

Qy   961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
Db  1066 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1125

Qy  1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Db  1126 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1185

Qy  1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
Db  1186 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAA---------- 1220

Qy  1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
Db  1221 --TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1278

Qy  1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
Db  1279 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1338

Qy  1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320
Db  1339 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1398

Qy  1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380
Db  1399 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1458

Qy  1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440
Db  1459 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1518

Qy  1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500
Db  1519 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1578

Qy  1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560
Db  1579 AAGTTTAAGGAAACATTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1638

Qy  1561 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620
Db  1639 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1698

Qy  1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680
Db  1699 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1758

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Db  1759 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1818

Qy  1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
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Qy       1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
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Db       1879 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1938

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Db       1939 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1998

Qy       1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
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Db       1999 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 2058

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Qy       2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
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Qy       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
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Qy       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
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Qy       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
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Db       2659 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2718

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Db       2719 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2772
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RESULT 9
AAH43634
ID AAH43634 standard; cDNA; 3111 BP.
XX
AC AAH43634;
XX
DT 21-JAN-2002 (first entry)
XX
DE Human ion-channel forming protein coding sequence.
XX
KW Ion-channel forming protein; voltage-gated potassium channel; fetal;
KW brain; thymus; prostate; heart; skeletal muscle; probe; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 59. .2831
FT /*tag= a
FT /product= "Human ion-channel forming protein"
XX
PN WO200175108-A1.
XX
PD 11-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US010875.
XX
PR 03-APR-2000; 2000US-0194255P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;
PI Sands AT;
XX
DR WPI; 2001-656987/75.
DR P-PSDB; AAB47678.
XX
PT New human ion channel protein and polynucleotides encoding the protein,
PT useful in diagnosing or treating diseases, in drug screening, and in
PT clinical trial monitoring.
XX
PS Disclosure; Page 37-38; 41pp; English.
XX
CC The sequences in AAH43633-34 encode a novel ion-channel forming protein.
CC The protein shares structural similarity with mammalian ion channel
CC proteins, particularly voltage-gated potassium channel proteins. The
CC protein is expressed in many human cell lines including fetal brain,
CC brain, thymus,prostate, heart and skeletal muscle. The novel protein can
CC be used in the diagnosis or treatment of diseases, in drug screening, and
CC in clinical trial monitoring. The oligonucleotides may be used as
CC hybridization probes for screening libraries, and assessing gene
CC expression patterns (particularly using a micro array or high throughput
CC chip format). The nucleic acids and novel protein can also be used in the
CC identification, selection and validation of novel molecular targets for
CC drug discovery, to screen collections of genetic material from patients
CC who have a particular medical condition, to identify mutations associated
CC with a particular disease, as a diagnostic or prognostic assay, and to
CC screen for drugs which can be used to treat symptomatic or phenotypic
CC manifestations of perturbing the normal function of novel human protein.
CC The polypeptides are further used in generating antibodies
XX
SQ Sequence 3111 BP; 814 A; 771 C; 789 G; 737 T; 0 U; 0 Other;

Query Match 97.4%; Score 2625.2; DB 5; Length 3111;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

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Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
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Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
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Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
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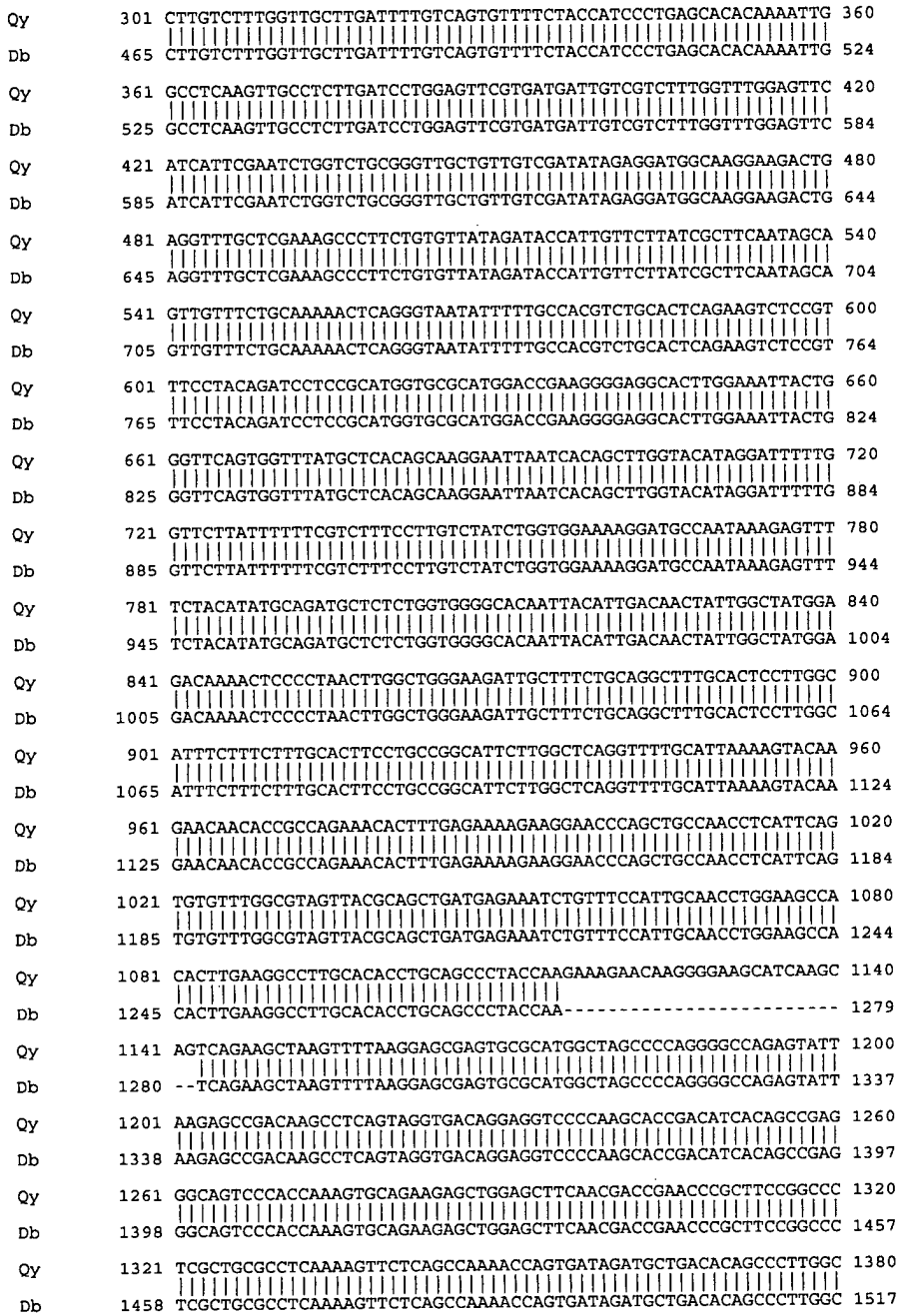

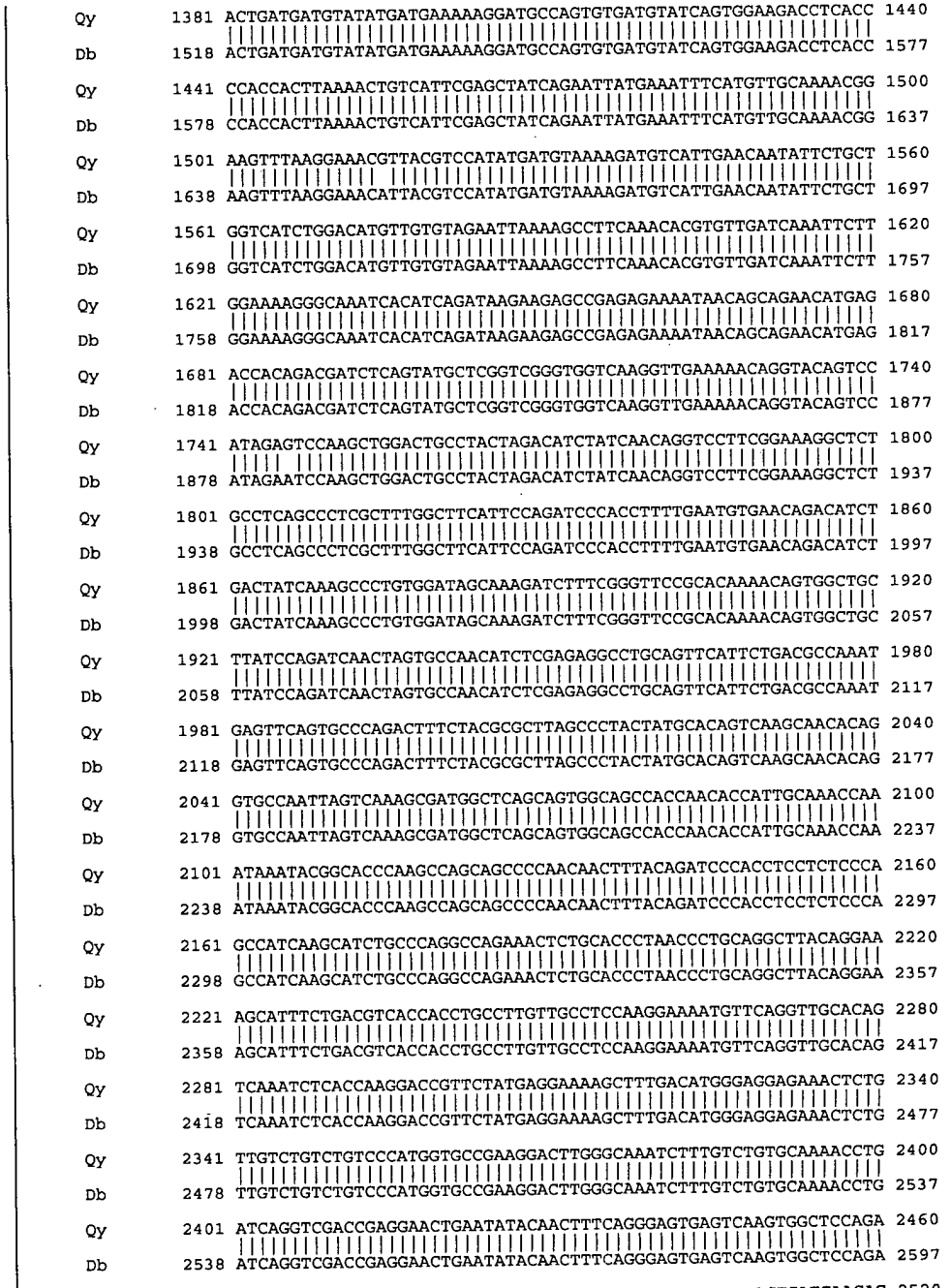

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Qy       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
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Db       2658 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2717

Qy       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2718 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2777

Qy       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2778 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2831


RESULT 10
AAC64371
ID   AAC64371 standard; cDNA; 3718 BP.
XX
AC   AAC64371;
XX
DT   07-FEB-2001  (first entry)
XX
DE   Human KCNQ5 (KCN6q) cDNA sequence SEQ ID NO:2.
XX
KW   Human; KCNQ5; KCN6q; chromosome 6; voltage-gated potassium channel;
KW   Stargardt-like macular dystrophy; cone-rod macular dystrophy;
KW   Salla disease; ophthalmological; auditory; central nervous system;
KW   cardioactive; anticonvulsant; gastrointestinal; muscular active;
KW   age-related macular degeneration; macular degeneration; deafness;
KW   epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
KW   gastrointestinal disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061606-A1.
XX
PD   19-OCT-2000.
XX
PF   10-APR-2000; 2000WO-US009587.
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PR   14-APR-1999;   99US-0129274P.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Petrukhin K,  Caskey CT,  Li W,  Metzker ML;
XX
DR   WPI; 2000-647417/62.
DR   P-PSDB; AAB24241.
XX
PT   Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
PT   inhibitors and activators which can treat e.g. Stargardt-like macular
PT   dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy.
XX
PS   Claim 3; Fig 2; 99pp; English.
XX
CC   The present sequence encodes the human KCNQ5 (also called KCN6q) protein,
CC   which is a voltage-gated potassium channel protein. Human KCNQ5 has
CC   ophthalmological, auditory, central nervous system (CNS), cardioactive,
CC   anticonvulsant, gastrointestinal and muscular active activities.
CC   Sequences and methods from the present invention are useful for
CC   identifying activators or inhibitors of KCNQ5 protein. These activators
CC   and inhibitors are useful for treating Stargardt-like macular dystrophy,
CC   cone-rod dystrophy, Salla disease, age-related macular degeneration,
CC   other forms of macular degeneration, deafness, epilepsy, and different
CC   forms of neuropsychiatric, heart, gastrointestinal, and muscle disorders.
CC   Stargardt-like macular dystrophy and cone-rod dystrophies are located at
CC   chromosome 6q
XX
SQ   Sequence 3718 BP; 1054 A; 845 C; 866 G; 953 T; 0 U; 0 Other;

  Query Match             96.0%;  Score 2585;  DB 3;  Length 3718;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 2591;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         94 ACGCTTGGTGGCGGCGGCGGTGGCCTGAGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGG 153
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Db        198 AAGTACCGGCGGGTGCAGAACTACCTGTACAACGTGCTGGAGAGACCCCGCGGCTGGGCG 257

Qy        274 TTCATCTACCACGCTTTCGTTTTTCTCCTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTT 333
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Db        258 TTCATCTACCACGCTTTCGTTTTTCTCCTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTT 317

Qy        334 TCTACCATCCCTGAGCACACAAAATTGGCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTG 393
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Db        318 TCTACCATCCCTGAGCACACAAAATTGGCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTG 377

Qy        394 ATGATTGTCGTCTTTGGTTTGGAGTTCATCATTCGAATCTGGTCTGCGGGTTGCTGTTGT 453
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Db        378 ATGATTGTCGTCTTTGGTTTGGAGTTCATCATTCGAATCTGGTCTGCGGGTTGCTGTTGT 437

Qy        454 CGATATAGAGGATGGCAAGGAAGACTGAGGTTTGCTCGAAAGCCCTTCTGTGTTATAGAT 513
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Db        438 CGATATAGAGGATGGCAAGGAAGACTGAGGTTTGCTCGAAAGCCCTTCTGTGTTATAGAT 497

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Db        498 ACCATTGTTCTTATCGCTTCAATAGCAGTTGTTTCTGCAAAAACTCAGGGTAATATTTTT 557

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Db        618 CGAAGGGGAGGCACTTGGAAATTACTGGGTTCAGTGGTTTATGCTCACAGCAAGGAATTA 677

Qy        694 ATCACAGCTTGGTACATAGGATTTTTGGTTCTTATTTTTTCGTCTTTCCTTGTCTATCTG 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 ATCACAGCTTGGTACATAGGATTTTTGGTTCTTATTTTTTCGTCTTTCCTTGTCTATCTG 737

Qy        754 GTGGAAAAGGATGCCAATAAAGAGTTTTCTACATATGCAGATGCTCTCTGGTGGGGCACA 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        738 GTGGAAAAGGATGCCAATAAAGAGTTTTCTACATATGCAGATGCTCTCTGGTGGGGCACA 797

Qy        814 ATTACATTGACAACTATTGGCTATGGAGACAAAACTCCCCTAACTTGGCTGGGAAGATTG 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        798 ATTACATTGACAACTATTGGCTATGGAGACAAAACTCCCCTAACTTGGCTGGGAAGATTG 857

Qy        874 CTTTCTGCAGGCTTTGCACTCCTTGGCATTTCTTTCTTTGCACTTCCTGCCGGCATTCTT 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        858 CTTTCTGCAGGCTTTGCACTCCTTGGCATTTCTTTCTTTGCACTTCCTGCCGGCATTCTT 917

Qy        934 GGCTCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAGAAACACTTTGAGAAAAGA 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        918 GGCTCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAGAAACACTTTGAGAAAAGA 977

Qy        994 AGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGTTACGCAGCTGATGAGAAA 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        978 AGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGTTACGCAGCTGATGAGAAA 1037

Qy       1054 TCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGCACACCTGCAGCCCTACC 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1038 TCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGCACACCTGCAGCCCTACC 1097

Qy       1114 AAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGC 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1098 AAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGC 1157
Qy       1174 ATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGG 1233
Db       1158 ATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGG 1217
Qy       1234 TCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGC 1293
Db       1218 TCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGC 1277
Qy       1294 TTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCA 1353
Db       1278 TTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCA 1337
Qy       1354 GTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAG 1413
Db       1338 GTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAG 1397
Qy       1414 TGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGA 1473
Db       1398 TGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGA 1457
Qy       1474 ATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATATGATGTA 1533
Db       1458 ATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACATTACGTCCATATGATGTA 1517
Qy       1534 AAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGC 1593
Db       1518 AAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGC 1577
Qy       1594 CTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGC 1653
Db       1578 CTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGC 1637
Qy       1654 CGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGTCGGGTG 1713
Db       1638 CGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGTCGGGTG 1697
Qy       1714 GTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGCTGGACTGCCTACTAGACATC 1773
Db       1698 GTCAAGGTTGAAAAACAGGTACAGTCCATAGAATCCAAGCTGGACTGCCTACTAGACATC 1757
Qy       1774 TATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTCCAGATC 1833
Db       1758 TATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTCCAGATC 1817
Qy       1834 CCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAAGATCTT 1893
Db       1818 CCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAAGATCTT 1877
Qy       1894 TCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATCTCGAGA 1953
Db       1878 TCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATCTCGAGA 1937
Qy       1954 GGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCGCTTAGC 2013
Db       1938 GGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCGCTTAGC 1997
Qy       2014 CCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCAGCAGTG 2073
Db       1998 CCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCAGCAGTG 2057
Qy       2074 GCAGCCACCAACACCATTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCCCCAACA 2133
Db       2058 GCAGCCACCAACACCATTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCCCCAACA 2117
Qy       2134 ACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAAACTCTG 2193
Db       2118 ACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAAACTCTG 2177
Qy       2194 CACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTTGTTGCC 2253
Db       2178 CACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTTGTTGCC 2237
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Qy       2254 TCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATGAGGAAA 2313
Db       2238 TCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATGAGGAAA 2297
Qy       2314 AGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAGGACTTG 2373
Db       2298 AGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAGGACTTG 2357
Qy       2374 GGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATACAACTT 2433
Db       2358 GGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATACAACTT 2417
Qy       2434 TCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGGAGGGAA 2493
Db       2418 TCAGGGAGTGAGTCAAGTGCCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGGAGGGAA 2477
Qy       2494 TCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGACACTTTT 2553
Db       2478 TCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGACACTTTT 2537
Qy       2554 GATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGGACTGGA 2613
Db       2538 GATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGGACTGGA 2597
Qy       2614 AGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTCAGCTTG 2673
Db       2598 AGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTCAGCTTG 2657
Qy       2674 CCTCATGTCAAACTGAAATAA 2694
Db       2658 CCTCATGTCAAACTGAAATAA 2678
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RESULT 11
AAC64370
ID AAC64370 standard; DNA; 125910 BP.
XX
AC AAC64370;
XX
DT 07-FEB-2001 (first entry)
XX
DE Human KCNQ5 (KCN6q) gene sequence SEQ ID NO:1.
XX
KW Human; KCNQ5; KCN6q; chromosome 6; voltage-gated potassium channel;
KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;
KW Salla disease; ophthalmological; auditory; central nervous system;
KW cardioactive; anticonvulsant; gastrointestinal; muscular active;
KW age-related macular degeneration; macular degeneration; deafness;
KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
KW gastrointestinal disorder; ds.
XX
OS Homo sapiens.
XX
PN WO200061606-A1.
XX
PD 19-OCT-2000.
XX
PF 10-APR-2000; 2000WO-US009587.
XX
PR 14-APR-1999; 99US-0129274P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Petrukhin K, Caskey CT, Li W, Metzker ML;
XX
DR WPI; 2000-647417/62.
DR P-PSDB; AAB24241.
XX
PT Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
PT inhibitors and activators which can treat e.g. Stargardt-like macular
PT dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy.
XX

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PS   Claim 3; Fig 1; 99pp; English.
XX
CC   The present sequence represents the human KCNQ5 (also called KCN6q) gene,
CC   which encodes a voltage-gated potassium channel protein. Human KCNQ5 has
CC   ophthalmological, auditory, central nervous system (CNS), cardioactive,
CC   anticonvulsant, gastrointestinal and muscular active activities.
CC   Sequences and methods from the present invention are useful for
CC   identifying activators or inhibitors of KCNQ5 protein. These activators
CC   and inhibitors are useful for treating Stargardt-like macular dystrophy,
CC   cone-rod dystrophy, Salla disease, age-related macular degeneration,
CC   other forms of macular degeneration, deafness, epilepsy, and different
CC   forms of neuropsychiatric, heart, gastrointestinal, and muscle disorders.
CC   Stargardt-like macular dystrophy and cone-rod dystrophies are located at
CC   chromosome 6q
XX
SQ   Sequence 125910 BP; 40132 A; 24180 C; 23166 G; 38360 T; 0 U; 72 Other;

  Query Match             35.8%;  Score 963.4;  DB 3;  Length 125910;
  Best Local Similarity   99.9%;  Pred. No. 1.9e-272;
  Matches  964;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1730 AGGTACAGTCCATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTC 1789
             ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db     123624 AGGTACAGTCCATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTC 123683

Qy       1790 GGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTG 1849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123684 GGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTG 123743

Qy       1850 AACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAA 1909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123744 AACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAA 123803

Qy       1910 ACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTC 1969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123804 ACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTC 123863

Qy       1970 TGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTC 2029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123864 TGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTC 123923

Qy       2030 AAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCA 2089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123924 AAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCA 123983

Qy       2090 TTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCAC 2149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123984 TTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCAC 124043

Qy       2150 CTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAG 2209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124044 CTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAG 124103

Qy       2210 GCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTC 2269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124104 GCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTC 124163

Qy       2270 AGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAG 2329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124164 AGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAG 124223

Qy       2330 GAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTG 2389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124224 GAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTG 124283

Qy       2390 TGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAA 2449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124284 TGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAA 124343

Qy       2450 GTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAA 2509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124344 GTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAA 124403

Qy       2510 CTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGC 2569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124404 CTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGC 124463

Qy       2570 CTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTC 2629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124464 CTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTC 124523

Qy       2630 AGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGA 2689
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124524 AGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGA 124583

Qy       2690 AATAA 2694
             |||||
Db     124584 AATAA 124588


RESULT 12
AAA47618
ID   AAA47618 standard; cDNA; 2335 BP.
XX
AC   AAA47618;
XX
DT   08-NOV-2000  (first entry)
XX
DE   KCNQ4 Potassium channel gene.
XX
KW   KCNQ4; potassium channel; cardiac arrhythmia; neonatal epilepsy;
KW   deafness; probes; treatment; therapy; transgenic animal; antibody;
KW   agonist; antagonist; tinnitus; hearing loss; neonatal deafness;
KW   presbyacusis; affective disorder, Alzheimer's disease; anxiety; ataxia;
KW   cognitive deficits; compulsive behavior; dementia; depression;
KW   Huntington's disease; mania; memory impairment; motor disorders;
KW   neurodegenerative disease; Parkinson's disease; Pick's disease;
KW   psychosis; schizophrenia; spinal cord damage; stroke; tremor; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             83. .2170
FT                   /*tag=  a
FT                   /product= "KCNQ4 Potassium channel polypeptide"
XX
PN   WO200044786-A1.
XX
PD   03-AUG-2000.
XX
PF   19-JAN-2000; 2000WO-DK000024.
XX
PR   26-JAN-1999;   99DK-00000076.
PR   19-MAY-1999;   99DK-00000693.
XX
PA   (NEUR-) NEUROSEARCH AS.
XX
PI   Jentsch TJ;
XX
DR   WPI; 2000-548813/50.
DR   P-PSDB; AAB01476.
XX
PT   Nucleic acids encoding the novel KCNQ4 potassium channel subunit, useful
PT   e.g. for treating tinnitus, deafness, Alzheimer's and Parkinson's
PT   diseases.
XX
PS   Claim 1; Page 43-48; 65pp; English.
XX
CC   Mutations in 3 known genes of the KCNQ branch of the potassium channel
CC   gene family underlie inherited cardiac arrhythmia's, neonatal epilepsy
CC   and in some cases associated with deafness. KCNQ4 has been mapped to the
CC   DFNA2 locus for autosomal dominant hearing loss, and a dominant negative
CC   KCNQ4 mutation that causes deafness in a DFNA2 pedigree has been
CC   identified. KCNQ4 is the first potassium channel gene underlying non-
CC   syndromic deafness. KCNQ4 forms heteromeric channels with other KCNQ
CC   channel subunits, especially KCNQ3. Nucleotides encoding the KCNQ4
```

CC protein and the protein itself may be used in the prevention, treatment
CC and diagnosis of diseases associated with inappropriate KCNQ4 expression.
CC The nucleotides may also be used as DNA probes in diagnostic assays (e.g.
CC polymerase chain reactions (PCR)) to detect and quantitate the presence
CC of similar nucleic acid sequences in samples and to identify mutations
CC within them, and hence which patients may be in need of restorative
CC therapy. They may also be used to study the expression and function of
CC KCNQ4 polypeptides and their role in metabolism, for example through the
CC production of transgenic animals. The KCNQ4 polypeptides may be used as
CC antigens in the production of antibodies and to identify modulators
CC (agonists and antagonists) of KCNQ4 expression and activity. The anti-
CC KCNQ4 antibodies and KCNQ4 antagonists may also be used to down regulate
CC KCNQ4 expression and activity. They may be used in this way to treat
CC tinnitus, loss of hearing (especially progressive hearing loss, neonatal
CC deafness and presbyacusis (deafness of the elderly)) and disease or
CC adverse conditions of the central nervous system (CNS) such as affective
CC disorder, Alzheimer's disease, anxiety, ataxia, CNS damage caused by
CC trauma, stroke or neurodegenerative illness, cognitive deficits,
CC compulsive behavior, dementia, depression, Huntington's disease, mania,
CC memory impairment, memory disorders and dysfunctions, motion disorders,
CC motor disorders, neurodegenerative diseases, Parkinson's disease,
CC Parkinson-like motor disorders, phobias, Pick's disease, psychosis,
CC schizophrenia, spinal cord damage, stroke and/or tremor. Conversely,
CC antisense nucleic acid molecules may be administered to down regulate
CC KCNQ4 expression by binding with the cells own KCNQ4 genes and preventing
CC their expression
XX
SQ Sequence 2335 BP; 396 A; 812 C; 719 G; 408 T; 0 U; 0 Other;

Query Match 19.2%; Score 518.4; DB 3; Length 2335;
Best Local Similarity 60.1%; Pred. No. 8.5e-142;
Matches 1103; Conservative 0; Mismatches 566; Indels 165; Gaps 8;

```
Qy        217 TACCGGCGGGTGCAGAACTACCTGTACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTC 276
Db        320 TACCGCCGCCTGCAGAACTGGGTCTACAACGTGCTGGAGCGGCCCCGCGGCTGGGCCTTC 379

Qy        277 ATCTACCACGCTTTCGTTTTTCTCCTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCT 336
Db        380 GTCTACCACGTCTTCATATTTTTGCTGGTCTTCAGCTGCCTGGTGCTGTCTGTGCTGTCC 439

Qy        337 ACCATCCCTGAGCACACAAAATTGGCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATG 396
Db        440 ACTATCCAGGAGCACCAGGAACTTGCCAACGAGTGTCTCCTCATCTTGGAATTCGTGATG 499

Qy        397 ATTGTCGTCTTTGGTTTGGAGTTCATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGA 456
Db        500 ATCGTGGTTTTCGGCTTGGAGTACATCGTCCGGGTCTGGTCCGCCGGATGCTGCTGCCGC 559

Qy        457 TATAGAGGATGGCAAGGAAGACTGAGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACC 516
Db        560 TACCGAGGATGGCAGGGTCGCTTCCGCTTTGCCAGAAAGCCCTTCTGTGTCATCGACTTC 619

Qy        517 ATTGTTCTTATCGCTTCAATAGCAGTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCC 576
Db        620 ATCGTGTTCGTGGCCTCGGTGGCCGTCATCGCCGCGGGTACCCAGGGCAACATCTTCGCC 679

Qy        577 ACGTCTGCACTCAGAAGTCTCCGTTTCCTACAGATCCTCCGCATGGTGCGCATGGACCGA 636
Db        680 ACGTCCGCGCTGCGCAGCATGCGCTTCCTGCAGATCCTGCGCATGGTGCGCATGGACCGC 739

Qy        637 AGGGGAGGCACTTGGAAATTACTGGGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATC 696
Db        740 CGCGGCGGCACCTGGAAGCTGCTGGGCTCAGTGGTCTACGCGCATAGCAAGGAGCTGATC 799

Qy        697 ACAGCTTGGTACATAGGATTTTTGGTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTG 756
Db        800 ACCGCCTGGTACATCGGGTTCCTGGTGCTCATCTTCGCCTCCTTCCTGGTCTACCTGGCC 859

Qy        757 GAAAAGGATGCCAATAAAGAGTTTTCTACATATGCAGATGCTCTCTGGTGGGGCACAATT 816
Db        860 GAGAAGGACGCCAACTCCGACTTCTCCTCCTACGCCGACTCGCTCTGGTGGGGGACGATT 919

Qy        817 ACATTGACAACTATTGGCTATGGAGACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTT 876
Db        920 ACATTGACAACCATCGGCTATGGTGACAAGACACCGCACACATGGCTGGGCAGGGTCCTG 979

Qy        877 TCTGCAGGCTTTGCACTCCTTGGCATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGC 936
Db        980 GCTGCTGGCTTCGCCTTACTGGGCATCTCTTTCTTTGCCCTGCCTGCCGGCATCCTAGGC 1039

Qy        937 TCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAGAAACACTTTGAGAAAAGAAGG 996
Db       1040 TCCGGCTTTGCCCTGAAGGTCCAGGAGCAGCACCGGCAGAAGCACTTCGAGAAGCGGAGG 1099

Qy        997 AACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCT 1056
Db       1100 ATGCCGGCAGCCAACCTCATCCAGGCTGCCTGGCGCCTGTACTCCACCGATATGAGCCGG 1159

Qy       1057 GTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGCACACCTGCAGC--------- 1107
Db       1160 GCCTACCTGACAGCCACCTGGTACTACTATGACAGTATCCTCCCATCCTTCAGAGAGCTG 1219

Qy       1108 CCTACCAAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGCTA---------------- 1152
Db       1220 GCCCTCTTGTTTGAGCACGTGCAACGGGCCCGCAATGGGGGCCTACGGCCCCTGGAGGTG 1279

Qy       1153 ---------------------------------------------------------- 1152
Db       1280 CGGCGGGCGCCGGTACCCGACGGAGCACCCTCCCGTTACCCGCCCGTTGCCACCTGCCAC 1339

Qy       1153 ----------------------------------------------AGTTTTAAGGAGCGA 1167
Db       1340 CGGCCGGGCAGCACCTCCTTCTGCCCTGGGGAAAGCAGCCGGATGGGCATCAAAGACCGC 1399

Qy       1168 GTGCGCATGGCTAGCCCCAGGGGCCAGA------GTATTAAGAGCCGACAAGCCTCAGTA 1221
Db       1400 ATCCGCATGGGCAGCTCCCAGCGGCGGACGGGTCCTTCCAAGCAGCAGCTGGCACCTCCA 1459

Qy       1222 GGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAGG---GCAGTCCCACCAAAGTG 1278
Db       1460 ACAATGCCCACCTCCCCAAGCAGCGAGCAGGTGGGTGAGGCCACCAGCCCCACCAAGGTG 1519

Qy       1279 CAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGT 1338
Db       1520 CAAAAGAGCTGGAGCTTCAATGACCGCACCCGCTTCCGGGCATCTCTGAGACTC------ 1573

Qy       1339 TCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGAT 1398
Db       1574 ---------AAACCCCGCACCTCTGCTGAGGATGCCC---CCTCAGAGGAAGTAGCAGAG 1621

Qy       1399 GAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTC 1458
Db       1622 GAGAAGAGCTACCAGTGTGAGCTCACGGTGGACGACATCATGCCTGCTGTGAAGACAGTC 1681

Qy       1459 ATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTA 1518
Db       1682 ATCCGCTCCATCAGGATTCTCAAGTTCCTGGTGGCCAAAAGGAAATTCAAGGAGACACTG 1741

Qy       1519 CGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTG 1578
Db       1742 CGACCGTACGACGTGAAGGACGTCATTGAGCAGTACTCAGCAGGCCACCTGGACATGCTG 1801

Qy       1579 TGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGC---AAATC 1635
Db       1802 GGCCGGATCAAGAGCCTGCAAACTCGGGTGGACCAAATTGTGGGTCGGGGGCCCGGGGAC 1861

Qy       1636 ACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTC 1695
Db       1862 AGGAAGGCCCGGGAGAAGGGCGACAAGGGGCCCTCCGACGCGGAGGTGGTGGATGAAATC 1921

Qy       1696 AGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGCTG 1755
Db       1922 AGCATGATGGGACGCGTGGTCAAGGTGGAGAAGCAGGTGCAGTCCATCGAGCACAAGCTG 1981

Qy       1756 GACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCT 1815
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Db       1982 GACCTGCTGTTGGGCTTCTATTCGCGCTGCCTGC------GCTCTGGCACCTCGGCCAGC 2035

Qy       1816 TTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCT 1875

Db       2036 CTGGGCGCCGTGCAAGTGCCGCTGTTCGACCCCGACATCACCTCCGACTACCACAGCCCT 2095

Qy       1876 GTGGATAGCAAAGATCTTTCGGGTTCCGCACAAA 1909

Db       2096 GTGGACCACGAGGACATCTCCGTCTCCGCACAGA 2129
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RESULT 13
ADE31698
ID ADE31698 standard; DNA; 2335 BP.
XX
AC ADE31698;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 32394 gene #SEQ ID 55.
XX
KW Antiarteriosclerotic; cardiant; vasotropic; antiinflammatory;
KW thrombolytic; antiarrhythmic; antianginal; hypotensive; gene therapy;
KW cardiovascular; disorder; ischaemia; aortic bending;
KW vascular heart disease; endocarditis; atrial fibrillation; heart failure;
KW angina; cardiomyopathy; cardiac death; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003065984-A2.
XX
PD 14-AUG-2003.
XX
PF 29-JAN-2003; 2003WO-US002571.
XX
PR 01-FEB-2002; 2002US-0353224P.
PR 15-MAR-2002; 2002US-0364529P.
PR 19-APR-2002; 2002US-0373861P.
PR 29-APR-2002; 2002US-0376287P.
PR 12-JUN-2002; 2002US-0388080P.
PR 24-JUN-2002; 2002US-0390971P.
PR 03-JUL-2002; 2002US-0394130P.
PR 10-JUL-2002; 2002US-0394797P.
PR 21-AUG-2002; 2002US-0404904P.
PR 23-AUG-2002; 2002US-0405450P.
PR 04-SEP-2002; 2002US-0408070P.
PR 06-NOV-2002; 2002US-0424300P.
PR 05-DEC-2002; 2002US-0431042P.
PR 05-DEC-2002; 2002US-0431079P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Logan TJ, Chun M, Galvin KM, Healy A, Acton SL, Donaghue M;
PI Stagliano N, Perodin J, Rodrigue-Way A;
XX
DR WPI; 2003-731468/69.
DR P-PSDB; ADE31699.
XX
PT Identifying a compound capable of treating a cardiovascular disorder
PT (e.g. atherosclerosis) comprises assaying the ability of the compound to
PT modulate the expression or activity of e.g. 1682, 6169 or 6193
PT polypeptide or nucleic acid.
XX
PS Disclosure; SEQ ID NO 55; 328pp; English.
XX
CC The invention relates to a method for identifying a compound capable of
CC treating a cardiovascular disorder. The present invention identifies the
CC differential expression of 1682, 6169, 6193, 7771, 14395, 29002, 33216,
CC 43726, 69292, 21656, 32427, 2402, 7747, 1720, 9151, 60491, 1371, 7077,
CC 33207, 1419, 18036, 16105, 38650, 14245, 58848, 1870, 25856, 32394, 3484,
CC 345, 9252, 9135, 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912,
CC 2868, 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914, 51130,
CC 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474, 9792, 15400, 1452 or
CC 6585 genes in cardiovascular disease states. The methods are useful in
CC diagnosing, preventing and treating cardiovascular disorders, such as
CC atherosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury,
CC restenosis, arterial inflammation, vascular wall remodeling, coronary
CC microembolism, tachycardia, bradycardia, pressure overload, aortic
CC bending, coronary artery ligation, vascular heart disease, valvular
CC disease, including but not limited to, valvular degeneration caused by
CC calcification, rheumatic heart disease, endocarditis, or complications of
CC artificial valves; atrial fibrillation, long-QT syndrome, congestive
CC heart failure, sinus node dysfunction, angina, heart failure,
CC hypertension, atrial fibrillation, atrial flutter, pericardial disease,
CC including but not limited to, pericardial effusion and pericarditis;
CC cardiomyopathies, e.g. dilated cardiomyopathy or idiopathic
CC cardiomyopathy, myocardial infarction, coronary artery disease, coronary
CC artery spasm, ischaemic disease, arrhythmia, sudden cardiac death and
CC cardiovascular developmental disorders. The methods may also be used for
CC identifying compounds that modulate cardiovascular disorders. Sequences
CC given in ADE31644-ADE31769 represent the genes and proteins that may be
CC regulated by a compound of the invention.
XX
SQ Sequence 2335 BP; 396 A; 812 C; 719 G; 408 T; 0 U; 0 Other;

Query Match 19.2%; Score 518.4; DB 10; Length 2335;
Best Local Similarity 60.1%; Pred. No. 8.5e-142;
Matches 1103; Conservative 0; Mismatches 566; Indels 165; Gaps 8;

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Qy        217 TACCGGCGGGTGCAGAACTACCTGTACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTC 276

Db        320 TACCGCCGCCTGCAGAACTGGGTCTACAACGTGCTGGAGCGGCCCCGCGGCTGGGCCTTC 379

Qy        277 ATCTACCACGCTTTCGTTTTTCTCCTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCT 336

Db        380 GTCTACCACGTCTTCATATTTTTGCTGGTCTTCAGCTGCCTGGTGCTGTCTGTGCTGTCC 439

Qy        337 ACCATCCCTGAGCACACAAAATTGGCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATG 396

Db        440 ACTATCCAGGAGCACCAGGAACTTGCCAACGAGTGTCTCCTCATCTTGGAATTCGTGATG 499

Qy        397 ATTGTCGTCTTTGGTTTGGAGTTCATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGA 456

Db        500 ATCGTGGTTTTCGGCTTGGAGTACATCGTCCGGGTCTGGTCCGCCGGATGCTGCTGCCGC 559

Qy        457 TATAGAGGATGGCAAGGAAGACTGAGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACC 516

Db        560 TACCGAGGATGGCAGGGTCGCTTCCGCTTTGCCAGAAAGCCCTTCTGTGTCATCGACTTC 619

Qy        517 ATTGTTCTTATCGCTTCAATAGCAGTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCC 576

Db        620 ATCGTGTTCGTGGCCTCGGTGGCCGTCATCGCCGCGGGTACCCAGGGCAACATCTTCGCC 679

Qy        577 ACGTCTGCACTCAGAAGTCTCCGTTTCCTACAGATCCTCCGCATGGTGCGCATGGACCGA 636

Db        680 ACGTCCGCGCTGCGCAGCATGCGCTTCCTGCAGATCCTGCGCATGGTGCGCATGGACCGC 739

Qy        637 AGGGGAGGCACTTGGAAATTACTGGGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATC 696

Db        740 CGCGGCGGCACCTGGAAGCTGCTGGGCTCAGTGGTCTACGCGCATAGCAAGGAGCTGATC 799

Qy        697 ACAGCTTGGTACATAGGATTTTTGGTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTG 756

Db        800 ACCGCCTGGTACATCGGGTTCCTGGTGCTCATCTTCGCCTCCTTCCTGGTCTACCTGGCC 859

Qy        757 GAAAAGGATGCCAATAAAGAGTTTTCTACATATGCAGATGCTCTCTGGTGGGGCACAATT 816

Db        860 GAGAAGGACGCCAACTCCGACTTCTCCTCCTACGCCGACTCGCTCTGGTGGGGGACGATT 919

Qy        817 ACATTGACAACTATTGGCTATGGAGACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTT 876

Db        920 ACATTGACAACCATCGGCTATGGTGACAAGACACCGCACACATGGCTGGGCAGGGTCCTG 979

Qy        877 TCTGCAGGCTTTGCACTCCTTGGCATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGC 936
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Db        980 GCTGCTGGCTTCGCCTTACTGGGCATCTCTTTCTTTGCCCTGCCTGCCGGCATCCTAGGC 1039

Qy        937 TCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAGAAACACTTTGAGAAAAGAAGG 996

Db       1040 TCCGGCTTTGCCCTGAAGGTCCAGGAGCAGCACCGGCAGAAGCACTTCGAGAAGCGGAGG 1099

Qy        997 AACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCT 1056

Db       1100 ATGCCGGCAGCCAACCTCATCCAGGCTGCCTGGCGCCTGTACTCCACCGATATGAGCCGG 1159

Qy       1057 GTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGCACACCTGCAGC---------- 1107

Db       1160 GCCTACCTGACAGCCACCTGGTACTACTATGACAGTATCCTCCCATCCTTCAGAGAGCTG 1219

Qy       1108 CCTACCAAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGCTA--------------- 1152

Db       1220 GCCCTCTTGTTTGAGCACGTGCAACGGGCCCGCAATGGGGGCCTACGGCCCCTGGAGGTG 1279

Qy       1153 ------------------------------------------------------------ 1152

Db       1280 CGGCGGGCGCCGGTACCCGACGGAGCACCCTCCCGTTACCCGCCCGTTGCCACCTGCCAC 1339

Qy       1153 ----------------------------------------------AGTTTTAAGGAGCGA 1167

Db       1340 CGGCCGGGCAGCACCTCCTTCTGCCCTGGGGAAAGCAGCCGGATGGGCATCAAAGACCGC 1399

Qy       1168 GTGCGCATGGCTAGCCCCAGGGGCCAGA------GTATTAAGAGCCGACAAGCCTCAGTA 1221

Db       1400 ATCCGCATGGGCAGCTCCCAGCGGCGGACGGGTCCTTCCAAGCAGCAGCTGGCACCTCCA 1459

Qy       1222 GGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAGG---GCAGTCCCACCAAAGTG 1278

Db       1460 ACAATGCCCACCTCCCCAAGCAGCGAGCAGGTGGGTGAGGCCACCAGCCCCACCAAGGTG 1519

Qy       1279 CAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGT 1338

Db       1520 CAAAAGAGCTGGAGCTTCAATGACCGCACCCGCTTCCGGGCATCTCTGAGACTC------ 1573

Qy       1339 TCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGAT 1398

Db       1574 ---------AAACCCCGCACCTCTGCTGAGGATGCCC---CCTCAGAGGAAGTAGCAGAG 1621

Qy       1399 GAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTC 1458

Db       1622 GAGAAGAGCTACCAGTGTGAGCTCACGGTGGACGACATCATGCCTGCTGTGAAGACAGTC 1681

Qy       1459 ATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTA 1518

Db       1682 ATCCGCTCCATCAGGATTCTCAAGTTCCTGGTGGCCAAAAGGAAATTCAAGGAGACACTG 1741

Qy       1519 CGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTG 1578

Db       1742 CGACCGTACGACGTGAAGGACGTCATTGAGCAGTACTCAGCAGGCCACCTGGACATGCTG 1801

Qy       1579 TGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGC---AAATC 1635

Db       1802 GGCCGGATCAAGAGCCTGCAAACTCGGGTGGACCAAATTGTGGGTCGGGGGCCCGGGGAC 1861

Qy       1636 ACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTC 1695

Db       1862 AGGAAGGCCCGGGAGAAGGGCGACAAGGGGCCCTCCGACGCGGAGGTGGTGGATGAAATC 1921

Qy       1696 AGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGCTG 1755

Db       1922 AGCATGATGGGACGCGTGGTCAAGGTGGAGAAGCAGGTGCAGTCCATCGAGCACAAGCTG 1981

Qy       1756 GACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCT 1815

Db       1982 GACCTGCTGTTGGGCTTCTATTCGCGCTGCCTGC------GCTCTGGCACCTCGGCCAGC 2035

Qy       1816 TTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCT 1875

Db       2036 CTGGGCGCCGTGCAAGTGCCGCTGTTCGACCCCGACATCACCTCCGACTACCACAGCCCT 2095

Qy       1876 GTGGATAGCAAAGATCTTTCGGGTTCCGCACAAA 1909

Db       2096 GTGGACCACGAGGACATCTCCGTCTCCGCACAGA 2129


RESULT 14
AAX57140
ID   AAX57140 standard; DNA; 2273 BP.
XX
AC   AAX57140;
XX
DT   22-JUL-1999  (first entry)
XX
DE   Mouse KCNQ2 cDNA.
XX
KW   KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
KW   benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy; JME;
KW   rolandic epilepsy; mutant; treatment; screening; epilepsy; detection;
KW   gene therapy; drug screening; ss.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2273
FT                   /*tag=  a
FT                   /product= "KCNQ2"
FT                   /note= "Partial sequence, no stop codon given"
XX
PN   WO9921875-A1.
XX
PD   06-MAY-1999.
XX
PF   23-OCT-1998;   98WO-US022375.
XX
PR   24-OCT-1997;   97US-0063147P.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
XX
PI   Singh NA,  Leppert MF,  Charlier C;
XX
DR   WPI; 1999-312938/26.
DR   P-PSDB; AAY08345.
XX
PT   Nucleic acid encoding potassium channels KCNQ2 and 3.
XX
PS   Claim 1; Page 153-156; 195pp; English.
XX
CC   This invention describes novel human and mouse potassium channel proteins
CC   KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
CC   KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
CC   prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic
CC   epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)
CC   that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
CC   in cell-free form) are used to screen for agents that can be used to
CC   treat or prevent these forms of epilepsy. Fragments of the encoding
CC   nucleic acids are used as probes or primers, either for detecting
CC   mutations or for isolation of related sequences, while the complete
CC   sequences may be used in gene therapy to provide wild-type protein.
CC   Antibodies specific for mutant or wild-type proteins are used as
CC   diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
CC   useful in rational design of drugs and therapeutically (in replacement
CC   therapies). The forms of epilepsy associated with mutations in KCNQ2 and
CC   3 sequences can now be diagnosed early (before symptoms are manifest),
CC   and better treatment options will be available
XX
SQ   Sequence 2273 BP; 486 A; 670 C; 653 G; 448 T; 0 U; 16 Other;

  Query Match           19.2%;  Score 516;  DB 2;  Length 2273;
  Best Local Similarity  57.6%;  Pred. No. 4.3e-141;
  Matches 1030;  Conservative    2;  Mismatches  684;  Indels   72;  Gaps    4;

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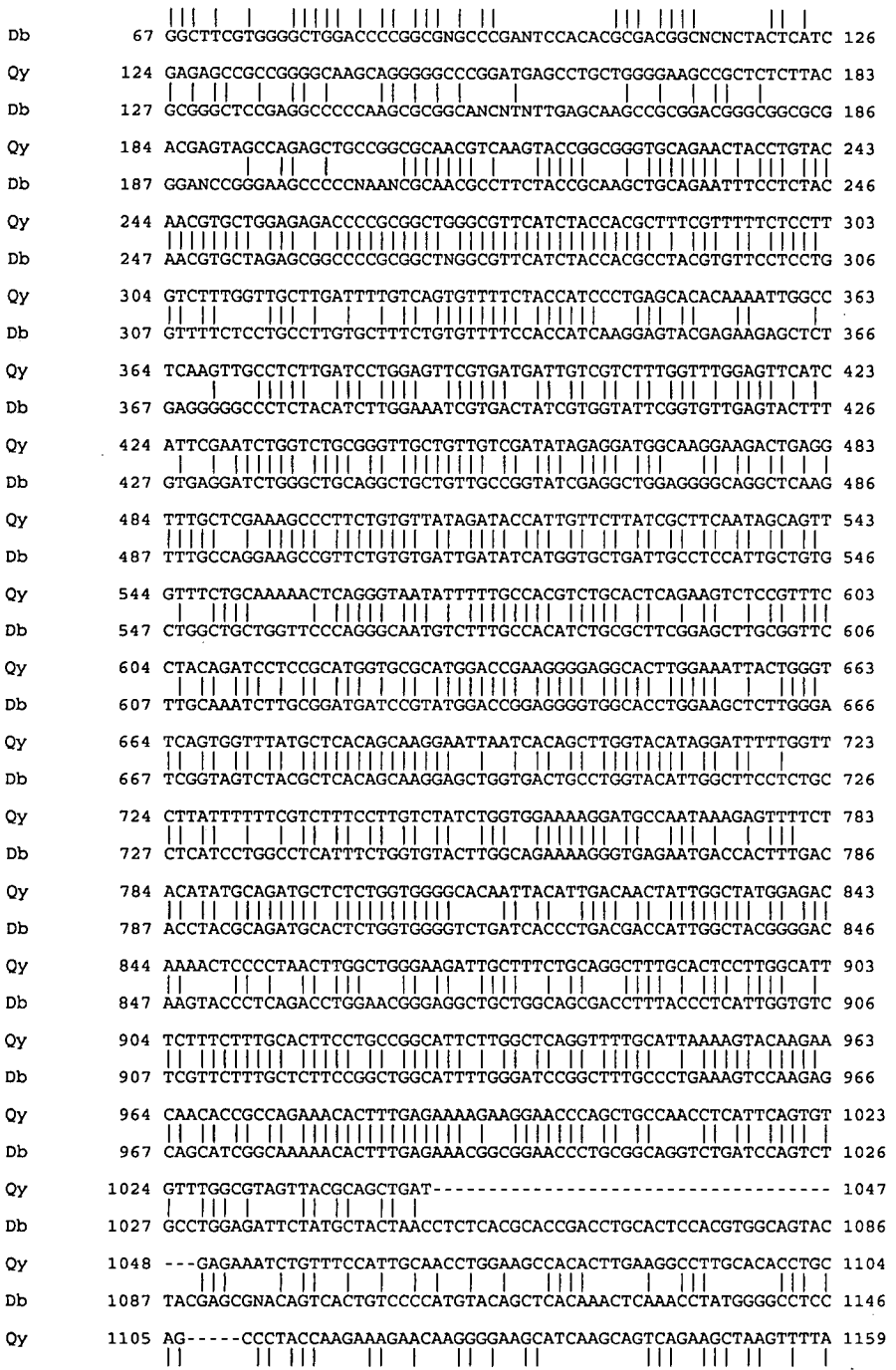
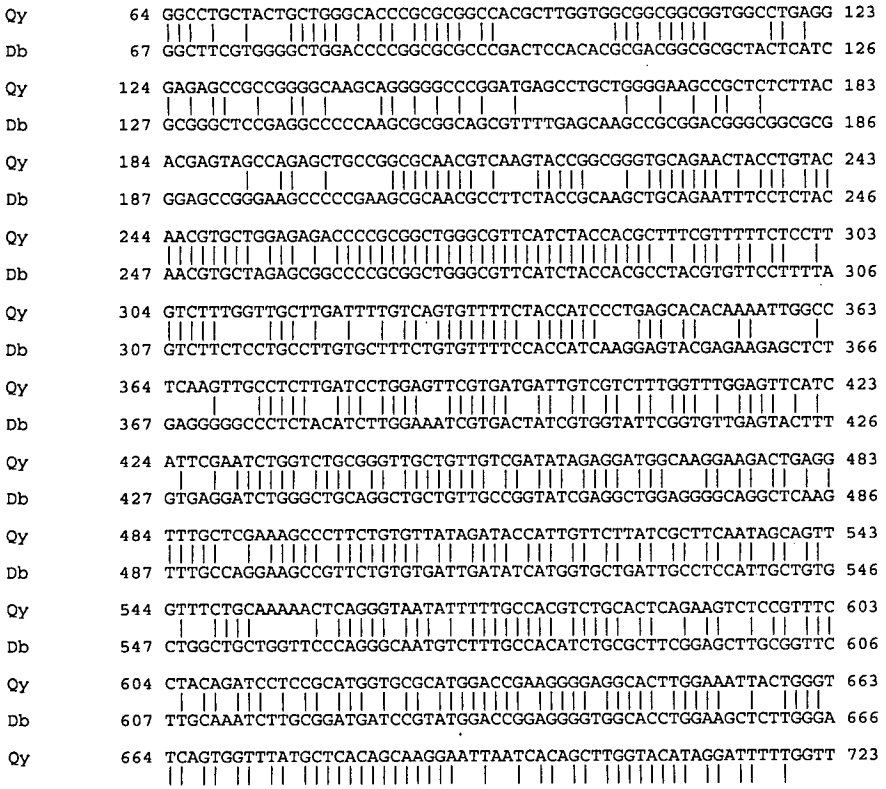
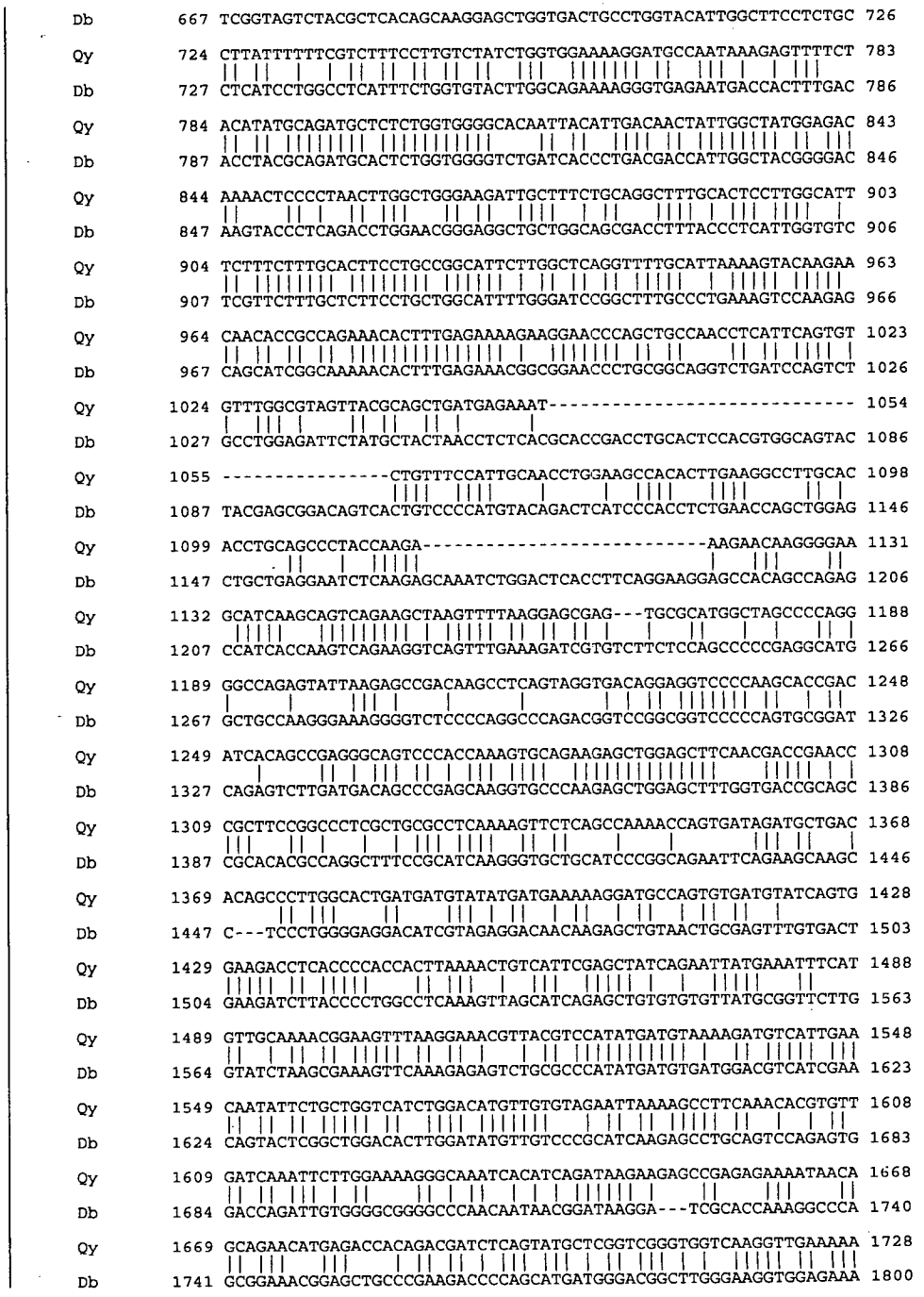


RESULT 15
AAX26588
ID AAX26588 standard; DNA; 2169 BP.
XX
AC AAX26588;
XX
DT 16-JUN-1999 (first entry)
XX
DE Nucleotide sequence of murine KCNQ2 (formerly known as (KvLR1).
XX
KW KCNQ protein; nervous system-specific potassium channel;
KW neuronal excitability; neurotransmitter release; KCNQ modulator; ataxia;
KW myokymia; seizure; Alzheimer's disease; Parkinson's disease;
KW age-associated memory loss; learning deficiency; motor neuron disease;
KW epilepsy; stroke; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 1. .2169
FT /*tag= a
XX
PN WO9907832-A1.
XX
PD 18-FEB-1999.
XX

PF 26-JUN-1998; 98WO-US013276.
XX
PR 12-AUG-1997; 97US-0055599P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Blanar MA, Dworetzky S, Yang W, Levesque PC, Gribkoff VK;
PI Neubauer MG, Little WA;
XX
DR WPI; 1999-190047/16.
DR P-PSDB; AAY01530.
XX
PT New potassium channels, KCNQ2 and KCNQ3 - may be involved in
PT neurotransmission and neuroprotection, used to treat, e.g. ataxia.
XX
PS Claim 7; Fig 10A-D; 64pp; English.
XX
CC The present sequence encodes murine KCNQ2/KvLR1. KCNQ proteins are
CC nervous system-specific potassium channels. In neurons, potassium
CC channels regulate neuronal excitability, action potential shape and
CC firing pattern, and neurotransmitter release. KCNQ modulators may be used
CC to treat disorders such as ataxia, myokymia, seizures, Alzheimer's
CC disease, Parkinson's disease, age-associated memory loss, learning
CC deficiencies, motor neuron diseases, epilepsy, and stroke
XX
SQ Sequence 2169 BP; 466 A; 622 C; 635 G; 446 T; 0 U; 0 Other;

Query Match 18.9%; Score 510; DB 2; Length 2169;
Best Local Similarity 58.1%; Pred. No. 2.5e-139;
Matches 1043; Conservative 0; Mismatches 670; Indels 81; Gaps 5;





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Qy       1729 CAGGTACAGTCCATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAG 1782
              |||||   ||||||||    ||||| |||| | |  |   |||||||  ||||
Db       1801 CAGGTCTTGTCCATGGAAAAGAAGCTCGACTTCTTGGTGAGCATCTATACACAG 1854
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Perfect score: 2694
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

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2	2694	100.0	2694	9	US-09-810-796-2	Sequence 2, Appli
3	2694	100.0	2694	19	US-10-948-493-1	Sequence 1, Appli
4	2690.4	99.9	3071	9	US-09-810-796-1	Sequence 1, Appli
5	2689.2	99.8	3137	18	US-10-661-629-1	Sequence 1, Appli
6	2681.2	99.5	3074	9	US-09-813-148-1	Sequence 1, Appli
7	2630	97.6	2667	9	US-09-810-796-3	Sequence 3, Appli
8	2625.2	97.4	2772	9	US-09-825-147-1	Sequence 1, Appli
9	2625.2	97.4	2772	18	US-10-803-268-1	Sequence 1, Appli
10	2625.2	97.4	3111	9	US-09-825-147-3	Sequence 3, Appli
11	2625.2	97.4	3111	18	US-10-803-268-3	Sequence 3, Appli
12	518.4	19.2	2335	17	US-10-353-690-55	Sequence 55, Appl
13	518.4	19.2	2335	19	US-10-850-928-1	Sequence 1, Appli
14	516	19.2	2273	16	US-10-096-578-88	Sequence 88, Appl
15	510	18.9	2169	13	US-10-128-870-22	Sequence 22, Appl
16	510	18.9	2169	14	US-10-131-685-22	Sequence 22, Appl
17	509.8	18.9	582	15	US-10-313-542-303	Sequence 303, App
18	500.6	18.6	7411	18	US-10-335-053-6	Sequence 6, Appli
19	500.6	18.6	7420	17	US-10-295-027-281	Sequence 281, App
20	500.6	18.6	7420	18	US-10-643-795A-75	Sequence 75, Appl
21	500.6	18.6	7420	19	US-10-948-518-75	Sequence 75, Appl
22	500.6	18.6	7863	15	US-10-084-817-335	Sequence 335, App
23	478.4	17.8	5595	18	US-10-820-307-8	Sequence 8, Appli
24	465.8	17.3	2766	18	US-10-820-307-6	Sequence 6, Appli
25	465.4	17.3	896	13	US-10-128-870-1	Sequence 1, Appli
26	465.4	17.3	896	14	US-10-131-685-1	Sequence 1, Appli
27	465	17.3	548	10	US-09-826-734-269	Sequence 269, App
28	464	17.2	2814	16	US-10-096-578-90	Sequence 90, Appl
29	460.8	17.1	2565	13	US-10-128-870-26	Sequence 26, Appl
30	460.8	17.1	2565	14	US-10-131-685-26	Sequence 26, Appl
31	460.8	17.1	2914	16	US-10-096-578-6	Sequence 6, Appli
32	457.4	17.0	2755	18	US-10-820-307-4	Sequence 4, Appli
33	455.8	16.9	1848	18	US-10-744-796-5	Sequence 5, Appli
34	454.2	16.9	4512	15	US-10-084-817-334	Sequence 334, App
35	452	16.8	575	15	US-10-313-542-305	Sequence 305, App
36	432.2	16.0	1878	18	US-10-744-796-3	Sequence 3, Appli
37	432.2	16.0	4596	18	US-10-723-860-7636	Sequence 7636, Ap
38	425.4	15.8	455	17	US-10-242-535A-25396	Sequence 25396, A
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40	425	15.8	3287	13	US-10-128-870-19	Sequence 19, Appl
41	425	15.8	3287	14	US-10-131-685-19	Sequence 19, Appl
42	423.4	15.7	1425	10	US-09-960-706-511	Sequence 511, App
43	423.4	15.7	1425	10	US-09-873-319-313	Sequence 313, App
44	423.4	15.7	1425	16	US-10-116-712-662	Sequence 662, App
45	423.4	15.7	1932	18	US-10-744-796-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-866-020-1
; Sequence 1, Application US/09866020
; Publication No. US20020040000A1
; GENERAL INFORMATION:
; APPLICANT: DWORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIBKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 3053-4091US1
; CURRENT APPLICATION NUMBER: US/09/866,020
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/207,389
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-020-1

Query Match 100.0%; Score 2694; DB 9; Length 2694;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
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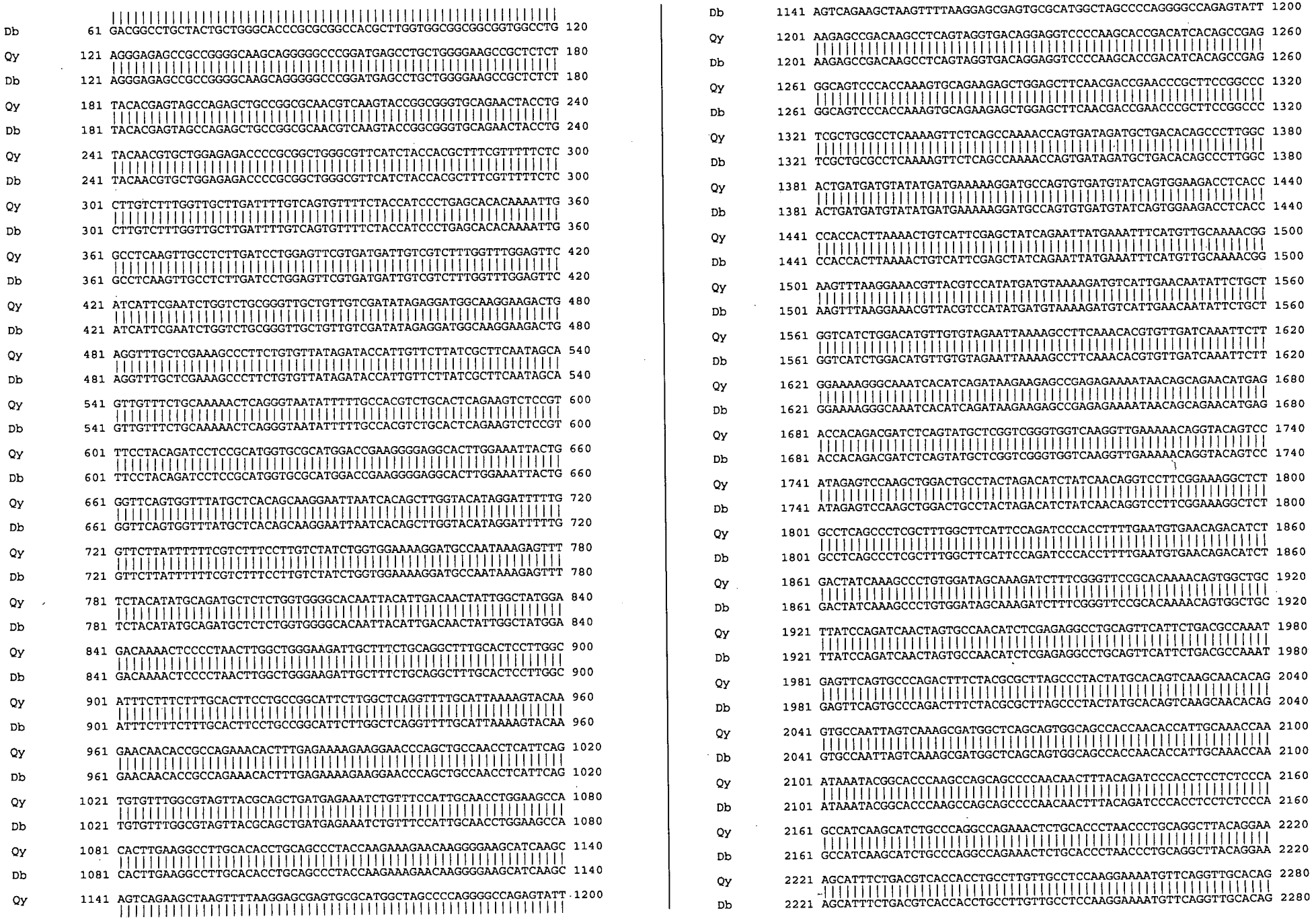
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Db 121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
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Db 721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
Qy 781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
Db 781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
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Db 1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
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Db 1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
Qy 1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
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Db 1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
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Db 1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
Qy 1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
Db 1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
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Db 1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
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Db 1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
Qy 1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
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Qy 2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
Db 2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
Qy 2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
Db 2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
Qy 2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
Db 2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
Qy 2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280
Db 2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280

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Db       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340

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Db       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400

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Db       2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460

Qy       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
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RESULT 2
US-09-810-796-2
; Sequence 2, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAgen, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly-rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-1 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(2694)
; OTHER INFORMATION: KCNQ5-1
US-09-810-796-2

Query Match 100.0%; Score 2694; DB 9; Length 2694;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
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Db        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900

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Db        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960

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Db       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140

Qy       1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
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Db       1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200

Qy       1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
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Db       1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260

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Qy       1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
Db       1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
Qy       1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
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Qy       2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280
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Db       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
Qy       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
Db       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
Qy       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
Db       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
Qy       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
Db       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
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RESULT 3
US-10-948-493-1
; Sequence 1, Application US/10948493
; Publication No. US20050064491A1
; GENERAL INFORMATION:
; APPLICANT: DWORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIBKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: D0023 DIV
; CURRENT APPLICATION NUMBER: US/10/948,493
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: 60/207,389
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-948-493-1

Query Match 100.0%; Score 2694; DB 19; Length 2694;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
Db          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
Db         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
Db        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
Db        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
Db        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
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Db        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
Db        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
Db        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
Db        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
Db        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
Db        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
Db        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
Db        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
Qy        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
Db        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
Qy        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
Db        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
Db        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
Db        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Db       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Qy       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
Db       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
Qy       1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
Db       1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
Qy       1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
Db       1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
Qy       1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320
Db       1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320
Qy       1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380
Db       1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380
Qy       1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440
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Db       1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440
Qy       1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500
Db       1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500
Qy       1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560
Db       1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560
Qy       1561 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620
Db       1561 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620
Qy       1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680
Db       1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680
Qy       1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
Db       1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
Qy       1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
Db       1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
Qy       1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
Db       1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
Qy       1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
Db       1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
Qy       1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
Db       1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
Qy       1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
Db       1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
Qy       2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
Db       2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
Qy       2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
Db       2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
Qy       2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
Db       2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
Qy       2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280
Db       2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280
Qy       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
Db       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
Qy       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400
Db       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400
Qy       2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460
Db       2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460
Qy       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
Db       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
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Qy       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580

Qy       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640

Qy       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694


RESULT 4
US-09-810-796-1
; Sequence 1, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
;  APPLICANT: Jegla, Timothy James
;  APPLICANT:  ICAgen, Inc.
;  TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
;  FILE REFERENCE: 018512-005010US
;  CURRENT APPLICATION NUMBER: US/09/810,796
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: US 60/190,954
;  PRIOR FILING DATE: 2000-03-21
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 3071
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: human outwardly rectifying, voltage-gated
;   OTHER INFORMATION: potassium channel KCNQ5-1
;   NAME/KEY: CDS
;   LOCATION: (10)..(2703)
;   OTHER INFORMATION: KCNQ5-1
US-09-810-796-1

  Query Match           99.9%;  Score 2690.4;  DB 9;  Length 3071;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 2691;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 69

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 129

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 189

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 249

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 309

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 369

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 429

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 489

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 549

Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 609

Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 669

Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 729

Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 789

Qy        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 849

Qy        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 909

Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 969

Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1029

Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1089

Qy       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1149

Qy       1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1150 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1209

Qy       1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1210 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1269

Qy       1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1329

Qy       1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1389

Qy       1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1449

Qy       1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1509

Qy       1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560
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Db       1510 AAGTTTAAGGAAACRTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1569

Qy       1561 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1570 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1629

Qy       1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1630 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1689

Qy       1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1690 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1749

Qy       1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1750 ATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1809

Qy       1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
             |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1810 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGTTCCCACCTTTTGAATGTGAACAGACATCT 1869

Qy       1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1870 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1929

Qy       1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1930 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1989

Qy       1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1990 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2049

Qy       2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2050 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2109

Qy       2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2110 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2169

Qy       2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2170 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2229

Qy       2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2230 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2289

Qy       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2290 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2349

Qy       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2350 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2409

Qy       2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2410 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2469

Qy       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2470 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2529

Qy       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2530 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2589

Qy       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       2590 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2649

Qy       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
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Db       2650 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2703


RESULT 5
US-10-661-629-1
; Sequence 1, Application US/10661629
; Publication No. US20040180405A1
; GENERAL INFORMATION:
;  APPLICANT: JENTSCH, Thomas
;  TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANN
;  FILE REFERENCE: 2815-0236P
;  CURRENT APPLICATION NUMBER: US/10/661,629
;  CURRENT FILING DATE:  2003-09-15
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 3137
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2691)
US-10-661-629-1

  Query Match             99.8%;  Score 2689.2;  DB 18;  Length 3137;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2691;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTCGGTGGCGGCGGCGGTGGCCTG 120

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540

Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600

Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
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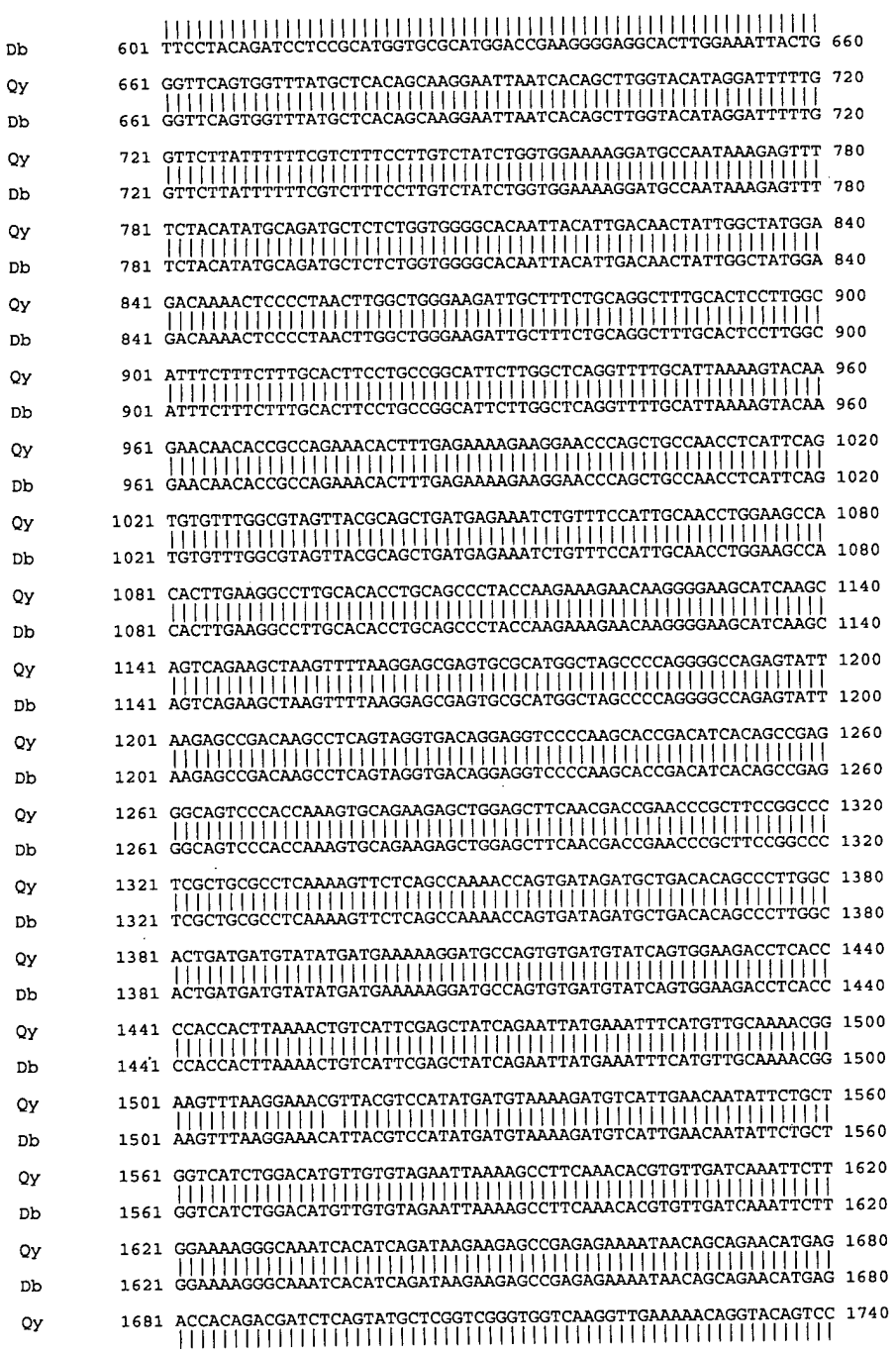

RESULT 6
US-09-813-148-1
; Sequence 1, Application US/09813148
; Patent No. US20020076809A1
; GENERAL INFORMATION:
; APPLICANT: STEINMEYER, Klaus

```
;  APPLICANT:  LERCHE, Christian
;  APPLICANT:  SCHERER, Constanze
;  APPLICANT:  SEEBOHM, Guiscard
;  APPLICANT:  BUSCH, Andreas E.
;  TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN
;  TITLE OF INVENTION:  NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
;  FILE REFERENCE: 38005-119
;  CURRENT APPLICATION NUMBER: US/09/813,148
;  CURRENT FILING DATE:  2001-03-21
;  PRIOR APPLICATION NUMBER: DE 100 13 732.6
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: US 60/194,041
;  PRIOR FILING DATE: 2000-04-03
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 3074
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-813-148-1

  Query Match             99.5%;  Score 2681.2;  DB 9;  Length 3074;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 2686;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 274

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 334

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              |||||||||||||||||||||||||||||||||||||||||||||||| |   |  ||||||
Db        335 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGAAGCCGCCTCTCT 394

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
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Db        395 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 454

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        455 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTCCTC 514

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 574

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        575 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 634

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        635 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 694

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        695 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 754

Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        755 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 814

Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        815 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 874

Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        875 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 934

Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        935 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 994

Qy        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
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Db        995 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 1054

Qy        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
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Db       1055 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 1114

Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
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Db       1115 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 1174

Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
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Db       1175 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1234

Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1235 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1294

Qy       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1295 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1354

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Qy       1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
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Db       1415 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1474

Qy       1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1475 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1534

Qy       1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1535 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1594

Qy       1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440
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Db       1595 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1654

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Db       1655 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1714

Qy       1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560
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Db       1715 AAGTTTAAGGAAACATTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1774

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Db       1775 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1834

Qy       1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1835 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1894

Qy       1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1895 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1954

Qy       1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
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Db       1955 ATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 2014

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Qy       1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
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Db       2135 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 2194

Qy       1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
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Db       2435 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2494

Qy       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2495 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2554

Qy       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2555 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2614

Qy       2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2615 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2674

Qy       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
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Db       2675 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2734

Qy       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2735 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2794

Qy       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2795 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2854

Qy       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
                ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2855 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2908
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RESULT 7
US-09-810-796-3
; Sequence 3, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAgen, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21

; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-2 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(2667)
; OTHER INFORMATION: KCNQ5-2
US-09-810-796-3

Query Match 97.6%; Score 2630; DB 9; Length 2667;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2667; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

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Db          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540

Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600

Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660

Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
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Db        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720

Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
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Db        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780

Qy        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
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Db        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
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Qy       841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
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Db       841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900

Qy       901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960

Qy       961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
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Db       961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020

Qy      1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
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Db      1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080

Qy      1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
            ||||||||||||||||||||||||||||||||
Db      1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAA---------------------------- 1115

Qy      1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1116 --TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1173

Qy      1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1174 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1233

Qy      1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320
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Db      1234 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1293

Qy      1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380
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Db      1294 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1353

Qy      1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1354 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1413

Qy      1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1414 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1473

Qy      1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560
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Db      1474 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1533

Qy      1561 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1534 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1593

Qy      1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1594 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1653

Qy      1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
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Db      1654 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1713

Qy      1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
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Db      1714 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1773

Qy      1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1774 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1833

Qy      1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
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Db      1834 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1893

Qy      1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
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Db      1894 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1953

Qy      1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
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Db      1954 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2013

Qy      2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
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Db      2014 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2073

Qy      2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
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Db      2074 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2133

Qy      2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
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Db      2134 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2193

Qy      2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280
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Db      2194 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2253

Qy      2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
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Db      2254 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2313

Qy      2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400
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Db      2314 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2373

Qy      2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460
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Db      2374 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2433

Qy      2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
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Db      2434 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2493

Qy      2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
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Db      2494 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2553

Qy      2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
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Qy      2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
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Db      2614 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2667
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RESULT 8
US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3

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;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 2772
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-825-147-1

  Query Match             97.4%;  Score 2625.2;  DB 9;  Length 2772;
  Best Local Similarity   98.9%;  Pred. No. 0;
  Matches 2664;  Conservative    0;  Mismatches    3;  Indels   27;  Gaps    1;

Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
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Db        106 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 165

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Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 405

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 465

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
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Db        466 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 525

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
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Db        526 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 585

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
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Db        646 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 705

Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 765

Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
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Db        766 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 825

Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
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Db        826 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 885

Qy        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
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Db        886 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 945

Qy        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 1005

Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       1006 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 1065

Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
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Db       1066 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1125

Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
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Db       1126 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1185

Qy       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
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Db       1186 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAA---------------------------- 1220

Qy       1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
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Db       1221 --TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1278

Qy       1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1338

Qy       1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320
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Db       1339 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1398

Qy       1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1458

Qy       1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1518

Qy       1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500
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Db       1519 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1578

Qy       1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1579 AAGTTTAAGGAAACATTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1638

Qy       1561 GGTCATCTGGACATGTTGTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1639 GGTCATCTGGACATGTTGTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1698

Qy       1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1699 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1758

Qy       1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
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Db       1759 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1818

Qy       1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
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Db       1819 ATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1878

Qy       1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
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Db       1879 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1938

Qy       1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1939 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1998

Qy       1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
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Db       1999 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 2058

Qy       1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2059 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2118
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Qy       2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
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Db       2119 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2178

Qy       2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2179 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2238

Qy       2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2239 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2298

Qy       2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280
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Db       2299 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2358

Qy       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
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Db       2359 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2418

Qy       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400
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Db       2419 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2478

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Db       2479 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2538

Qy       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
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Db       2599 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2658

Qy       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
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Db       2659 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2718

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RESULT 9
US-10-803-268-1
; Sequence 1, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
;  APPLICANT: Hu, Yi
;  APPLICANT:  Kieke, James Alvin
;  APPLICANT:  Turner, C. Alexander Jr.
;  APPLICANT:  Nehls, Michael C.
;  APPLICANT:  Friedrich, Glenn
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: Novel Human Ion Channel Protein and
;  TITLE OF INVENTION:  Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0160-USA
;  CURRENT APPLICATION NUMBER: US/10/803,268
;  CURRENT FILING DATE:  2004-03-18
;  PRIOR APPLICATION NUMBER: US/09/825,147
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: US 60/194,255
;  PRIOR FILING DATE: 2000-04-03
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 2772
;   TYPE: DNA
;   ORGANISM: homo sapiens
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US-10-803-268-1

Query Match 97.4%; Score 2625.2; DB 18; Length 2772;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

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Db        106 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 165

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              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        166 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTCGGTGGCGGCGGCGGTGGCCTG 225

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
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Db        226 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 285

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
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Db        346 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 405

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Db        406 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 465

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Db        466 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 525

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Db        826 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 885

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Db       1186 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAA---------------------------- 1220

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Db       1221 --TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1278

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Db       1279 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1338

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RESULT 10
US-09-825-147-3
; Sequence 3, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-3

Query Match 97.4%; Score 2625.2; DB 9; Length 3111;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

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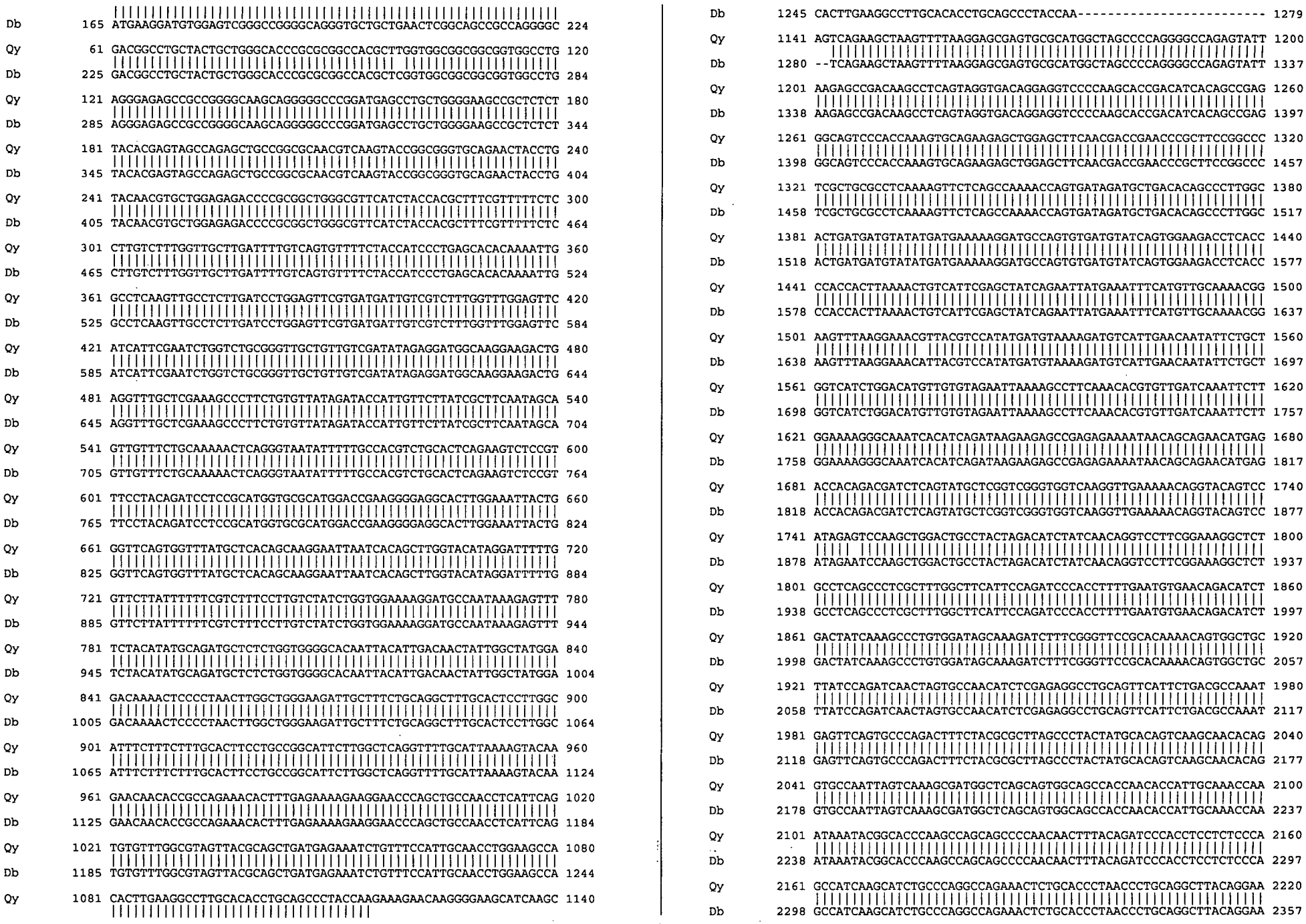
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Qy 781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
Db 945 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 1004
Qy 841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
Db 1005 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 1064
Qy 901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
Db 1065 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 1124
Qy 961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
Db 1125 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1184
Qy 1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Db 1185 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1244
Qy 1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
Db 1245 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAA---------- 1279
Qy 1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
Db 1280 --TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1337
Qy 1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
Db 1338 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1397
Qy 1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320
Db 1398 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1457
Qy 1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380
Db 1458 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1517
Qy 1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440
Db 1518 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1577
Qy 1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500
Db 1578 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1637
Qy 1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560
Db 1638 AAGTTTAAGGAAACATTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1697
Qy 1561 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620
Db 1698 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1757
Qy 1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680
Db 1758 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1817
Qy 1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
Db 1818 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1877
Qy 1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
Db 1878 ATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1937
Qy 1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
Db 1938 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1997
Qy 1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
Db 1998 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 2057
Qy 1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
Db 2058 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 2117
Qy 1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
Db 2118 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2177
Qy 2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
Db 2178 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2237
Qy 2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
Db 2238 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2297
Qy 2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
Db 2298 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2357

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Qy       2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2358 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2417

Qy       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2418 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2477

Qy       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2478 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2537

Qy       2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2538 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2597

Qy       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2598 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2657

Qy       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2658 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2717

Qy       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2718 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2777

Qy       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2778 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2831
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RESULT 11
US-10-803-268-3
; Sequence 3, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-3

Query Match 97.4%; Score 2625.2; DB 18; Length 3111;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

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Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 224

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
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Db        225 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTCGGTGGCGGCGGCGGTGGCCTG 284

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 344

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 404

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 464

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 524

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 584

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 644

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 704

Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        705 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 764

Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 824

Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        825 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 884

Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        885 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 944

Qy        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        945 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 1004

Qy        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1005 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 1064

Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1065 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 1124

Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1125 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1184

Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1185 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1244

Qy       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
              ||||||||||||||||||||||||||||||||||
Db       1245 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAA---------------------------- 1279

Qy       1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1280 --TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1337
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Qy       1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1338 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1397

Qy       1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1398 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1457

Qy       1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1458 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1517

Qy       1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1518 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1577

Qy       1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1578 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1637

Qy       1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1638 AAGTTTAAGGAAACATTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1697

Qy       1561 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1698 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1757

Qy       1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1758 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1817

Qy       1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1818 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1877

Qy       1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1878 ATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1937

Qy       1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1938 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1997

Qy       1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1998 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 2057

Qy       1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2058 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 2117

Qy       1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2118 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2177

Qy       2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2178 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2237

Qy       2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2238 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2297

Qy       2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2298 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2357

Qy       2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2358 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2417

Qy       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2418 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2477

Qy       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2478 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2537

Qy       2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2538 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2597

Qy       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2598 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2657

Qy       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2658 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2717

Qy       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2718 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2777

Qy       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
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Db       2778 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2831
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RESULT 12
US-10-353-690-55
; Sequence 55, Application US/10353690
; Publication No. US20030215840A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Donoghue, Mary
; APPLICANT: Stagliano, Nancy
; APPLICANT: Perodin, Jacquelin
; APPLICANT: Rodrigue-Way, Amelie
; TITLE OF INVENTION: Methods and compositions for treating
; TITLE OF INVENTION: cardiovascular disease using 1682, 6169, 6193, 7771, 14395,
; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 1720,
; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
; TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,
; TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,
; TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,
; TITLE OF INVENTION: 9792, 15400, 1452 or 6585 molecules
; FILE REFERENCE: MPI02-018P1RNOMNIM
; CURRENT APPLICATION NUMBER: US/10/353,690
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 60/353,224
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/364,529
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/373,861
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/376,287
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 60/388,080
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: 60/390,971
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/394,130
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/394,797
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/404,904
; PRIOR FILING DATE: 2002-08-21

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;  PRIOR APPLICATION NUMBER: 60/405,450
;  PRIOR FILING DATE: 2002-08-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 55
;    LENGTH: 2335
;    TYPE: DNA
;    ORGANISM: Homo Sapiens
US-10-353-690-55

  Query Match           19.2%;  Score 518.4;  DB 17;  Length 2335;
  Best Local Similarity  60.1%;  Pred. No. 1.8e-148;
  Matches 1103;  Conservative    0;  Mismatches  566;  Indels  165;  Gaps    8;

Qy        217 TACCGGCGGGTGCAGAACTACCTGTACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTC 276
Db        320 TACCGCCGCCTGCAGAACTGGGTCTACAACGTGCTGGAGCGGCCCCGCGGCTGGGCCTTC 379

Qy        277 ATCTACCACGCTTTCGTTTTTCTCCTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCT 336
Db        380 GTCTACCACGTCTTCATATTTTTGCTGGTCTTCAGCTGCCTGGTGCTGTCTGTGCTGTCC 439

Qy        337 ACCATCCCTGAGCACACAAAATTGGCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATG 396
Db        440 ACTATCCAGGAGCACCAGGAACTTGCCAACGAGTGTCTCCTCATCTTGGAATTCGTGATG 499

Qy        397 ATTGTCGTCTTTGGTTTGGAGTTCATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGA 456
Db        500 ATCGTGGTTTTCGGCTTGGAGTACATCGTCCGGGTCTGGTCCGCCGGATGCTGCTGCCGC 559

Qy        457 TATAGAGGATGGCAAGGAAGACTGAGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACC 516
Db        560 TACCGAGGATGGCAGGGTCGCTTCCGCTTTGCCAGAAAGCCCTTCTGTGTCATCGACTTC 619

Qy        517 ATTGTTCTTATCGCTTCAATAGCAGTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCC 576
Db        620 ATCGTGTTCGTGGCCTCGGTGGCCGTCATCGCCGCGGGTACCCAGGGCAACATCTTCGCC 679

Qy        577 ACGTCTGCACTCAGAAGTCTCCGTTTCCTACAGATCCTCCGCATGGTGCGCATGGACCGA 636
Db        680 ACGTCCGCGCTGCGCAGCATGCGCTTCCTGCAGATCCTGCGCATGGTGCGCATGGACCGC 739

Qy        637 AGGGGAGGCACTTGGAAATTACTGGGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATC 696
Db        740 CGCGGCGGCACCTGGAAGCTGCTGGGCTCAGTGGTCTACGCGCATAGCAAGGAGCTGATC 799

Qy        697 ACAGCTTGGTACATAGGATTTTTGGTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTG 756
Db        800 ACCGCCTGGTACATCGGGTTCCTGGTGCTCATCTTCGCCTCCTTCCTGGTCTACCTGGCC 859

Qy        757 GAAAAGGATGCCAATAAAGAGTTTTCTACATATGCAGATGCTCTCTGGTGGGGCACAATT 816
Db        860 GAGAAGGACGCCAACTCCGACTTCTCCTCCTACGCCGACTCGCTCTGGTGGGGGACGATT 919

Qy        817 ACATTGACAACTATTGGCTATGGAGACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTT 876
Db        920 ACATTGACAACCATCGGCTATGGTGACAAGACACCGCACACATGGCTGGGCAGGGTCCTG 979

Qy        877 TCTGCAGGCTTTGCACTCCTTGGCATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGC 936
Db        980 GCTGCTGGCTTCGCCTTACTGGGCATCTCTTTCTTTGCCCTGCCTGCCGGCATCCTAGGC 1039

Qy        937 TCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAGAAACACTTTGAGAAAAGAAGG 996
Db       1040 TCCGGCTTTGCCCTGAAGGTCCAGGAGCAGCACCGGCAGAAGCACTTCGAGAAGCGGAGG 1099

Qy        997 AACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCT 1056
Db       1100 ATGCCGGCAGCCAACCTCATCCAGGCTGCCTGGCGCCTGTACTCCACCGATATGAGCCGG 1159

Qy       1057 GTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGCACACCTGCAGC--------- 1107

Db       1160 GCCTACCTGACAGCCACCTGGTACTACTATGACAGTATCCTCCCATCCTTCAGAGAGCTG 1219

Qy       1108 CCTACCAAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGCTA--------------- 1152

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Qy       1153 ------------------------------------------------------------ 1152

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Qy       1153 ----------------------------------------------AGTTTTAAGGAGCGA 1167

Db       1340 CGGCCGGGCAGCACCTCCTTCTGCCCTGGGGAAAGCAGCCGGATGGGCATCAAAGACCGC 1399

Qy       1168 GTGCGCATGGCTAGCCCCAGGGGCCAGA------GTATTAAGAGCCGACAAGCCTCAGTA 1221

Db       1400 ATCCGCATGGGCAGCTCCCAGCGGCGGACGGGTCCTTCCAAGCAGCAGCTGGCACCTCCA 1459

Qy       1222 GGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAGG---GCAGTCCCACCAAAGTG 1278

Db       1460 ACAATGCCCACCTCCCCAAGCAGCGAGCAGGTGGGTGAGGCCACCAGCCCCACCAAGGTG 1519

Qy       1279 CAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGT 1338

Db       1520 CAAAAGAGCTGGAGCTTCAATGACCGCACCCGCTTCCGGGCATCTCTGAGACTC------ 1573

Qy       1339 TCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGAT 1398

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Qy       1399 GAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTC 1458

Db       1622 GAGAAGAGCTACCAGTGTGAGCTCACGGTGGACGACATCATGCCTGCTGTGAAGACAGTC 1681

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Db       1682 ATCCGCTCCATCAGGATTCTCAAGTTCCTGGTGGCCAAAAGGAAATTCAAGGAGACACTG 1741

Qy       1519 CGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTG 1578

Db       1742 CGACCGTACGACGTGAAGGACGTCATTGAGCAGTACTCAGCAGGCCACCTGGACATGCTG 1801

Qy       1579 TGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGC---AAATC 1635

Db       1802 GGCCGGATCAAGAGCCTGCAAACTCGGGTGGACCAAATTGTGGGTCGGGGGCCCGGGGAC 1861

Qy       1636 ACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTC 1695

Db       1862 AGGAAGGCCCGGGAGAAGGGCGACAAGGGGCCCTCCGACGCGGAGGTGGTGGATGAAATC 1921

Qy       1696 AGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGCTG 1755

Db       1922 AGCATGATGGGACGCGTGGTCAAGGTGGAGAAGCAGGTGCAGTCCATCGAGCACAAGCTG 1981

Qy       1756 GACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCT 1815

Db       1982 GACCTGCTGTTGGGCTTCTATTCGCGCTGCCTGC------GCTCTGGCACCTCGGCCAGC 2035

Qy       1816 TTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCT 1875

Db       2036 CTGGGCGCCGTGCAAGTGCCGCTGTTCGACCCCGACATCACCTCCGACTACCACAGCCCT 2095

Qy       1876 GTGGATAGCAAAGATCTTTCGGGTTCCGCACAAA 1909

Db       2096 GTGGACCACGAGGACATCTCCGTCTCCGCACAGA 2129

RESULT 13
US-10-850-928-1
; Sequence 1, Application US/10850928
; Publication No. US20050037460A1
; GENERAL INFORMATION:
;  APPLICANT: JENTSCH, Thomas J.
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;  TITLE OF INVENTION: POTASSIUM CHANNELS AND GENES ENCODING THESE
;  TITLE OF INVENTION:  POTASSIUM CHANNELS
;  FILE REFERENCE: 2815-127PUS2
;  CURRENT APPLICATION NUMBER: US/10/850,928
;  CURRENT FILING DATE:  2004-05-20
;  PRIOR APPLICATION NUMBER: 09/492,361
;  PRIOR FILING DATE: 2000-01-27
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 2335
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (1)..(2335)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (83)..(2170)
US-10-850-928-1

  Query Match             19.2%;  Score 518.4;  DB 19;  Length 2335;
  Best Local Similarity   60.1%;  Pred. No. 1.8e-148;
  Matches 1103;  Conservative    0;  Mismatches  566;  Indels  165;  Gaps    8;

Qy        217 TACCGGCGGGTGCAGAACTACCTGTACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTC 276
              ||||| ||  |||||||||    | ||||||||||||||| | ||||||||||||| |||
Db        320 TACCGCCGCCTGCAGAACTGGGTCTACAACGTGCTGGAGCGGCCCCGCGGCTGGGCCTTC 379

Qy        277 ATCTACCACGCTTTCGTTTTTCTCCTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCT 336
              ||||||||  ||| | ||| | || |||||  | ||| || |  |||| ||| | ||
Db        380 GTCTACCACGTCTTCATATTTTTGCTGGTCTTCAGCTGCCTGGTGCTGTCTGTGCTGTCC 439

Qy        337 ACCATCCCTGAGCACACAAAATTGGCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATG 396
              || ||||  ||||||    || | |||       || ||| | ||| |||| |||||||||
Db        440 ACTATCCAGGAGCACCAGGAACTTGCCAACGAGTGTCTCCTCATCTTGGAATTCGTGATG 499

Qy        397 ATTGTCGTCTTTGGTTTGGAGTTCATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGA 456
              || || || || || ||||||| |||| | ||  ||||||| || || ||||| || ||
Db        500 ATCGTGGTTTTCGGCTTGGAGTACATCGTCCGGGTCTGGTCCGCCGGATGCTGCTGCCGC 559

Qy        457 TATAGAGGATGGCAAGGAAGACTGAGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACC 516
              ||  ||||||||||  ||   | | |||||  ||||||||||||||| || ||   |
Db        560 TACCGAGGATGGCAGGGTCGCTTCCGCTTTGCCAGAAAGCCCTTCTGTGTCATCGACTTC 619

Qy        517 ATTGTTCTTATCGCTTCAATAGCAGTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCC 576
              || ||  |  | || ||  | || ||  |  | ||     || ||||| || || || |||
Db        620 ATCGTGTTCGTGGCCTCGGTGGCCGTCATCGCCGCGGGTACCCAGGGCAACATCTTCGCC 679

Qy        577 ACGTCTGCACTCAGAAGTCTCCGTTTCCTACAGATCCTCCGCATGGTGCGCATGGACCGA 636
              ||||| || ||  | ||  | || ||||| |||||||| ||||||||||||||||||||
Db        680 ACGTCCGCGCTGCGCAGCATGCGCTTCCTGCAGATCCTGCGCATGGTGCGCATGGACCGC 739

Qy        637 AGGGGAGGCACTTGGAAATTACTGGGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATC 696
              | || |||||  ||||  | ||||| ||||||| || || || ||||||||  | |||
Db        740 CGCGGCGGCACCTGGAAGCTGCTGGGCTCAGTGGTCTACGCGCATAGCAAGGAGCTGATC 799

Qy        697 ACAGCTTGGTACATAGGATTTTTGGTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTG 756
              || || |||||||| || ||  |||| || || ||  | || |||||  ||||| ||||
Db        800 ACCGCCTGGTACATCGGGTTCCTGGTGCTCATCTTCGCCTCCTTCCTGGTCTACCTGGCC 859

Qy        757 GAAAAGGATGCCAATAAAGAGTTTTCTACATATGCAGATGCTCTCTGGTGGGGCACAATT 816
              || ||||| |||||    || || ||  | || || ||  | ||||||||||| || |||
Db        860 GAGAAGGACGCCAACTCCGACTTCTCCTCCTACGCCGACTCGCTCTGGTGGGGGACGATT 919

Qy        817 ACATTGACAACTATTGGCTATGGAGACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTT 876
              |||||||||| || |||||||| ||||| || || |  || |||||||| ||  | ||
Db        920 ACATTGACAACCATCGGCTATGGTGACAAGACACCGCACACATGGCTGGGCAGGGTCCTG 979

Qy        877 TCTGCAGGCTTTGCACTCCTTGGCATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGC 936
              |||| ||||| ||  | || ||||| |||||||||| || ||||||||||| || |||
Db        980 GCTGCTGGCTTCGCCTTACTGGGCATCTCTTTCTTTGCCCTGCCTGCCGGCATCCTAGGC 1039

Qy        937 TCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAGAAACACTTTGAGAAAAGAAGG 996
              || || |||||  | || || || || || ||||| ||||| ||||| |||||  | |||
Db       1040 TCCGGCTTTGCCCTGAAGGTCCAGGAGCAGCACCGGCAGAAGCACTTCGAGAAGCGGAGG 1099

Qy        997 AACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCT 1056
              |  || || |||||||||||| |||  ||  |||||     ||| |  | |||  ||
Db       1100 ATGCCGGCAGCCAACCTCATCCAGGCTGCCTGGCGCCTGTACTCCACCGATATGAGCCGG 1159

Qy       1057 GTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGCACACCTGCAGC--------- 1107
              |  | | |  || ||      |    |||  |     | | | | | | |  |
Db       1160 GCCTACCTGACAGCCACCTGGTACTACTATGACAGTATCCTCCCATCCTTCAGAGAGCTG 1219

Qy       1108 CCTACCAAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGCTA--------------- 1152
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Db       1220 GCCCTCTTGTTTGAGCACGTGCAACGGGCCCGCAATGGGGGCCTACGGCCCCTGGAGGTG 1279

Qy       1153 ------------------------------------------------------------ 1152

Db       1280 CGGCGGGCGCCGGTACCCGACGGAGCACCCTCCCGTTACCCGCCCGTTGCCACCTGCCAC 1339

Qy       1153 ---------------------------------------------AGTTTTAAGGAGCGA 1167
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Db       1340 CGGCCGGGCAGCACCTCCTTCTGCCCTGGGGAAAGCAGCCGGATGGGCATCAAAGACCGC 1399

Qy       1168 GTGCGCATGGCTAGCCCCAGGGGCCAGA------GTATTAAGAGCCGACAAGCCTCAGTA 1221
              | |||||||  ||| ||  | | | ||        |  |||   |  |  ||  |   |
Db       1400 ATCCGCATGGGCAGCTCCCAGCGGCGGACGGGTCCTTCCAAGCAGCAGCTGGCACCTCCA 1459

Qy       1222 GGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAGG---GCAGTCCCACCAAAGTG 1278
                |  |||||||||| |||       |  ||||    ||| ||||||||| |||
Db       1460 ACAATGCCCACCTCCCCAAGCAGCGAGCAGGTGGGTGAGGCCACCAGCCCCACCAAGGTG 1519

Qy       1279 CAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGT 1338
              || ||||||||||||||||| ||||| |||||||||||| | || ||| | |||
Db       1520 CAAAAGAGCTGGAGCTTCAATGACCGCACCCGCTTCCGGGCATCTCTGAGACTC------ 1573

Qy       1339 TCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGAT 1398
                  |||||    |  ||||||   ||||   | | || || |||   ||
Db       1574 ---------AAACCCCGCACCTCTGCTGAGGATGCCC---CCTCAGAGGAAGTAGCAGAG 1621

Qy       1399 GAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTC 1458
              || ||  | | |||||||||  |  | |||||  ||| |||  ||  |  | || || |||
Db       1622 GAGAAGAGCTACCAGTGTGAGCTCACGGTGGACGACATCATGCCTGCTGTGAAGACAGTC 1681

Qy       1459 ATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTA 1518
              || ||  | ||||| ||| | || || |  || || ||| |||| || ||||| ||  |
Db       1682 ATCCGCTCCATCAGGATTCTCAAGTTCCTGGTGGCCAAAAGGAAATTCAAGGAGACACTG 1741

Qy       1519 CGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTG 1578
              || || || || || || || |||||||| || || || || || || |||||||||  ||
Db       1742 CGACCGTACGACGTGAAGGACGTCATTGAGCAGTACTCAGCAGGCCACCTGGACATGCTG 1801

Qy       1579 TGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGC---AAATC 1635
              |  | || || ||||| ||||| || || || ||||||  | ||     ||||       |
Db       1802 GGCCGGATCAAGAGCCTGCAAACTCGGGTGGACCAAATTGTGGGTCGGGGGCCCGGGGAC 1861

Qy       1636 ACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTC 1695
              |     |   | |||  | || ||    |  | ||   |||     || ||  ||
Db       1862 AGGAAGGCCCGGGAGAAGGGCGACAAGGGGCCCTCCGACGCGGAGGTGGTGGATGAAATC 1921

Qy       1696 AGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGCTG 1755
              || ||| | || || |||||||||| || |||||  |||||||| |||  |||||||
Db       1922 AGCATGATGGGACGCGTGGTCAAGGTGGAGAAGCAGGTGCAGTCCATCGAGCACAAGCTG 1981

Qy       1756 GACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCT 1815
              |||   ||  | | | |||||    |   ||| |     |||||| | |  |   |
Db       1982 GACCTGCTGTTGGGCTTCTATTCGCGCTGCCTGC------GCTCTGGCACCTCGGCCAGC 2035

Qy       1816 TTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCT 1875
              |||   |  | ||  | || |  || ||    ||    || || ||||| || ||||||
Db       2036 CTGGGCGCCGTGCAAGTGCCGCTGTTCGACCCCGACATCACCTCCGACTACCACAGCCCT 2095

Qy       1876 GTGGATAGCAAAGATCTTTCGGGTTCCGCACAAA 1909
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Db       2096 GTGGACCACGAGGACATCTCCGTCTCCGCACAGA 2129


RESULT 14
US-10-096-578-88
; Sequence 88, Application US/10096578
; Publication No. US20030165874A1
; GENERAL INFORMATION:
;  APPLICANT: Leppert, Mark F.
;  APPLICANT:  Singh, Nanda
;  APPLICANT:  Charlier, Carole
;  TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
;  TITLE OF INVENTION:  MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
;  TITLE OF INVENTION:  AND OTHER EPILEPSIES
;  FILE REFERENCE: 2323-160
;  CURRENT APPLICATION NUMBER: US/10/096,578
;  CURRENT FILING DATE:  2002-03-14
;  PRIOR APPLICATION NUMBER: US 09/177,650
;  PRIOR FILING DATE: 1998-10-23
;  PRIOR APPLICATION NUMBER: US 60/063,147
;  PRIOR FILING DATE: 1997-10-24
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
;  LENGTH: 2273
;  TYPE: DNA
;  ORGANISM: Mus musculus
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)..(2271)
;  NAME/KEY: misc_feature
;  LOCATION: (1)..(2273)
;  OTHER INFORMATION: n may be any nucleotide except at position
;  OTHER INFORMATION: 272 at which n may be t, c or g.
;  NAME/KEY: PEPTIDE
;  LOCATION: (1)..(757)
;  OTHER INFORMATION: Xaa may be: S or R at 18, 19 and 69; V, A, E or G
;  OTHER INFORMATION: at 31; D or E at 33; S, P, T or A at 39; I, T, N or
;  OTHER INFORMATION: S at 52; F, L, I, M or V at 53; S, P, T or A at 64;
;  OTHER INFORMATION: P at 68; L, S or W at 91; R at 365; V at 509 and 516.
US-10-096-578-88

  Query Match           19.2%;  Score 516;  DB 16;  Length 2273;
  Best Local Similarity  57.6%;  Pred. No. 9.7e-148;
  Matches 1030;  Conservative    2;  Mismatches  684;  Indels   72;  Gaps    4;

Qy         64 GGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTGAGG 123
Db         67 GGCTTCGTGGGGCTGGACCCCGGCGNGCCCGANTCCACACGCGACGGCNCNCTACTCATC 126

Qy        124 GAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCTTAC 183
Db        127 GCGGGCTCCGAGGCCCCCAAGCGCGGCANCNTNTTGAGCAAGCCGCGGACGGGCGGCGCG 186

Qy        184 ACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTGTAC 243
Db        187 GGANCCGGGAAGCCCCCNAANCGCAACGCCTTCTACCGCAAGCTGCAGAATTTCCTCTAC 246

Qy        244 AACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTCCTT 303
Db        247 AACGTGCTAGAGCGGCCCCGCGGCTNGGCGTTCATCTACCACGCCTACGTGTTCCTCCTG 306

Qy        304 GTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTGGCC 363
Db        307 GTTTTCTCCTGCCTTGTGCTTTCTGTGTTTTCCACCATCAAGGAGTACGAGAAGAGCTCT 366

Qy        364 TCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTCATC 423
Db        367 GAGGGGGCCCTCTACATCTTGGAAATCGTGACTATCGTGGTATTCGGTGTTGAGTACTTT 426

Qy        424 ATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTGAGG 483

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Qy        484 TTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCAGTT 543
Db        487 TTTGCCAGGAAGCCGTTCTGTGTGATTGATATCATGGTGCTGATTGCCTCCATTGCTGTG 546

Qy        544 GTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGTTTC 603
Db        547 CTGGCTGCTGGTTCCCAGGGCAATGTCTTTGCCACATCTGCGCTTCGGAGCTTGCGGTTC 606

Qy        604 CTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTGGGT 663
Db        607 TTGCAAATCTTGCGGATGATCCGTATGGACCGGAGGGGTGGCACCTGGAAGCTCTTGGGA 666

Qy        664 TCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTGGTT 723
Db        667 TCGGTAGTCTACGCTCACAGCAAGGAGCTGGTGACTGCCTGGTACATTGGCTTCCTCTGC 726

Qy        724 CTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTTTCT 783
Db        727 CTCATCCTGGCCTCATTTCTGGTGTACTTGGCAGAAAAGGGTGAGAATGACCACTTTGAC 786

Qy        784 ACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGAGAC 843
Db        787 ACCTACGCAGATGCACTCTGGTGGGGTCTGATCACCCTGACGACCATTGGCTACGGGGAC 846

Qy        844 AAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGCATT 903
Db        847 AAGTACCCTCAGACCTGGAACGGGAGGCTGCTGGCAGCGACCTTTACCCTCATTGGTGTC 906

Qy        904 TCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAAGAA 963
Db        907 TCGTTCTTTGCTCTTCCGGCTGGCATTTTGGGATCCGGCTTTGCCCTGAAAGTCCAAGAG 966

Qy        964 CAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAGTGT 1023
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Db       1087 TACGAGCGNACAGTCACTGTCCCCATGTACAGCTCACAAACTCAAACCTATGGGGCCTCC 1146

Qy       1105 AG-----CCCTACCAAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGCTAAGTTTTA 1159
Db       1147 AGACTCATCCCACCTCTGAACCAGCTGGAGCTGCTGAGGAATCTCAAGAGCAAATCTGGA 1206

Qy       1160 AGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAG 1219
Db       1207 CTCACCTTCAGGAAGGAGCCACAGCCAGAGCCATCACCAAGCCCCCGAGGCATGGCTGCC 1266

Qy       1220 TAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGC---------------------- 1256
Db       1267 AAGGGAAAGGGGTCTCCCCAGGCCCAGACGGTCCGGCGGTCCCCCAGTGCGGATCAGAGT 1326

Qy       1257 --CGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTC 1314
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Qy       1315 CGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCC 1374
Db       1387 CGCCAGGCTTTCCGCATCAAGGGTGCTGCATCCCGGCAGAATTCAGAAGAAGCAAGCCTC 1446

Qy       1375 CTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGAC 1434
Db       1447 CCTGGGGAGGACATCGTAGAGGACAACAAGAGCTGTAACTGCGAGTTTGTGACTGAAGAT 1506

Qy       1435 CTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCA 1494
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Qy       1495 AAACGGAAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATAT 1554
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RESULT 15
US-10-128-870-22
; Sequence 22, Application US/10128870
; Publication No. US20020168724A1
; GENERAL INFORMATION:
;  APPLICANT: Blanar, Michael A.
;  APPLICANT:  Dworetzky, Steven
;  APPLICANT:  Gribkoff, Valentin K.
;  APPLICANT:  Levesque, Paul C.
;  APPLICANT:  Little, Wayne A.
;  APPLICANT:  Neubauer, Michael G.
;  APPLICANT:  Yang, Wen-Pin
;  TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
;  FILE REFERENCE: DC58aDIV
;  CURRENT APPLICATION NUMBER: US/10/128,870
;  CURRENT FILING DATE:  2002-04-24
;  PRIOR APPLICATION NUMBER: 09/105,058
;  PRIOR FILING DATE: June 26, 1998
;  PRIOR APPLICATION NUMBER: 60/055,599
;  PRIOR FILING DATE: August 12, 1997
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 2169
;   TYPE: DNA
;   ORGANISM: MOUSE
US-10-128-870-22

  Query Match             18.9%;  Score 510;  DB 13;  Length 2169;
  Best Local Similarity   58.1%;  Pred. No. 6.7e-146;
  Matches 1043;  Conservative    0;  Mismatches  670;  Indels   81;  Gaps    5;

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Qy        184 ACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTGTAC 243
Db        187 GGAGCCGGGAAGCCCCCGAAGCGCAACGCCTTCTACCGCAAGCTGCAGAATTTCCTCTAC 246

Qy        244 AACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTCCTT 303
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Qy        304 GTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTGGCC 363
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Qy       1189 GGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGAC 1248
Db       1267 GCTGCCAAGGGAAAGGGGTCTCCCCAGGCCCAGACGGTCCGGCGGTCCCCCAGTGCGGAT 1326

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              ||||| || |||||     ||'|||   |  |||  ||||| |   |  |||||    ||
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Job time : 1523.51 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 09:10:16 ; Search time 8514.67 Seconds
(without alignments)
12043.352 Million cell updates/sec

Title: US-09-810-796-2
Perfect score: 2694
Sequence: 1 atgaaggatgtggagtcggg.....ctcatgtcaaactgaaataa 2694

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
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9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	2105.2	78.1	2729	9	AY407015	AY407015 Mus muscu
	3	1822.2	67.6	2014	9	AY407014	AY407014 Pan trogl
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c	8	656.2	24.4	717	6	CD629766	CD629766 55049391J
c	9	647.8	24.0	678	6	CD629758	CD629758 55049351J
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ALIGNMENTS

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ACCESSION AY407013
VERSION AY407013.1 GI:39762984
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2733)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2733)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
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gene <1. .>2733
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/locus_tag="HCM2749"
ORIGIN

Query Match 97.1%; Score 2616.6; DB 9; Length 2733;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 2656; Conservative 0; Mismatches 11; Indels 27; Gaps 1;

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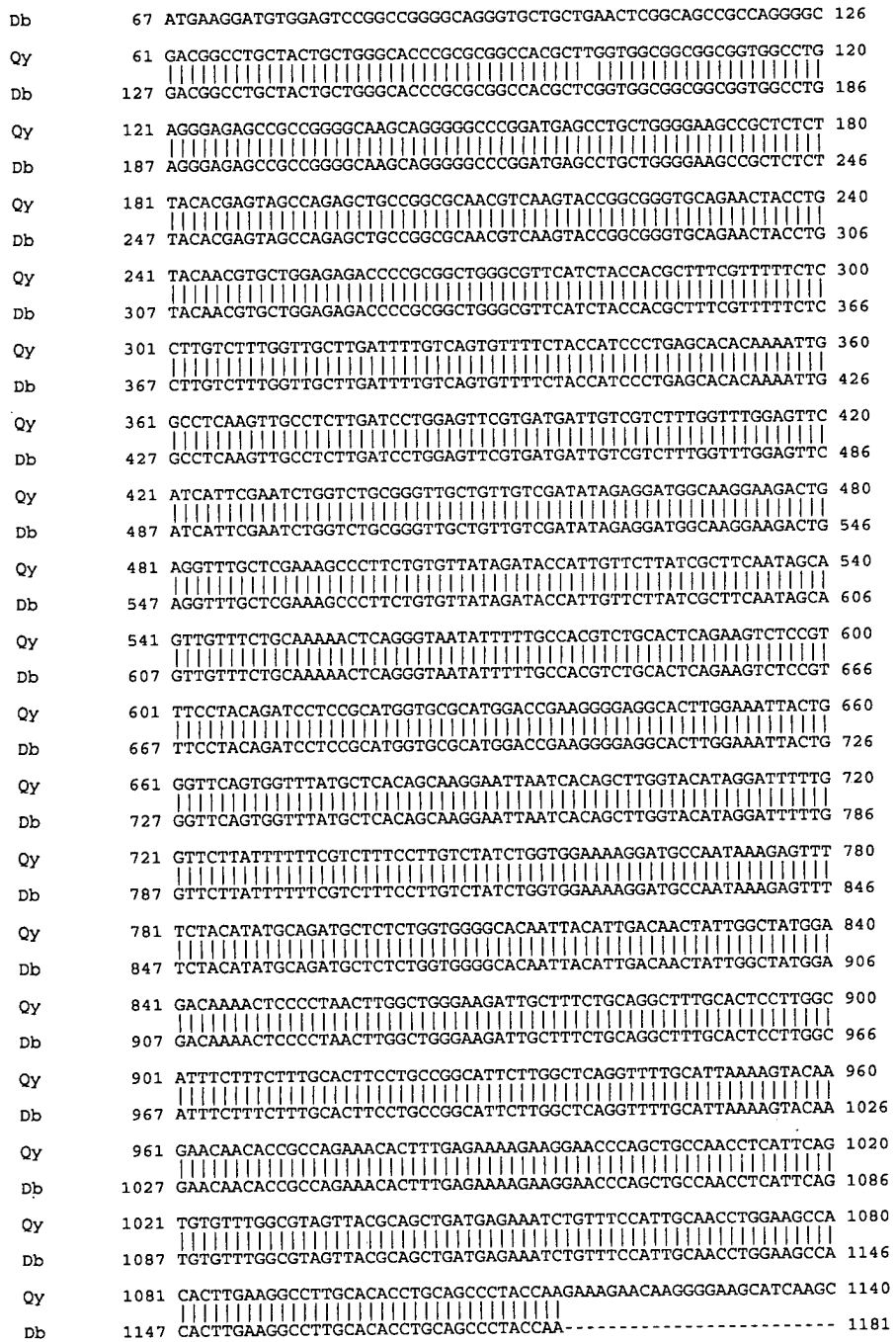
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Qy 1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
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Qy 1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
Db 2020 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2079
Qy 2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
Db 2080 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2139
Qy 2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
Db 2140 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2199
Qy 2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
Db 2200 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2259

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Qy       2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280
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Db       2260 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2319

Qy       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2320 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2379

Qy       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400
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Db       2380 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2439

Qy       2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460
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Db       2440 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2499

Qy       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
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Db       2500 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2559

Qy       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
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Db       2560 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2619

Qy       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2620 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2679

Qy       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
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Db       2680 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2733
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RESULT 2
AY407015
LOCUS       AY407015                2729 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Mus musculus KCNQ5 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY407015
VERSION     AY407015.1  GI:39762986
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2729)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2729)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match 78.1%; Score 2105.2; DB 9; Length 2729;
Best Local Similarity 87.7%; Pred. No. 0;
Matches 2363; Conservative 0; Mismatches 258; Indels 73; Gaps 3;

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Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
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Db        109 ATGAAGGATGTGGAGTCCGGCCGCGGCAGGGTGCTGCTGAACTCGGCGGCCGCCAGGGGC 168

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              ||||||||||  |||| ||||||||||||||  |||| || || |||||||| ||| ||
Db        169 GACGGCCTGCTGTTGCTCGGCACCCGCGCGGCGGCGCTCGGCGGAGGCGGCGGCGGCTTG 228

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
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Db        229 AGAGAGAGCCGCCGGGGCAAGCAGGGGGCCCGAATGAGCCTGCTGGGGAAGCCGCTCTCC 288

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
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Db        289 TACACCAGCAGCCAGAGCTGTCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTATCTG 348

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
              |||||||||||||||                                        |||||||
Db        349 TACAACGTGCTGGA----------------------------------------TTTTCTC 369

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              ||||| ||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        370 CTTGTGTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCATACAAAATTG 429

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
              || |||||||||||||| || |||||||||||||||| || |||||||| |||||||||
Db        430 GCTTCAAGTTGCCTCTTAATTCTGGAGTTCGTGATGATCGTTGTCTTTGGCTTGGAGTTC 489

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
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Db        490 ATCATTCGAATCTGGTCTGCAGGTTGCTGTTGTCGTTATAGAGGATGGCAAGGAAGACTG 549

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
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Db        550 AGGTTTGCTCGAAAACCATTCTGTGTAATAGATACCATTGTTCTCATCGCTTCAATAGCA 609

Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
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Db        610 GTTGTCTCTGCAAAAACTCAGGGTAATATTTTCGCCACGTCAGCGCTCAGAAGTCTCCGG 669

Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
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Db        670 TTCCTACAGATCCTGCGTATGGTGCGCATGGACAGAAGGGGAGGGACCTGGAAGCTGCTC 729

Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
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Db        730 GGCTCTGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCCTGGTACATTGGATTTCTG 789

Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
              |||||||||||||| || |||||||||||| |||||||||||||||||||||||||||||
Db        790 GTTCTTATTTTTTCATCCTTCCTTGTCTATCTTGTGGAAAAGGATGCCAATAAAGAGTTT 849

Qy        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
              || |||||||| |||||||||||||||||||||||||||| ||| ||||||| ||||||||||
Db        850 TCGACATATGCGGATGCTCTCTGGTGGGGCACAATCACACTGACAACCATTGGCTATGGA 909

Qy        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
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Db        910 GACAAAACACCCCTAACGTGGCTGGGAAGACTGCTCTCTGCAGGCTTCGCACTCCTTGGC 969

Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        970 ATTTCTTTCTTTGCACTTCCTGCTGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAG 1029

Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
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Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
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Qy       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
Db       1150 CATCTGAAGGCCTTGCACACCTGCAGCCCTACCAA---------------------------- 1184
Qy       1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
Db       1185 --TCAGAAGCTGAGCTTTAAGGAGCGAGTGCGCATGGCTAGCCCAAGGGGCCAGAGCATT 1242
Qy       1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
Db       1243 AAGAGCAGACAAGCATCAGTAGGTGACAGGAGATCCCCGAGCACTGACATCACTGCCGAG 1302
Qy       1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320
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Qy       1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380
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Qy       1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560
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Qy       1561 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620
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Qy       1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680
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Qy       1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
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Qy       1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
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Qy       1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860
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Qy       1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
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Qy       1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
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Qy       1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
Db       2016 GAGTTCAGTGCTCAGACTTTCTATGCGCTTAGCCCTACTATGCACAGCCAAGCTACCCAG 2075
Qy       2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
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Db       2136 ATAAGCGCCGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCTCCTCCTCTCTCG 2195
Qy       2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220
Db       2196 GCCATCAAGCACTTGTCCAGGCCAGAACCTCTGCTCTCAAACCCCACCGGCTTACAAGAG 2255
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Qy       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340
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Qy       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520
Db       2496 GGCAGTCAAGATTTTTATCCCAAGTGGAGAGAATCCAAATTGTTTATAACTGATGAGGAG 2555
Qy       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580
Db       2556 GTCGGTGCCGAAGAGACAGAAACAGATACTTTTGACGGCACCCCACCGCCTGCGGGGGAG 2615
Qy       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
Db       2616 GCTGCTTTCTCATCAGACTCTCTAAGGACTGGAAGGTCACGGTCATCTCAGAACATTTGT 2675
Qy       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
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RESULT 3
AY407014

LOCUS	AY407014 2014 bp DNA linear GSS 15-DEC-2003
DEFINITION	Pan troglodytes KCNQ5 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION	AY407014
VERSION	AY407014.1 GI:39762985
KEYWORDS	GSS.
SOURCE	Pan troglodytes (chimpanzee)
ORGANISM	Pan troglodytes Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE	1 (bases 1 to 2014)
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL	Science 302 (5652), 1960-1963 (2003)
PUBMED	14671302
REFERENCE	2 (bases 1 to 2014)
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Direct Submission
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES	Location/Qualifiers
source	1. .2014

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ORIGIN

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Qy         31 GTGCTGCTGAACTCGGCAGCCGCCAGGGGCGACGGCCTGCTACTGCTGGGCACCCGCGCG 90
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Qy         91 GCCACGCTTGGTGGCGGCGGCGGTGGCCTGAGGGAGAGCCGCCGGGGCAAGCAGGGGGCC 150
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Db         61 GCCACGCTCGGTGGCGGCGGCGGTGGCCTGAGGGAGAGCCGCCGGGGCAAGCAGGGGGCC 120

Qy        151 CGGATGAGCCTGCTGGGGAAGCCGCTCTCTTACACGAGTAGCCAGAGCTGCCGGCGCAAC 210
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Db        121 CGGATGNNNCTGCTGGGGANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 180

Qy        211 GTCAAGTACCGGCGGGTGCAGAACTACCTGTACAACGTGCTGGAGAGACCCCGCGGCTGG 270

Db        181 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 240

Qy        271 GCGTTCATCTACCACGCTTTCGTTTTTCTCCTTGTCTTTGGTTGCTTGATTTTGTCAGTG 330
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Db        241 NNNNNNNNNNNNNNNNNNNNNNTTTTCTCCTTGTCTTTGGTTGCTTGATTTTGTCAGTG 300

Qy        331 TTTTCTACCATCCCTGAGCACACAAAATTGGCCTCAAGTTGCCTCTTGATCCTGGAGTTC 390
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Db        301 TTTTCTACCATCCCTGAGCACACAAAATTGGCCTCAAGTTGCCTCTTGATCCTGGAGTTC 360

Qy        391 GTGATGATTGTCGTCTTTGGTTTGGAGTTCATCATTCGAATCTGGTCTGCGGGTTGCTGT 450
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Db        361 GTGATGATTGTCGTCTTTGGTTTGGAGTTCATCATTCGAATCTGGTCTGCGGGTTGCTGT 420

Qy        451 TGTCGATATAGAGGATGGCAAGGAAGACTGAGGTTTGCTCGAAAGCCCTTCTGTGTTATA 510
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Db        421 TGTCGATATAGAGGATGGCAAGGAAGACTGAGGTTTGCTCGAAAGCCCTTCTGTGTTATA 480

Qy        511 GATACCATTGTTCTTATCGCTTCAATAGCAGTTGTTTCTGCAAAAACTCAGGGTAATATT 570
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Db        481 GATACCATTGTTCTTATCGCTTCAATAGCAGTTGTTTCTGCAAAAACTCAGGGTAATATT 540

Qy        571 TTTGCCACGTCTGCACTCAGAAGTCTCCGTTTCCTACAGATCCTCCGCATGGTGCGCATG 630
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Db        541 TTTGCCACGTCTGCACTCAGAAGTCTCCGTTTCCTACAGATCCTCCGCATGGTGCGCATG 600

Qy        631 GACCGAAGGGGAGGCACTTGGAAATTACTGGGTTCAGTGGTTTATGCTCACAGCAAGGAA 690
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Db        601 GACCGAAGGGGAGGCACTTGGAAATTACTGGGTTCAGTGGTTTATGCTCACAGCAAGGAA 660

Qy        691 TTAATCACAGCTTGGTACATAGGATTTTTGGTTCTTATTTTTTCGTCTTTCCTTGTCTAT 750
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Db        661 TTAATCACAGCTTGGTACATAGGATTTTTGGTTCTTATTTTTTCGTCTTTCCTTGTCTAT 720

Qy        751 CTGGTGGAAAAGGATGCCAATAAAGAGTTTTCTACATATGCAGATGCTCTCTGGTGGGGC 810
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Db        721 CTGGTGGAAAAGGATGCCAATAAAGAGTTTTCTACATATGCAGATGCTCTCTGGTGGGGC 780

Qy        811 ACAATTACATTGACAACTATTGGCTATGGAGACAAAACTCCCCTAACTTGGCTGGGAAGA 870
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Db        781 ACAATTACATTGACAACTATTGGCTATGGAGACAAAACTCCCCTAACTTGGCTGGGAAGA 840

Qy        871 TTGCTTTCTGCAGGCTTTGCACTCCTTGGCATTTCTTTCTTTGCACTTCCTGCCGGCATT 930
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Qy        931 CTTGGCTCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAGAAACACTTTGAGAAA 990
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Db        901 CTTGGCTCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAGAAACACTTTGAGAAA 960

Qy        991 AGAAGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGTTACGCAGCTGATGAG 1050
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Db        961 AGAAGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGTTATGCAGCTGATGAG 1020

Qy       1051 AAATCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGCACACCTGCAGCCCT 1110
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Qy       1111 ACCAAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGCTAAGTTTTAAGGAGCGAGTG 1170
              |||||                          ||||||||||||||||||||||||||
Db       1081 ACCAA--------------------------TCAGAAGCTAAGTTTTAAGGAGCGAGTG 1113

Qy       1171 CGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGG 1230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 CGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGG 1173

Qy       1231 AGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGG 1290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 AGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGG 1233

Qy       1291 AGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAA 1350
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Db       1234 AGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAA 1293

Qy       1351 CCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGATGC 1410
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db       1294 CCAGTGATAGATGNNNACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGATGC 1353

Qy       1411 CAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCTATC 1470
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db       1354 CAGTGTGATGTATCAGTGGAAGANNTCACCCCACCACTTAAAACTGTCATTCGAGCTATC 1413

Qy       1471 AGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATATGAT 1530
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Db       1414 AGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATATGAT 1473

Qy       1531 GTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATTAAA 1590
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Qy       1591 AGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAGAAG 1650
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Qy       1651 AGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGTCGG 1710
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Qy       1711 GTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGCTGGACTGCCTACTAGAC 1770
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Db       1654 GTGGTCAAGGTNNNNNNNNNGTACAGTCCATAGAGTCCAAGCTGGACTGCCTACTAGAC 1713

Qy       1771 ATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTCCAG 1830
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Db       1714 ATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTCCAG 1773

Qy       1831 ATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAAGAT 1890
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Db       1834 CTTTCGGGTTCTGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATCTCG 1893

Qy       1951 AGAGGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCGCTT 2010
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Qy       2011 AGCCCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCAGCA 2070
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Db       1954 AGCCCTACTATGCACAGTCAAGCANCACAGGTGCNAATTAGTCAAAGCGATGGCTCAGCA 2013

Qy       2071 G 2071
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Db       2014 G 2014


RESULT 4
AK033079
LOCUS       AK033079               2276 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult male cortex cDNA, RIKEN full-length enriched
            library, clone:7730402H11 product:potassium voltage-gated channel,
            subfamily Q, member 5, full insert sequence.
ACCESSION   AK033079
VERSION     AK033079.1  GI:26328812
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2276)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
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            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1. .2276
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
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                     QMTSDKKSREKITAEHETTDDPSMLARVVKVEKQVQSIESKLDCLLDIYQQVLRKGYA
                     SALTLASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLTRSASANISRGLQFILTP
                     NEFSAQTFYALSPTMHSQATQVPMSQNDGSSVVATNNIANQISAAPKPAAPTTLQIPP
                     PLSAIKHLSRPEPLLSNPTGLQESISDVTTCLVASKESVQFAQSNLTKDRSLRKSFDM
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                     PHVKLN"
ORIGIN

  Query Match           52.5%;  Score 1413.8;  DB 3;  Length 2276;
  Best Local Similarity  88.8%;  Pred. No. 0;
  Matches 1529;  Conservative    0;  Mismatches  192;  Indels    0;  Gaps    0;

Qy        974 AGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTA 1033
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Db          1 AGAAGCATTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATCCAGTGTGTCTGGCGTA 60

Qy       1034 GTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCT 1093
              |||| |||||||||||| |||||||||||||||||||||||||||||||  |||||||||
Db         61 GTTATGCAGCTGATGAAAAATCTGTTTCCATTGCAACCTGGAAGCCACATCTGAAGGCCT 120

Qy       1094 TGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGCTAA 1153
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        121 TGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAGGCATCAAGCAGTCAGAAGCTGA 180

Qy       1154 GTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAG 1213
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Db        241 CATCAGTAGGTGACAGGAGATCCCCGAGCACTGACATCACTGCCGAGGGCAGCCCCACCA 300

Qy       1274 AAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCA 1333
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Db        361 AGAGTTCCCAGCCAAAGCCAGTGATAGACGCCGACACAGCCCTTGGCATTGATGATGTGT 420

Qy       1394 ATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAA 1453

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Db        601 TGCTTTGTAGAATAAAAAGCCTTCAGACACGCGTTGATCAAATTCTTGGAAAAGGACAAA 660

Qy       1634 TCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATC 1693

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Qy       1694 TCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGC 1753

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Db        781 TGGACTGCCTGCTGGATATCTATCAACAGGTCCTCCGGAAAGGCTATGCCTCCGCCCTCA 840

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Qy       1874 CTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAA 1933

Db        901 CTGTGGATAGCAAAGACCTGTCTGGCTCAGCACAAAACAGCGGCTGTTTAACGAGGTCAG 960

Qy       1934 CTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCC 1993

Db        961 CCAGTGCCAACATCTCAAGAGGCCTGCAGTTCATCCTAACACCAAATGAGTTCAGTGCTC 1020

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Qy       2054 AAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAAATAAATACGGCAC 2113

Db       1081 AAAATGACGGCTCCTCCGTGGTAGCCACCAATAACATTGCAAACCAAATAAGCGCCGCAC 1140

Qy       2114 CCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATC 2173

Db       1141 CCAAGCCAGCAGCCCCAACAACTTTACAGATCCCTCCTCCTCTCTCGGCCATCAAGCACT 1200

Qy       2174 TGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACG 2233

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Qy       2294 AGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTC 2353

Db       1321 AGGACCGTTCCCTGAGGAAAAGTTTCGACATGGGAGGAGAAACTCTGTTGTCTGTCCGCC 1380

Qy       2354 CCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCG 2413

Db       1381 CCATGGTGCCCAAGGATTTGGGCAAATCTCTGTCTGTACAAAACCTGATCAGGTCGACAG 1440

Qy       2414 AGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATT 2473

Db       1441 AAGAACTGAACTTACAGTTTTCAGGCAGCGAGTCAAGCGGCTCTCGAGGCAGTCAAGATT 1500

Qy       2474 TTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAG 2533

Db       1501 TTTATCCCAAGTGGAGAGAATCCAAATTGTTTATAACTGATGAGGAGGTCGGTGCCGAAG 1560

Qy       2534 AGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCAT 2593

Db       1561 AGACAGAAACAGATACTTTTGACGGCACCCCACCGCCTGCGGGGGAGGCTGCTTTCTCAT 1620

Qy       2594 CAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAA 2653

Db       1621 CAGACTCTCTAAGGACTGGAAGGTCACGGTCATCTCAGAACATTTGTAAGACAGGAGACA 1680

Qy       2654 GTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694

Db       1681 GTACAGGCGCCCTCAGTTTGCCTCACGTCAAACTGAACTAA 1721


RESULT 5
CD629762/c
LOCUS       CD629762                797 bp    mRNA    linear   EST 12-JAN-2004
DEFINITION  55049367J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD629762
VERSION     CD629762.1  GI:40278028
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 797)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches  754;  Conservative    0;  Mismatches    7;  Indels    2;  Gaps    2;

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Qy       1049 AGAAATCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGCACACCTGCAG-C 1107

Db        704 AGAAATCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGCACACCTGCAGCC 645

Qy       1108 CCTACCAAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGCTAAGTTTTAAGGAGCGA 1167

Db        644 CCTACCAAGAAAGGACAAGGGGAAGCATCAAGCAGTCAGAAGCTAAGTTTTAAGGAGCGA 585

Qy       1168 GTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGAC 1227

Db        584 GTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGAC 525

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Qy       1288 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 1347
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Db        284 ATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACATTACGTCCATAT 225

Qy       1528 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 1587
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Qy       1588 AAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAG 1647
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Qy       1708 CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCA 1750
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RESULT 6
CD629756/c
LOCUS       CD629756                732 bp    mRNA    linear   EST 12-JAN-2004
DEFINITION  55049343J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD629756
VERSION     CD629756.1  GI:40278022
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 732)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
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  Matches  727;  Conservative    0;  Mismatches    2;  Indels    4;  Gaps    4;

Qy       1014 CATTCAGTGTGTTTGGCGTAGTT-ACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCT 1072
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Qy       1073 GGAAGCCACACTTGAAGGCCTTGCACACCTGCAGCCCTA-CCAAGAAAGAACAA-GGGGA 1130
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Db        672 GGAAGCCACACTTGAAGGCCTTGCACACCTGCAGCCCTACCCAAGAAAGAACAAGGGGGA 613

Qy       1131 AGCATCAAGCAGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGG 1190
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Db        612 AGCATCAAGCAGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGG 553

Qy       1191 CCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACAT 1250
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Db        552 CCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACAT 493

Qy       1251 CACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCG 1310
                |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        492 CACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGGCCGAACCCG 433

Qy       1311 CTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACAC 1370
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 CTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACAC 373

Qy       1371 AGCCCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGA 1430
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Db        372 AGCCCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGA 313

Qy       1431 AGACCTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGT 1490
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Db        312 AGACCTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGT 253

Qy       1491 TGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACA 1550
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Qy       1551 ATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGA 1610
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Db        192 ATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGA 133

Qy       1611 TCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGC 1670
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Db        132 TCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGC 73

Qy       1671 AGAACATGAGACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACA 1730
                |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db          72 AGAACATGAGACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTC-AGGTTGAAAAACA 14

Qy       1731 GGTACAGTCCATA 1743
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Db          13 GGTACAGTCCATA 1
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RESULT 7
CD629754/c
LOCUS       CD629754                742 bp    mRNA    linear   EST 12-JAN-2004
DEFINITION  55049327J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD629754
VERSION     CD629754.1  GI:40278020
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 742)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
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                     /note="Vector: pDrive Cloning Vector"
ORIGIN

  Query Match             25.2%;  Score 679.2;  DB 6;  Length 742;
  Best Local Similarity   98.4%;  Pred. No. 4e-183;
  Matches  728;  Conservative    0;  Mismatches    8;  Indels    4;  Gaps    4;

Qy       1016 TTCAGTGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGA 1075
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Db        742 TTCAGTGTTTTGCCGTA-TTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACTGGGA 684

Qy       1076 AGCCACACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAA-CAAGGGGAAGCA 1134
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        683 AGCCACACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACCAAGGGGAAGCA 624

Qy       1135 TCAAGCAGTCAGAAGCTAAGTTTTAAGGAG-CGAGTGCGCATGGCTAGCCCCAGGGGCCA 1193
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Db        623 TCAAGCAGTCAGAAGCTAAGTTTTAAGGAGCCGAGTGCGCATGGCTAGCCCCAGGGGCCA 564

Qy       1194 GAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCAC 1253
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Db        563 GAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCAC 504

Qy       1254 AGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTT 1313
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 AGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTT 444

Qy       1314 CCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGC 1373
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 CCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGC 384

Qy       1374 CCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGA 1433
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 CCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGA 324

Qy       1434 CCTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGC 1493
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Db        323 CCTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGC 264

Qy       1494 AAAACGGAAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATA 1553
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Db        263 AAAACGGAAGTTTAAGTAAACATTACGTCCATATGATGTAAAAGATGTCATTGAACAATA 204

Qy       1554 TTCTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCA 1613
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 TTCTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCA 144

Qy       1614 AATTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGA 1673
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Db        143 AATTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGA 84

Qy       1674 ACATGAGACCACAGACGATCTCAGTATGCTCGGTCGGG-TGGTCAAGGTTGAAAAACAGG 1732
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Db          83 ACATGAGACCACAGACGATCTCAGTATGCTCGGTCGGGTTGGTCAAGGTTGAAAAACAGG 24

Qy       1733 TACAGTCCATAGAGTCCAAG 1752
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Db          23 TACAGTCCATAGAATCCTAG 4


RESULT 8
CD629766/c
LOCUS       CD629766                717 bp    mRNA    linear   EST 12-JAN-2004
DEFINITION  55049391J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD629766
VERSION     CD629766.1  GI:40278032
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 717)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .717
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                     /db_xref="taxon:9606"
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ORIGIN

  Query Match             24.4%;  Score 656.2;  DB 6;  Length 717;
  Best Local Similarity   98.3%;  Pred. No. 1.6e-176;
  Matches  705;  Conservative    0;  Mismatches    8;  Indels    4;  Gaps    4;

Qy       1031 GTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGG 1090
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Db         717 GTAGTTACGCAGCTGATGAGAAATCTGTTGCCATTGCAACCTGGAGGCCACACTTGAAGG 658

Qy       1091 CCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGC 1150
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Db         657 CTTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGC 598

Qy       1151 TAAGTT-TTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCC-G 1208
             ||||||  |||||||||||||||||||||||||||||||||||||||||||||||||| |
Db         597 TAAGTTATTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCGGAGTATTAAGAGCCGG 538

Qy       1209 ACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCC 1268
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Db         537 ACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCC 478

Qy       1269 CACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCG 1328
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         477 CACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCG 418

Qy       1329 CCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGA 1388
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Db         417 CCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGA 358

Qy       1389 TGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACT 1448
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Db         357 TGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACT 298

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Db         297 TAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAA 238

Qy       1509 GGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCT 1568
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Db         237 GTAAACATTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCT 178

Qy       1569 GGACATGTTGTGTAGAATTAAAAGCCTTCA-AACACGTGTTGATCAAATTCTTGGAAAAG 1627
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Db         177 GGACATGTTGTGTAGAATTAAAAGCCTTCATAACACGTGTTGATCAAATTCTTGGAAAAG 118

Qy       1628 GGCAAATCACATCAGATAAGAA-GAGCCGAGAGAAAATAACAGCAGAACATGAGACCACA 1686
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Db         117 GGCAAATCACATCAGATAAGAACGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACA 58

Qy       1687 GACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATA 1743
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RESULT 9
CD629758/c
LOCUS       CD629758                678 bp    mRNA    linear   EST 12-JAN-2004
DEFINITION  55049351J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD629758
VERSION     CD629758.1  GI:40278024
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 678)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .678
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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                     /note="Vector: pDrive Cloning Vector"
ORIGIN

  Query Match           24.0%;  Score 647.8;  DB 6;  Length 678;
  Best Local Similarity  99.4%;  Pred. No. 4.1e-174;
  Matches  671;  Conservative    0;  Mismatches    2;  Indels    2;  Gaps    2;

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Qy       1136 CAAGCAGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGA 1195
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Qy       1196 GTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAG 1255
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Db        558 GTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAG 499

Qy       1256 CCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCC 1315
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Db        498 CCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCC 439

Qy       1316 GGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCC 1375
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1376 TTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACC 1435
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Db        378 TTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACC 319

Qy       1436 TCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAA 1495
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Qy       1496 AACGGAAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATT 1555
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Qy       1556 CTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAA 1615
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Qy       1616 TTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAAC 1675
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Db        138 TTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAAC 79

Qy       1676 ATGAGACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTAC 1735
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Qy       1736 AGTCCATAGAGTCCA 1750
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RESULT 10
CD629755
LOCUS       CD629755                691 bp    mRNA    linear   EST 12-JAN-2004
DEFINITION  55049343H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD629755
VERSION     CD629755.1  GI:40278021
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 691)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .691
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
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ORIGIN

  Query Match           24.0%;  Score 647.6;  DB 6;  Length 691;
  Best Local Similarity  99.0%;  Pred. No. 4.7e-174;
  Matches  683;  Conservative    0;  Mismatches    4;  Indels    3;  Gaps    3;

Qy        796 GCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGAGACAAAACTCCCCTA 855
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGAGACAAAACTCCCCTA 60

Qy        856 ACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGCATTTCTTTCTTTGCA 915
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Db         61 ACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGCATTTCTTTCTTTGCA 120

Qy        916 CTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAG 975
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        976 AAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGT 1035
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Db        181 AAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGT 240

Qy       1036 TACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTG 1095
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Db        241 TACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTG 300

Qy       1096 CACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGCTAAGT 1155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGCTAAGT 360

Qy       1156 TTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCC 1215
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Qy       1216 TCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGA-GGGCAGTCCCACCAA 1274
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Db        420 TCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGGCAGTCCCACCAA 479

Qy       1275 AGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAA 1334
             |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        480 AGTGCAGAAGAGCTGGAGCTTCAACGGCCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAA 539

Qy       1335 AAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATA 1394
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 AAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATA 599

Qy       1395 TGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAAC 1454
             |||||||||||||||||||||||||||||||||||| |||||||| ||||| ||||
Db        600 TGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGAACTCACCCCCACACTT-AAAC 658

Qy       1455 TGTCATTCGAGCTATCAGAATTATGAAATT 1484
             |||||||||||||||||||||||||||||
Db        659 TGTCATTCGAGCTATCAGAATTATGAAATT 688


RESULT 11
CD629752/c
LOCUS       CD629752                724 bp    mRNA    linear   EST 12-JAN-2004
DEFINITION  55049303J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD629752
VERSION     CD629752.1  GI:40278018
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 724)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .724
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="FLP"
                     /note="Vector: pDrive Cloning Vector"
ORIGIN

  Query Match           22.8%;  Score 615.2;  DB 6;  Length 724;
  Best Local Similarity   97.1%;  Pred. No. 9.8e-165;
  Matches  701;  Conservative    0;  Mismatches   13;  Indels    8;  Gaps    7;

Qy       1038 CGCAGCTGATGAGAAATCTGT-TTCCATTGCAACCTGGAAGCCACACTT-GAAGGCCTTG 1095
             |||||||||||||||||||| | |||||||||| |||||||||||||| ||||||||||
Db        724 CGCAGCTGATGAGAAATCTGTGTCCCATTGCAACTTGGAAGCCACACTTGGAAGGCCTTG 665

Qy       1096 CACACC-TGCAGCCCTA-CCAAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGCTAA 1153
             |||||| |||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        664 CACACCTTGCAGCCCTACCCAAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGCTAA 605

Qy       1154 GTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAG 1213
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 GTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAG 545

Qy       1214 CCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCA 1273
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 CCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCA 485

Qy       1274 AAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCA 1333
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        484 AAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCA 425

Qy       1334 AAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTAT 1393
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTAT 365

Qy       1394 ATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAA 1453
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 ATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAA 305

Qy       1454 CTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAA 1513
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        304 CTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGTAAA 245

Qy       1514 CGTTACGTCCATATGATGTAAAAGA-TGTCATTGAACAATATTCTGCTGGTCATCTGGAC 1572
             | |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        244 CATTACGTCCATATGATGTAAAAGACTGTCATTGAACAATATTCTGCTGGTCATCTGGAC 185

Qy       1573 ATGTTGTGTAGAATTAAAAGCCTTCAAA--CACGTGTTGATCAAATTCTTGGAAAAGGGC 1630
             |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        184 ATGTTGTGTAGAATTAAAAGCCTTCAAAACACGTGTTTGATCAAATTCTTGGAAAAGGGC 125

Qy       1631 AAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACG 1690
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACG 65

Qy       1691 ATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCA 1750
             |||||||||||| |||||||||||||||||  |||||||||||||||||||| ||||
Db         64 ATCTCAGTATGCCCGGTCGGGTGGTCAAGGTT-TAAAACAGGTACAGTCCATAGAATCCA 6

Qy       1751 AG 1752
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Db           5 AG 4


RESULT 12
BE158938
LOCUS       BE158938                658 bp    mRNA    linear   EST 21-JUN-2000
DEFINITION  MR0-HT0404-210200-001-c04 HT0404 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE158938
VERSION     BE158938.1  GI:8621659
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 658)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=MR0-HT0404-210
            200-001-c04&t3=2000-02-21&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 657.
FEATURES             Location/Qualifiers
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     source          1. .658
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="HT0404"
                     /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

  Query Match             22.3%;  Score 600.2;  DB 2;  Length 658;
  Best Local Similarity   95.5%;  Pred. No. 2e-160;
  Matches  639;  Conservative    0;  Mismatches    3;  Indels   27;  Gaps    1;

Qy        831 TGGCTATGGAGACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGC 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 TGGCTATGGAGACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGC 76

Qy        891 ACTCCTTGGCATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATT 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 ACTCCTTGGCATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATT 136

Qy        951 AAAAGTACAAGAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAA 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 AAAAGTACAAGAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAA 196

Qy       1011 CCTCATTCAGTGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAAC 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 CCTCATTCAGTGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAAC 256

Qy       1071 CTGGAAGCCACACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGA 1130
              ||||||||||||||||||||||||||||||||||||||||||||
Db        257 CTGGAAGCCACACTTGAAGGCCTTGCACACCTGCAGCCCTACCAA--------------- 301

Qy       1131 AGCATCAAGCAGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGG 1190
                          ||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 ------------TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGG 349

Qy       1191 CCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACAT 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        350 CCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACGT 409

Qy       1251 CACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCG 1310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 CACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCG 469

Qy       1311 CTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACAC 1370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        470 CTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACAC 529

Qy       1371 AGCCCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGA 1430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        530 AGCCCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGA 589

Qy       1431 AGACCTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGT 1490
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        590 AGACCTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCTTGT 649

Qy       1491 TGCAAAACG 1499
              ||| |||||
Db        650 TGCCAAACG 658


RESULT 13
CD629765
LOCUS       CD629765                599 bp    mRNA    linear   EST 12-JAN-2004
DEFINITION  55049391H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD629765
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VERSION     CD629765.1  GI:40278031
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 599)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .599
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="FLP"
                     /note="Vector: pDrive Cloning Vector"
ORIGIN

  Query Match             22.1%;  Score 594.4;  DB 6;  Length 599;
  Best Local Similarity   99.8%;  Pred. No. 8.8e-159;
  Matches  595;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        796 GCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGAGACAAAACTCCCCTA 855
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGAGACAAAACTCCCCTA 60

Qy        856 ACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGCATTTCTTTCTTTGCA 915
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGCATTTCTTTCTTTGCA 120

Qy        916 CTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAG 975
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAG 180

Qy        976 AAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGT 1035
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGT 240

Qy       1036 TACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTG 1095
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTG 300

Qy       1096 CACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGCTAAGT 1155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGCTAAGT 360

Qy       1156 TTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCC 1215
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        361 TTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCGGAGTATTAAGAGCCGACAAGCC 420

Qy       1216 TCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAA 1275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAA 480

Qy       1276 GTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAA 1335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAA 540

Qy       1336 AGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGT 1391
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGT 596


RESULT 14
CD629760/c
LOCUS       CD629760                714 bp    mRNA    linear   EST 12-JAN-2004
```

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DEFINITION  55049359J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD629760
VERSION     CD629760.1  GI:40278026
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 714)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .714
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="FLP"
                     /note="Vector: pDrive Cloning Vector"
ORIGIN

  Query Match             21.7%;  Score 585.6;  DB 6;  Length 714;
  Best Local Similarity   96.3%;  Pred. No. 3.1e-156;
  Matches  643;  Conservative    0;  Mismatches   18;  Indels    7;  Gaps    4;

Qy       1068 AACCTGGAAGCCACA-CTTGAAGGCCTTGCA-CACCTGCAGCCCTACC----AAGAAAGA 1121
             | |||||||||||||| |||||||||||||||| ||||||||||||||    ||  ||
Db        688 ACCCTGGAAGCCACACCTTGAAGGCCTTGCACCACCTGCAGCCCTACCCAAGAAAGAACC 629

Qy       1122 ACAAGGGGAAGCATCAAGCAGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAG 1181
             | | ||| |    ||||||||||||||||||||||||||||||||||||||||||||||||
Db        628 AAAGGGGAAGCATTCAAGCAGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAG 569

Qy       1182 CCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAG 1241
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        568 CCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAG 509

Qy       1242 CACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAA-CG 1300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        508 CACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAAGCG 449

Qy       1301 ACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAG 1360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 ACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAG 389

Qy       1361 ATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATG 1420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 ATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATG 329

Qy       1421 TATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGA 1480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 TATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGA 269

Qy       1481 AATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATG 1540
             |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        268 AATTTCATGTTGCAAAACGGAAGTTTAAGGAAACATTACGTCCATATGATGTAAAAGATG 209

Qy       1541 TCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAA 1600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 TCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAA 149

Qy       1601 CACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGA 1660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        148 CACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGA 89

Qy       1661 AAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGG 1720
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |

Db         88 AAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAGGT 29

Qy       1721 TTGAAAAA 1728
                | ||| |
Db         28 TGAAAACA 21


RESULT 15
CD629751
LOCUS       CD629751                624 bp    mRNA    linear   EST 12-JAN-2004
DEFINITION  55049303H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD629751
VERSION     CD629751.1  GI:40278017
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 624)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .624
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="FLP"
                     /note="Vector: pDrive Cloning Vector"
ORIGIN

  Query Match             21.7%;  Score 584;  DB 6;  Length 624;
  Best Local Similarity   97.8%;  Pred. No. 8.7e-156;
  Matches  614;  Conservative    0;  Mismatches   10;  Indels    4;  Gaps    2;

Qy        796 GCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGAGACAAAACTCCCCTA 855
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGAGACAAAACTCCCCTA 60

Qy        856 ACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGCATTTCTTTCTTTGCA 915
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGCATTTCTTTCTTTGCA 120

Qy        916 CTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAG 975
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAG 180

Qy        976 AAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGT 1035
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Db        181 AAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGT 240

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Search completed: April 11, 2005, 21:31:56
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 09:27:56 ; Search time 422.362 Seconds
(without alignments)
10332.249 Million cell updates/sec

Title: US-09-810-796-3
Perfect score: 2667
Sequence: 1 atgaaggatgtggagtcggg.....ctcatgtcaaactgaaataa 2667

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2662.2	99.8	2772	4	US-09-825-147-1	Sequence 1, Appli
2	2662.2	99.8	3111	4	US-09-825-147-3	Sequence 3, Appli
3	2625.2	98.4	3137	4	US-09-590-304-1	Sequence 1, Appli
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5	509.8	19.1	582	4	US-09-495-050A-303	Sequence 303, App
6	492	18.4	2196	4	US-09-949-016-1823	Sequence 1823, Ap
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8	489.2	18.3	2273	3	US-09-177-650-88	Sequence 88, Appl
9	475.6	17.8	2169	3	US-09-105-058C-22	Sequence 22, Appl
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45	84.8	3.2	649	3	US-09-177-650-118	Sequence 118, App

ALIGNMENTS

RESULT 1
US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-1

Query Match 99.8%; Score 2662.2; DB 4; Length 2772;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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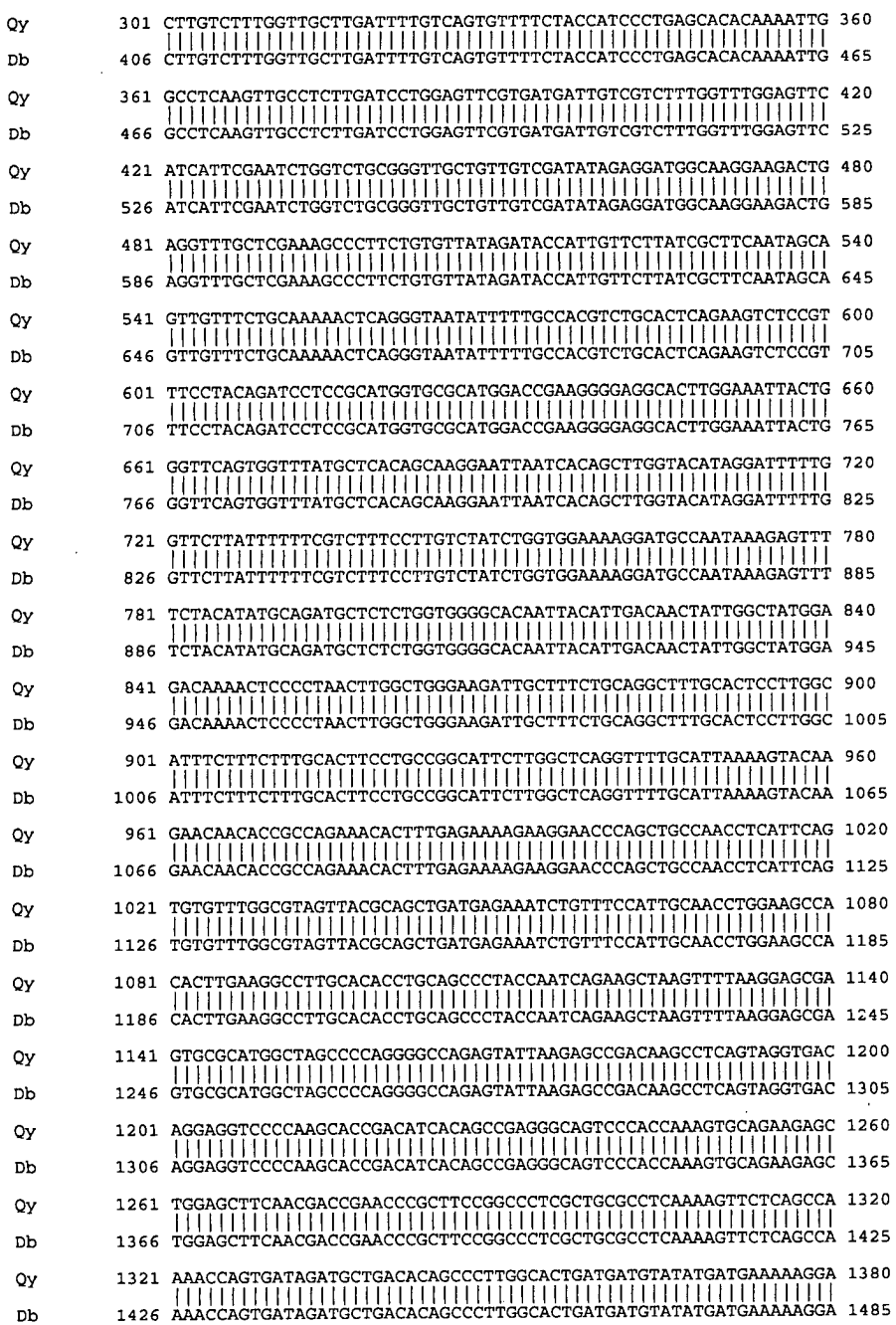
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; Sequence 3, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
;  APPLICANT: Hu, Yi
;  APPLICANT:  Kieke, James Alvin
;  APPLICANT:  Turner, C. Alexander Jr.
;  APPLICANT:  Nehls, Michael C.
;  APPLICANT:  Friedrich, Glenn
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and
;  TITLE OF INVENTION:  Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0160-USA
;  CURRENT APPLICATION NUMBER: US/09/825,147
;  CURRENT FILING DATE:  2001-04-03
;  PRIOR APPLICATION NUMBER: US 60/194,255
;  PRIOR FILING DATE: 2000-04-03
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 3111
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-825-147-3

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Db          825 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 884

Qy          721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
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Db          885 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 944

Qy          781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
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Db          945 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 1004

Qy          841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
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Db         1005 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 1064

Qy          901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1065 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 1124

Qy          961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
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Qy         1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
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Qy         1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAATCAGAAGCTAAGTTTTAAGGAGCGA 1140
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Db         1245 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAATCAGAAGCTAAGTTTTAAGGAGCGA 1304

Qy         1141 GTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGAC 1200
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Db         1305 GTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGAC 1364

Qy         1201 AGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGC 1260
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Db         1365 AGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGC 1424

Qy         1261 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1425 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 1484

Qy         1321 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 1380
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Db         1485 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 1544

Qy         1381 TGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCT 1440
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Db         1545 TGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCT 1604

Qy         1441 ATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATAT 1500
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Db         1605 ATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACATTACGTCCATAT 1664
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Qy       1501 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1665 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 1724

Qy       1561 AAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAG 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1725 AAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAG 1784

Qy       1621 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1785 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGT 1844

Qy       1681 CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGCTGGACTGCCTACTA 1740
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Db       1845 CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAATCCAAGCTGGACTGCCTACTA 1904

Qy       1741 GACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1800
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Db       1905 GACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1964

Qy       1801 CAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAA 1860
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Db       1965 CAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAA 2024

Qy       1861 GATCTTTCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATC 1920
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Qy       1921 TCGAGAGGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCG 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2101 CCAACAACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAA 2160
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Db       2265 CCAACAACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAA 2324

Qy       2161 ACTCTGCACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTT 2220
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Db       2325 ACTCTGCACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTT 2384

Qy       2221 GTTGCCTCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATG 2280
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Qy       2281 AGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAG 2340
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Db       2445 AGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAG 2504

Qy       2341 GACTTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATA 2400
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Db       2505 GACTTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATA 2564

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Db       2565 CAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGG 2624

Qy       2461 AGGGAATCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGAC 2520
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Qy       2521 ACTTTTGATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGG 2580
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Db       2685 ACTTTTGATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGG 2744

Qy       2581 ACTGGAAGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTC 2640
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RESULT 3
US-09-590-304-1
; Sequence 1, Application US/09590304
; Patent No. 6649371
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANN
; FILE REFERENCE: 2815-0136P
; CURRENT APPLICATION NUMBER: US/09/590,304
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2691)
US-09-590-304-1

Query Match 98.4%; Score 2625.2; DB 4; Length 3137;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

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Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
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Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
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Db        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240

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Db        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300

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Db        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360

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Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
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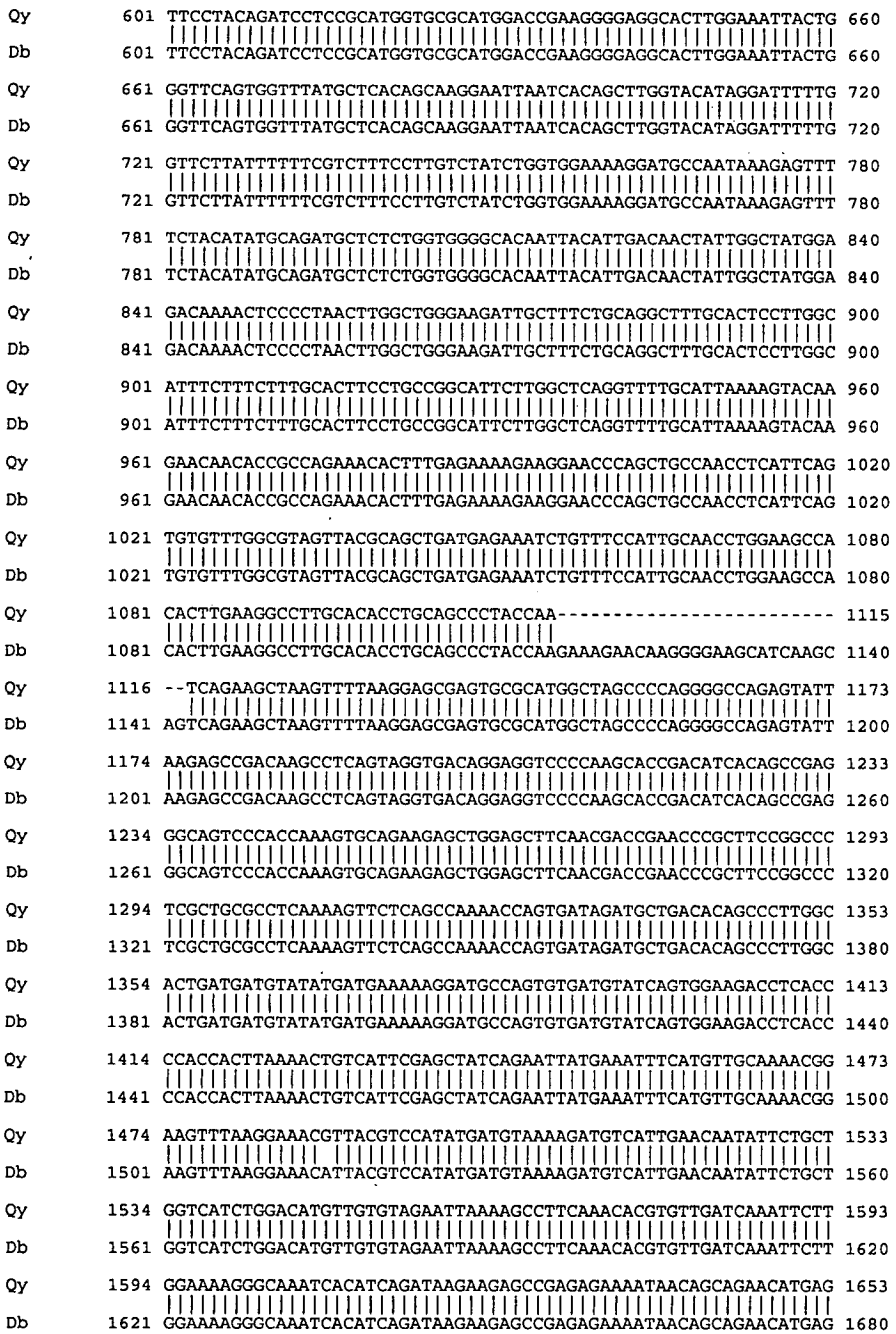

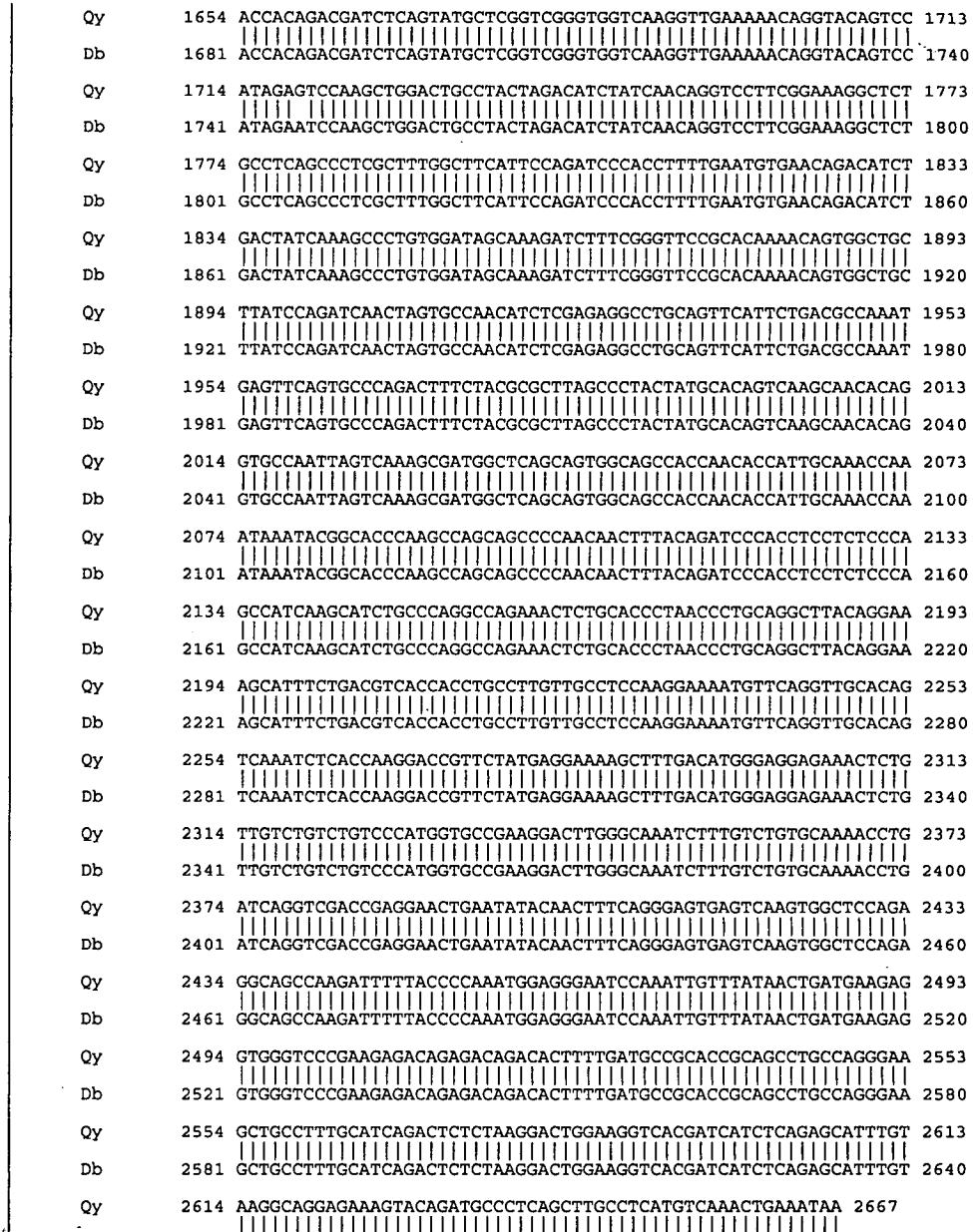

RESULT 4
US-09-813-148-1
; Sequence 1, Application US/09813148
; Patent No. 6617131

```
; GENERAL INFORMATION:
;  APPLICANT: STEINMEYER, Klaus
;  APPLICANT:  LERCHE, Christian
;  APPLICANT:  SCHERER, Constanze
;  APPLICANT:  SEEBOHM, Guiscard
;  APPLICANT:  BUSCH, Andreas E.
;  TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN
;  TITLE OF INVENTION:  NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
;  FILE REFERENCE: 38005-119
;  CURRENT APPLICATION NUMBER: US/09/813,148
;  CURRENT FILING DATE:  2001-03-21
;  PRIOR APPLICATION NUMBER: DE 100 13 732.6
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: US 60/194,041
;  PRIOR FILING DATE: 2000-04-03
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 3074
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-813-148-1

  Query Match             98.1%;  Score 2617.2;  DB 4;  Length 3074;
  Best Local Similarity   98.7%;  Pred. No. 0;
  Matches 2659;  Conservative    0;  Mismatches    8;  Indels   27;  Gaps    1;

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Db        275 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 334

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Db        455 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTCCTC 514

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
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Db        515 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 574

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Db        635 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 694

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Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
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Db        755 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 814

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Db        815 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 874

Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
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Db        875 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 934

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Db        935 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 994

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Db        995 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 1054

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Qy       1474 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1533
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1715 AAGTTTAAGGAAACATTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1774

Qy       1534 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1775 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1834

Qy       1594 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1835 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1894

Qy       1654 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1895 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1954

Qy       1714 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1773
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1955 ATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 2014
```

```
Qy       1774 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1833
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2015 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 2074

Qy       1834 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1893
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2075 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 2134

Qy       1894 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1953
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2135 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 2194

Qy       1954 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2013
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2195 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2254

Qy       2014 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2073
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2255 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2314

Qy       2074 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2133
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2315 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2374

Qy       2134 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2193
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2375 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2434

Qy       2194 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2253
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2435 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2494

Qy       2254 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2313
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2495 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2554

Qy       2314 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2373
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2555 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2614

Qy       2374 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2433
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2615 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2674

Qy       2434 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2493
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2675 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2734

Qy       2494 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2553
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2735 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2794

Qy       2554 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2613
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2795 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2854

Qy       2614 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2667
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2855 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2908


RESULT 5
US-09-495-050A-303
; Sequence 303, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
;  APPLICANT: Roopa, Reddy
;  APPLICANT:  Guegler, Karl, J.
;  APPLICANT:  Au-Young, Janice
;  TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
;  FILE REFERENCE: PA-0013 US
;  CURRENT APPLICATION NUMBER: US/09/495,050A
;  CURRENT FILING DATE:  2000-01-31
;  PRIOR APPLICATION NUMBER: 60/118,318
;  PRIOR FILING DATE: February 1, 1999
;  NUMBER OF SEQ ID NOS: 305
;  SOFTWARE: PERL Program
; SEQ ID NO 303
;    LENGTH: 582
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: misc_feature
;    OTHER INFORMATION: Incyte ID No. 6492505 4970006CT1
US-09-495-050A-303

  Query Match             19.1%;  Score 509.8;  DB 4;  Length 582;
  Best Local Similarity   99.4%;  Pred. No. 3.6e-145;
  Matches  522;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy       1594 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1653
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 60

Qy       1654 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1713
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 120

Qy       1714 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1773
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 180

Qy       1774 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1833
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 240

Qy       1834 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1893
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 300

Qy       1894 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1953
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 360

Qy       1954 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2013
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 420

Qy       2014 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2073
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 480

Qy       2074 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATC 2118
             ||||||||||||||| |||||||||| ||||||||||||||||||
Db        481 ATAAATACGGCACCAAAGCCAGCAG-CCCAACAACTTTACAGATC 524


RESULT 6
US-09-949-016-1823
; Sequence 1823, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
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;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1823
;   LENGTH: 2196
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-1823

  Query Match             18.4%;  Score 492;  DB 4;  Length 2196;
  Best Local Similarity   59.3%;  Pred. No. 2.7e-139;
  Matches 1087;  Conservative    0;  Mismatches  555;  Indels  192;  Gaps    7;

Qy       217 TACCGGCGGGTGCAGAACTACCTGTACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTC 276
Db       181 TACCGCCGCCTGCAGAACTGGGGGTACAACGTGCTGGAGCGGCCCCGCGGCTGGGCCTTC 240

Qy       277 ATCTACCACGCTTTCGTTTTTCTCCTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCT 336
Db       241 GTCTACCACGTCTTCATATTTTTGCTGGTCTTCAGCTGCCTGGTGCTGTCTGTGCTGTCC 300

Qy       337 ACCATCCCTGAGCACACAAAATTGGCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATG 396
Db       301 ACTATCCAGGAGCACCAGGAACTTGCCAACGAGTGTCTCCTCATCTTGGAATTCGTGATG 360

Qy       397 ATTGTCGTCTTTGGTTTGGAGTTCATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGA 456
Db       361 ATCGTGGTTTTCGGCTTGGAGTACATCGTCCGGGTCTGGTCCGCCGGATGCTGCTGCCGC 420

Qy       457 TATAGAGGATGGCAAGGAAGACTGAGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACC 516
Db       421 TACCGAGGATGGCAGGGTCGCTTCCGCTTTGCCAGAAAGCCCTTCTGTGTCATCGACTTC 480

Qy       517 ATTGTTCTTATCGCTTCAATAGCAGTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCC 576
Db       481 ATCGTGTTCGTGGCCTCGGTGGCCGTCATCGCCGCGGGTACCCAGGGCAACATCTTCGCC 540

Qy       577 ACGTCTGCACTCAGAAGTCTCCGTTTCCTACAGATCCTCCGCATGGTGCGCATGGACCGA 636
Db       541 ACGTCCGCGCTGCGCAGCATGCGCTTCCTGCAGATCCTGCGCATGGTGCGCATGGACCGC 600

Qy       637 AGGGGAGGCACTTGGAAATTACTGGGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATC 696
Db       601 CGCGGCGGCACCTGGAAGCTGCTGGGCTCAGTGGTCTACGCGCATAGCAAGGAGCTGATC 660

Qy       697 ACAGCTTGGTACATAGGATTTTTGGTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTG 756
Db       661 ACCGCCTGGTACATCGGGTTCCTGGTGCTCATCTTCGCCTCCTTCCTGGTCTACCTGGCT 720

Qy       757 GAAAAGGATGCCAATAAAGAGTTTTCTACATATGCAGATGCTCTCTGGTGGGGCACAATT 816
Db       721 GAGAAGGACGCCAACTCCGACTTCTCCTCCTACGCCGACTCGCTCTGGTGGGGGACGATT 780

Qy       817 ACATTGACAACTATTGGCTATGGAGACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTT 876
Db       781 ACATTGACAACCATCGGCTATGGTGACAAGACACCGCACACATGGCTGGGCAGGGTCCTG 840

Qy       877 TCTGCAGGCTTTGCACTCCTTGGCATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGC 936
Db       841 GCTGCTGGCTTCGCCTTACTGGGCATCTCTTTCTTTGCCCTGCCTGCCGGCATCCTAGGC 900

Qy       937 TCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAGAAACACTTTGAGAAAAGAAGG 996
Db       901 TCCGGCTTTGCCCTGAAGGTCCAGGAGCAGCACCGGCAGAAGCACTTCGAGAAGCGGAGG 960

Qy       997 AACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCT 1056
Db       961 ATGCCGGCAGCCAACCTCATCCAGGCTGCCTGGCGCCTGTACTCCACCGATATGAGCCGG 1020

Qy      1057 GTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGCACAC---------------- 1100
Db      1021 GCCTACCTGACAGCCACCTGGTACTACTATGACAGTATCCTCCCATCCTTCAGAGAGCTG 1080

Qy      1101 ------------------------------------------------------------ 1100

Db      1081 GCCCTCTTGTTTGAGCACGTGCAACGGGCCCGCAATGGGGGCCTACGGCCCCTGGAGGTG 1140

Qy      1101 ------------------------------------------------------------ 1100

Db      1141 CGGCGGGCGCCGGTACCCGACGGAGCACCCTCCCGTTACCCGCCCGTTGCCACCTGCCAC 1200

Qy      1101 --------------------CTGCAGCCCTACCAATCAGAAGCTAAGTTTTAAGGAGCGA 1140
Db      1201 CGGCCGGGCAGCACCTCCTTCTGCCCTGGGGAAAGCAGCCGGATGGGCATCAAAGACCGC 1260

Qy      1141 GTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT------AAGAGCCGACAAGCCTCAGTA 1194
Db      1261 ATCCGCATGGGCAGCTCCCAGCGGCGGACGGGTCCTTCCAAGCAGCATCTGGCACCTCCA 1320

Qy      1195 GGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAGG---GCAGTCCCACCAAAGTG 1251
Db      1321 ACAATGCCCACCTCCCCAAGCAGCGAGCAGGTGGGTGAGGCCACCAGCCCCACCAAGGTG 1380

Qy      1252 CAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGT 1311
Db      1381 CAAAAGAGCTGGAGCTTCAATGACCGCACCCGCTTCCGGGCATCTCTGAGACTC------ 1434

Qy      1312 TCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGAT 1371
Db      1435 ---------AAACCCCGCACCTCTGCTGAGGATGCCC---CCTCAGAGGAAGTAGCAGAG 1482

Qy      1372 GAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTC 1431
Db      1483 GAGAAGAGCTACCAGTGTGAGCTCACGGTGGACGACATCATGCCTGCTGTGAAGACAGTC 1542

Qy      1432 ATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTA 1491
Db      1543 ATCCGCTCCATCAGGATTCTCAAGTTCCTGGTGGCCAAAAGGAAATTCAAGGAGACACTG 1602

Qy      1492 CGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTG 1551
Db      1603 CGACCGTACGACGTGAAGGACGTCATTGAGCAGTACTCAGCAGGCCACCTGGACATGCTG 1662

Qy      1552 TGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGC---AAATC 1608
Db      1663 GGCCGGATCAAGAGCCTGCAAACTCGGGTGGACCAAATTGTGGGTCGGGGGCCCGGGGAC 1722

Qy      1609 ACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTC 1668
Db      1723 AGGAAGGCCCGGGAGAAGGGCGACAAGGGGCCCTCCGACGCGGAGGTGGTGGATGAAATC 1782

Qy      1669 AGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGCTG 1728
Db      1783 AGCATGATGGGACGCGTGGTCAAGGTGGAGAAGCAGGTGCAGTCCATCGAGCACAAGCTG 1842

Qy      1729 GACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCT 1788
Db      1843 GACCTGCTGTTGGGCTTCTATTCGCGCTGCCTGC------GCTCTGGCACCTCGGCCAGC 1896

Qy      1789 TTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCT 1848
Db      1897 CTGGGCGCCGTGCAAGTGCCGCTGTTCGACCCCGACATCACCTCCGACTACCACAGCCCT 1956

Qy      1849 GTGGATAGCAAAGATCTTTCGGGTTCCGCACAAA 1882
Db      1957 GTGGACCACGAGGACATCTCCGTCTCCGCACAGA 1990


RESULT 7
US-09-492-361-1
; Sequence 1, Application US/09492361
; Patent No. 6794161
; GENERAL INFORMATION:
;  APPLICANT: JENTSCH, Thomas J.
;  TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
;  TITLE OF INVENTION:  POTASSIUM CHANNELS
;  FILE REFERENCE: 2815-127P
;  CURRENT APPLICATION NUMBER: US/09/492,361
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;  CURRENT FILING DATE:  2000-01-27
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 2335
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (1)..(2335)
;   NAME/KEY: CDS
;   LOCATION: (83)..(2170)
US-09-492-361-1

  Query Match             18.4%;  Score 492;  DB 4;  Length 2335;
  Best Local Similarity   59.3%;  Pred. No. 2.9e-139;
  Matches 1087;  Conservative    0;  Mismatches  555;  Indels  192;  Gaps    7;

Qy        217 TACCGGCGGGTGCAGAACTACCTGTACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTC 276
              ||||| ||  |||||||||   | ||||||||||||||| | ||||||||||||| |||
Db        320 TACCGCCGCCTGCAGAACTGGGTCTACAACGTGCTGGAGCGGCCCCGCGGCTGGGCCTTC 379

Qy        277 ATCTACCACGCTTTCGTTTTTCTCCTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCT 336
              |||||||||  ||| | ||| | || |||||  | ||| || |  |||| ||| | ||
Db        380 GTCTACCACGTCTTCATATTTTTGCTGGTCTTCAGCTGCCTGGTGCTGTCTGTGCTGTCC 439

Qy        337 ACCATCCCTGAGCACACAAAATTGGCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATG 396
              || ||||  |||||   || | |||      || ||| | ||| |||| |||||||||
Db        440 ACTATCCAGGAGCACCAGGAACTTGCCAACGAGTGTCTCCTCATCTTGGAATTCGTGATG 499

Qy        397 ATTGTCGTCTTTGGTTTGGAGTTCATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGA 456
              || || || || ||||||| |||| | ||  |||||| || || ||||| || ||
Db        500 ATCGTGGTTTTCGGCTTGGAGTACATCGTCCGGGTCTGGTCCGCCGGATGCTGCTGCCGC 559

Qy        457 TATAGAGGATGGCAAGGAAGACTGAGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACC 516
              ||  |||||||||| ||  |  |  | |||||  |||||||||||||||| || ||   |
Db        560 TACCGAGGATGGCAGGGTCGCTTCCGCTTTGCCAGAAAGCCCTTCTGTGTCATCGACTTC 619

Qy        517 ATTGTTCTTATCGCTTCAATAGCAGTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCC 576
              || ||  |  | || ||  | || ||  |  | ||    || ||||| || || || |||
Db        620 ATCGTGTTCGTGGCCTCGGTGGCCGTCATCGCCGCGGGTACCCAGGGCAACATCTTCGCC 679

Qy        577 ACGTCTGCACTCAGAAGTCTCCGTTTCCTACAGATCCTCCGCATGGTGCGCATGGACCGA 636
              ||||| || ||  | ||  | || ||||| |||||||| ||||||||||||||||||||
Db        680 ACGTCCGCGCTGCGCAGCATGCGCTTCCTGCAGATCCTGCGCATGGTGCGCATGGACCGC 739

Qy        637 AGGGGAGGCACTTGGAAATTACTGGGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATC 696
              | || ||||| |||||  | ||||| |||||||| || || || ||||||||  | |||
Db        740 CGCGGCGGCACCTGGAAGCTGCTGGGCTCAGTGGTCTACGCGCATAGCAAGGAGCTGATC 799

Qy        697 ACAGCTTGGTACATAGGATTTTTGGTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTG 756
              || || |||||||| || ||  |||| || || ||  | || ||||| ||||| ||||
Db        800 ACCGCCTGGTACATCGGGTTCCTGGTGCTCATCTTCGCCTCCTTCCTGGTCTACCTGGCC 859

Qy        757 GAAAAGGATGCCAATAAAGAGTTTTCTACATATGCAGATGCTCTCTGGTGGGGCACAATT 816
              || ||||| |||||     || || ||  | || || ||  | ||||||||||| || |||
Db        860 GAGAAGGACGCCAACTCCGACTTCTCCTCCTACGCCGACTCGCTCTGGTGGGGGACGATT 919

Qy        817 ACATTGACAACTATTGGCTATGGAGACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTT 876
              |||||||||| || |||||||| ||||| || || |  || |||||||| ||  | ||
Db        920 ACATTGACAACCATCGGCTATGGTGACAAGACACCGCACACATGGCTGGGCAGGGTCCTG 979

Qy        877 TCTGCAGGCTTTGCACTCCTTGGCATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGC 936
              |||| ||||| ||  | || ||||| |||||||||| || ||||||||||| || |||
Db        980 GCTGCTGGCTTCGCCTTACTGGGCATCTCTTTCTTTGCCCTGCCTGCCGGCATCCTAGGC 1039

Qy        937 TCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAGAAACACTTTGAGAAAAGAAGG 996
              || || |||||  | || || || || ||||| ||||| ||||| |||||  | |||
Db       1040 TCCGGCTTTGCCCTGAAGGTCCAGGAGCAGCACCGGCAGAAGCACTTCGAGAAGCGGAGG 1099

Qy        997 AACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCT 1056
              |  || || |||||||||| ||| ||  |||||    ||| |  | |||  ||
Db       1100 ATGCCGGCAGCCAACCTCATCCAGGCTGCCTGGCGCCTGTACTCCACCGATATGAGCCGG 1159

Qy       1057 GTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGCACAC---------------- 1100
              | | | |  || ||      |    |||   |     | | | |
Db       1160 GCCTACCTGACAGCCACCTGGTACTACTATGACAGTATCCTCCCATCCTTCAGAGAGCTG 1219

Qy       1101 ------------------------------------------------------------ 1100

Db       1220 GCCCTCTTGTTTGAGCACGTGCAACGGGCCCGCAATGGGGGCCTACGGCCCCTGGAGGTG 1279

Qy       1101 ------------------------------------------------------------ 1100

Db       1280 CGGCGGGCGCCGGTACCCGACGGAGCACCCTCCCGTTACCCGCCCGTTGCCACCTGCCAC 1339

Qy       1101 --------------------CTGCAGCCCTACCAATCAGAAGCTAAGTTTTAAGGAGCGA 1140
                                   ||||          |     | |  |  | || || ||
Db       1340 CGGCCGGGCAGCACCTCCTTCTGCCCTGGGGAAAGCAGCCGGATGGGCATCAAAGACCGC 1399

Qy       1141 GTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT------AAGAGCCGACAAGCCTCAGTA 1194
              | |||||||  ||| ||  | | | ||    |     |||  |  |  ||  |   |
Db       1400 ATCCGCATGGGCAGCTCCCAGCGGCGGACGGGTCCTTCCAAGCAGCAGCTGGCACCTCCA 1459

Qy       1195 GGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAGG---GCAGTCCCACCAAAGTG 1251
                      | ||||||||||| |||       |  ||||    ||| |||||||| |||
Db       1460 ACAATGCCCACCTCCCCAAGCAGCGAGCAGGTGGGTGAGGCCACCAGCCCCACCAAGGTG 1519

Qy       1252 CAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGT 1311
              || |||||||||||||||| ||||| |||||||||||| | || ||| | |||
Db       1520 CAAAAGAGCTGGAGCTTCAATGACCGCACCCGCTTCCGGGCATCTCTGAGACTC------ 1573

Qy       1312 TCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGAT 1371
                   |||||   |  ||||||  ||||   | | || || |||   ||
Db       1574 ---------AAACCCCGCACCTCTGCTGAGGATGCCC---CCTCAGAGGAAGTAGCAGAG 1621

Qy       1372 GAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTC 1431
              || ||  | | |||||||||  |  | ||||| ||| |||  ||  |  | || || |||
Db       1622 GAGAAGAGCTACCAGTGTGAGCTCACGGTGGACGACATCATGCCTGCTGTGAAGACAGTC 1681

Qy       1432 ATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTA 1491
              || ||  | ||||| ||| | || || |  || || ||| |||| || ||||| ||  |
Db       1682 ATCCGCTCCATCAGGATTCTCAAGTTCCTGGTGGCCAAAAGGAAATTCAAGGAGACACTG 1741

Qy       1492 CGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTG 1551
              || || || || || || || |||||||| || || || || || || |||||||||  ||
Db       1742 CGACCGTACGACGTGAAGGACGTCATTGAGCAGTACTCAGCAGGCCACCTGGACATGCTG 1801

Qy       1552 TGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGC---AAATC 1608
              |  | || || ||||| ||||| || || || ||||||  | ||    ||||       |
Db       1802 GGCCGGATCAAGAGCCTGCAAACTCGGGTGGACCAAATTGTGGGTCGGGGGCCCGGGGAC 1861

Qy       1609 ACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTC 1668
              |      |   | |||   | || ||      |  | ||     |||       || ||  ||
Db       1862 AGGAAGGCCCGGGAGAAGGGCGACAAGGGGCCCTCCGACGCGGAGGTGGTGGATGAAATC 1921

Qy       1669 AGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGCTG 1728
              || ||| | || || |||||||||| || || ||||| |||||||| |||  |||||||
Db       1922 AGCATGATGGGACGCGTGGTCAAGGTGGAGAAGCAGGTGCAGTCCATCGAGCACAAGCTG 1981

Qy       1729 GACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCT 1788
              |||   ||  | | | |||||     |   ||| |      ||||||  |  |   |
Db       1982 GACCTGCTGTTGGGCTTCTATTCGCGCTGCCTGC------GCTCTGGCACCTCGGCCAGC 2035

Qy       1789 TTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCT 1848
              |||   |  | ||  | || |  || ||    ||    || || ||||| || ||||||
Db       2036 CTGGGCGCCGTGCAAGTGCCGCTGTTCGACCCCGACATCACCTCCGACTACCACAGCCCT 2095

Qy       1849 GTGGATAGCAAAGATCTTTCGGGTTCCGCACAAA 1882
              |||||  | | ||  | || |  |||||||| |
Db       2096 GTGGACCACGAGGACATCTCCGTCTCCGCACAGA 2129


RESULT 8
US-09-177-650-88
; Sequence 88, Application US/09177650
```
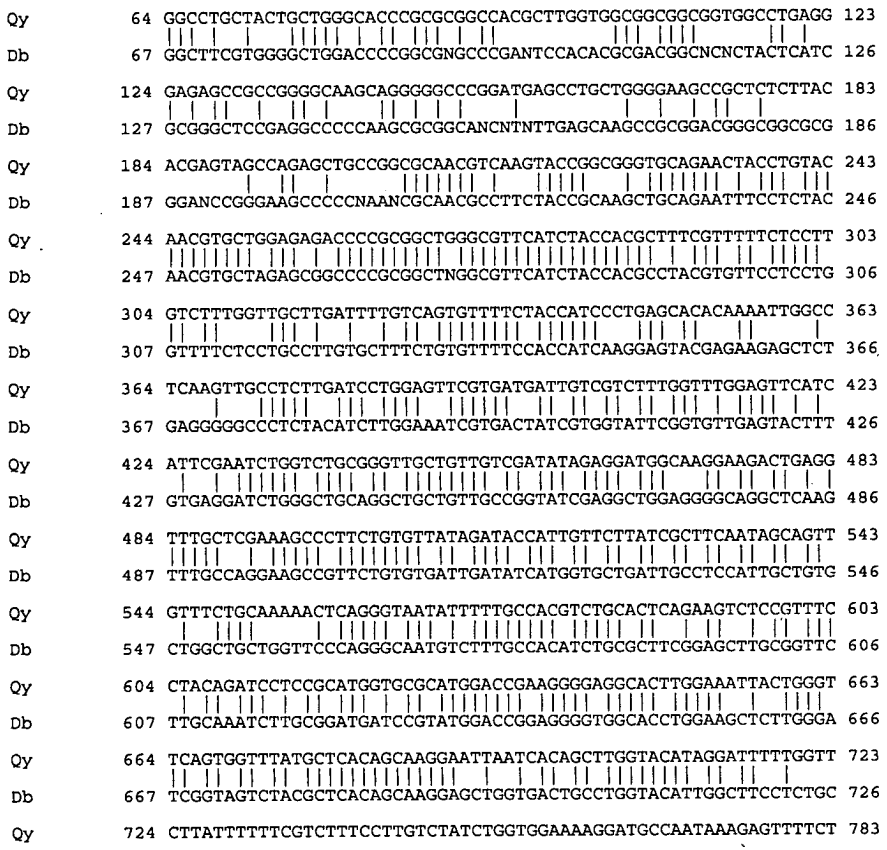
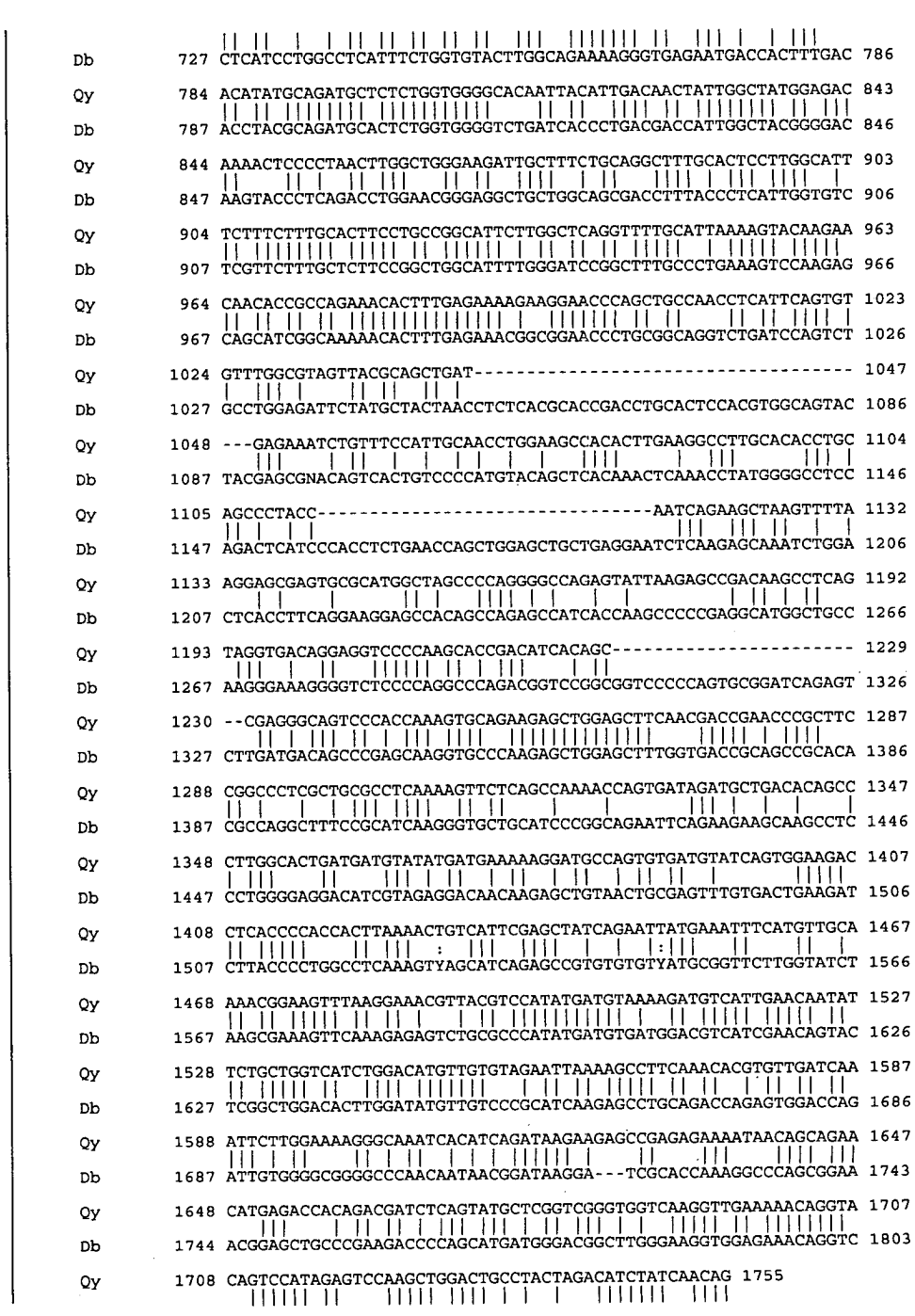

; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; TITLE OF INVENTION: AND OTHER EPILEPSIES
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 2273
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2271)
US-09-177-650-88

Query Match 18.3%; Score 489.2; DB 3; Length 2273;
Best Local Similarity 57.0%; Pred. No. 2e-138;
Matches 1020; Conservative 2; Mismatches 667; Indels 99; Gaps 4;





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Db       1804 TTGTCCATGGAAAAGAAGCTCGACTTCTTGGTGAGCATCTATACACAG 1851


RESULT 9
US-09-105-058C-22
; Sequence 22, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
;  APPLICANT:  Blanar, Michael A.
;  APPLICANT:  Dworetzky, Steven
;  APPLICANT:  Gribkoff, Valentin K.
;  APPLICANT:  Levesque, Paul C.
;  APPLICANT:  Little, Wayne A.
;  APPLICANT:  Neubauer, Michael G.
;  APPLICANT:  Yang, Wen-Pin
;  TITLE OF INVENTION:  KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
;  FILE REFERENCE:  3053-4052
;  CURRENT APPLICATION NUMBER: US/09/105,058C
;  CURRENT FILING DATE:  1998-06-26
;  PRIOR APPLICATION NUMBER:  US 60/055,599
;  PRIOR FILING DATE:  1997-08-12
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 2169
;   TYPE: DNA
;   ORGANISM: mouse
US-09-105-058C-22

  Query Match             17.8%;  Score 475.6;  DB 3;  Length 2169;
  Best Local Similarity   57.0%;  Pred. No. 2.9e-134;
  Matches 1022;  Conservative    0;  Mismatches  664;  Indels  108;  Gaps    4;

Qy         64 GGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTGAGG 123
Db         67 GGCTTCGTGGGGCTGGACCCCGGCGCGCCCGACTCCACACGCGACGGCGCGCTACTCATC 126

Qy        124 GAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCTTAC 183
Db        127 GCGGGCTCCGAGGCCCCCAAGCGCGGCAGCGTTTTGAGCAAGCCGCGGACGGGCGGCGCG 186

Qy        184 ACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTGTAC 243
Db        187 GGAGCCGGGAAGCCCCCGAAGCGCAACGCCTTCTACCGCAAGCTGCAGAATTTCCTCTAC 246

Qy        244 AACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTCCTT 303
Db        247 AACGTGCTAGAGCGGCCCCGCGGCTGGGCGTTCATCTACCACGCCTACGTGTTCCTTTTA 306

Qy        304 GTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTGGCC 363
Db        307 GTCTTCTCCTGCCTTGTGCTTTCTGTGTTTTCCACCATCAAGGAGTACGAGAAGAGCTCT 366

Qy        364 TCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTCATC 423
Db        367 GAGGGGGCCCTCTACATCTTGGAAATCGTGACTATCGTGGTATTCGGTGTTGAGTACTTT 426

Qy        424 ATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTGAGG 483
Db        427 GTGAGGATCTGGGCTGCAGGCTGCTGTTGCCGGTATCGAGGCTGGAGGGGCAGGCTCAAG 486

Qy        484 TTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCAGTT 543
Db        487 TTTGCCAGGAAGCCGTTCTGTGTGATTGATATCATGGTGCTGATTGCCTCCATTGCTGTG 546

Qy        544 GTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGTTTC 603
Db        547 CTGGCTGCTGGTTCCCAGGGCAATGTCTTTGCCACATCTGCGCTTCGGAGCTTGCGGTTC 606

Qy        604 CTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTGGGT 663
Db        607 TTGCAAATCTTGCGGATGATCCGTATGGACCGGAGGGGTGGCACCTGGAAGCTCTTGGGA 666

Qy        664 TCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTGGTT 723
Db        667 TCGGTAGTCTACGCTCACAGCAAGGAGCTGGTGACTGCCTGGTACATTGGCTTCCTCTGC 726

Qy        724 CTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTTTCT 783
Db        727 CTCATCCTGGCCTCATTTCTGGTGTACTTGGCAGAAAAGGGTGAGAATGACCACTTTGAC 786

Qy        784 ACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGAGAC 843
Db        787 ACCTACGCAGATGCACTCTGGTGGGGTCTGATCACCCTGACGACCATTGGCTACGGGGAC 846

Qy        844 AAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGCATT 903
Db        847 AAGTACCCTCAGACCTGGAACGGGAGGCTGCTGGCAGCGACCTTTACCCTCATTGGTGTC 906

Qy        904 TCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAAGAA 963
Db        907 TCGTTCTTTGCTCTTCCTGCTGGCATTTTGGGATCCGGCTTTGCCCTGAAAGTCCAAGAG 966

Qy        964 CAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAGTGT 1023
Db        967 CAGCATCGGCAAAAACACTTTGAGAAACGGCGGAACCCTGCGGCAGGTCTGATCCAGTCT 1026

Qy       1024 GTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCACAC 1083
Db       1027 GCCTGGAGATTCTATGCTACTAACCTCTCACGCACCGACCTGCACTCCACGTGGCAGTAC 1086

Qy       1084 T---------------------------------------------------------- 1084
Db       1087 TACGAGCGGACAGTCACTGTCCCCATGTACAGACTCATCCCACCTCTGAACCAGCTGGAG 1146

Qy       1085 ----------------------------------------TGAAGGCCTTGCACACCTGC 1104
Db       1147 CTGCTGAGGAATCTCAAGAGCAAATCTGGACTCACCTTCAGGAAGGAGCCACAGCCAGAG 1206

Qy       1105 AGCCCTACCAATCAGAAGCTAAGTTTTAAGGAGCGAG---TGCGCATGGCTAGCCCCAGG 1161
Db       1207 CCATCACCAAGTCAGAAGGTCAGTTTGAAAGATCGTGTCTTCTCCAGCCCCCGAGGCATG 1266

Qy       1162 GGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGAC 1221
Db       1267 GCTGCCAAGGGAAAGGGGTCTCCCCAGGCCCAGACGGTCCGGCGGTCCCCCAGTGCGGAT 1326

Qy       1222 ATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACC 1281
Db       1327 CAGAGTCTTGATGACAGCCCGAGCAAGGTGCCCAAGAGCTGGAGCTTTGGTGACCGCAGC 1386

Qy       1282 CGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGAC 1341
Db       1387 CGCACACGCCAGGCTTTCCGCATCAAGGGTGCTGCATCCCGGCAGAATTCAGAAGCAAGC 1446

Qy       1342 ACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTG 1401
Db       1447 C---TCCCTGGGGAGGACATCGTAGAGGACAACAAGAGCTGTAACTGCGAGTTTGTGACT 1503

Qy       1402 GAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCAT 1461
Db       1504 GAAGATCTTACCCCTGGCCTCAAAGTTAGCATCAGAGCTGTGTGTGTTATGCGGTTCTTG 1563

Qy       1462 GTTGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAA 1521
Db       1564 GTATCTAAGCGAAAGTTCAAAGAGAGTCTGCGCCCATATGATGTGATGGACGTCATCGAA 1623

Qy       1522 CAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTT 1581
Db       1624 CAGTACTCGGCTGGACACTTGGATATGTTGTCCCGCATCAAGAGCCTGCAGTCCAGAGTG 1683

Qy       1582 GATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACA 1641
Db       1684 GACCAGATTGTGGGGCGGGGCCCAACAATAACGGATAAGGA---TCGCACCAAAGGCCCA 1740

Qy       1642 GCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAA 1701
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Db       1741 GCGGAAACGGAGCTGCCCGAAGACCCCAGCATGATGGGACGGCTTGGGAAGGTGGAGAAA 1800

Qy       1702 CAGGTACAGTCCATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAG 1755

Db       1801 CAGGTCTTGTCCATGGAAAAGAAGCTCGACTTCTTGGTGAGCATCTATACACAG 1854


RESULT 10
US-09-105-058C-1
; Sequence 1, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
;  APPLICANT:  Blanar, Michael A.
;  APPLICANT:  Dworetzky, Steven
;  APPLICANT:  Gribkoff, Valentin K.
;  APPLICANT:  Levesque, Paul C.
;  APPLICANT:  Little, Wayne A.
;  APPLICANT:  Neubauer, Michael G.
;  APPLICANT:  Yang, Wen-Pin
;  TITLE OF INVENTION:  KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
;  FILE REFERENCE:  3053-4052
;  CURRENT APPLICATION NUMBER: US/09/105,058C
;  CURRENT FILING DATE:  1998-06-26
;  PRIOR APPLICATION NUMBER:  US 60/055,599
;  PRIOR FILING DATE:  1997-08-12
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 896
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Consensus
;   OTHER INFORMATION: nucleotide sequence as shown in Fig. 16A-16D
;   OTHER INFORMATION: y=c or t; r=a or g; m=a or c; k=g or t; s=g or c;
;   OTHER INFORMATION: w=a or t; h=a, c, or t; b=g, t, or c; v=g, c, or a
US-09-105-058C-1

  Query Match             17.5%;  Score 465.4;  DB 3;  Length 896;
  Best Local Similarity   53.7%;  Pred. No. 2e-131;
  Matches  460;  Conservative  231;  Mismatches  162;  Indels    4;  Gaps    2;

Qy        190 AGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTGTACAACGTG 249

Db         13 RGSMRSCCMSYSAAGMGMAACGCCWWSTACCGSMRSMTSCARAMTTTSMTCTACRACGYS 72

Qy        250 CTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTCCTTGTCTTT 309

Db         73 CTRGAGMGRCCSCGSGGCTGGGCGYTSMTYTACCACGCSTWSGTGTTCCTBHTDGTYYTS 132

Qy        310 GGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTGGCCTCAAGT 369

Db        133 KSSTGCYTBRTKCTGKCTGTS-YKWCCACMWTCAAGGAGTAYGAGAMKRKYTCBGRRGRS 191

Qy        370 TGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTCATCATTCGA 429

Db        192 KSSCTYYWSWTMYTGGARAYMKTKRCYATYKTSRTVTTYGGHGYBGAGTWYKYYKTGMGR 251

Qy        430 ATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTGAGGTTTGCT 489

Db        252 ATCTGGGCYGCWGGMTGYTSYTGCCGRTACMRWGGCTGGMGGGGSMGRCTSAAGTTTGCC 311

Qy        490 CGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCAGTTGTTTCT 549

Db        312 MGGAARCCVCTSTGYRTGWTBGAYATCWTKGTGCTSATYGCCTCYRTKSCDGTGSTKGCY 371

Qy        550 GCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGTTTCCTACAG 609

Db        372 GYBGGHWMCCARGGCAAYGTYYTKGCYACVTCY---CTBCGRAGCYTGCGSTTCYTRCAR 428

Qy        610 ATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTGGGTTCAGTG 669

Db        429 ATYYTRCGSATGMTSCGBATGGACCGGMGRGGHGGCACCTGGAAGCTBYTGGGMTCDGYV 488

Qy        670 GTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTGGTTCTTATT 729

Db        489 RTCTRYGCYCACAGCAARGARCTSRTSACKGCSTGGTACATYGGYTTCCTBWSHCTCATC 548

Qy        730 TTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTTTCTACATAT 789

Db        549 CTKKCYTCRTTYCTKGTSTACYTGGYWGARAARSSDGAGRWBGAYSMMTTYGASACCTAY 608

Qy        790 GCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGAGACAAAACT 849

Db        609 GCRGATGCMCTSTGGTGGGGYCTGATCACVCTGRCVACCATTGGCTAYGGRGACAAGWMM 668

Qy        850 CCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGCATTTCTTTC 909

Db        669 CCYMARACSTGGRAMGGSMGKCTSHTDGCVGCVACSTTYWCCYTMATYGGYGTCTCVTTY 728

Qy        910 TTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAAGAACAACAC 969

Db        729 TTYGCBCTKCCWGCDGGCATYYTGGGRTCYGGSYTKGCCCTSAARGTBCARGAGCARCAY 788

Qy        970 CGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGG 1029

Db        789 MGKCARAARCACTTTGAGAARMGGMGGAABCCDGCDGCWGRBCTSATYCAGKCKGCCTGG 848

Qy       1030 CGTAGTTACGCAGCTGA 1046

Db        849 AGRTWYTAYGCYACYAA 865


RESULT 11
US-09-495-050A-305
; Sequence 305, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
;  APPLICANT: Roopa, Reddy
;  APPLICANT:  Guegler, Karl, J.
;  APPLICANT:  Au-Young, Janice
;  TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
;  FILE REFERENCE: PA-0013 US
;  CURRENT APPLICATION NUMBER: US/09/495,050A
;  CURRENT FILING DATE:  2000-01-31
;  PRIOR APPLICATION NUMBER: 60/118,318
;  PRIOR FILING DATE: February 1, 1999
;  NUMBER OF SEQ ID NOS: 305
;  SOFTWARE: PERL Program
; SEQ ID NO 305
;   LENGTH: 575
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6492505 4970006F6
;   NAME/KEY: unsure
;   LOCATION: 486, 510, 552, 573
;   OTHER INFORMATION: a, t, c, g, or other
US-09-495-050A-305

  Query Match             16.9%;  Score 452;  DB 4;  Length 575;
  Best Local Similarity   95.0%;  Pred. No. 1.8e-127;
  Matches  509;  Conservative    0;  Mismatches   22;  Indels    5;  Gaps    4;

Qy       1594 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1653

Db          1 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 60

Qy       1654 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1713

Db         61 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 120

Qy       1714 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1773
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Db        121 ATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 180
Qy       1774 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1833
Db        181 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 240
Qy       1834 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1893
Db        241 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 300
Qy       1894 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1953
Db        301 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCA-TCTGACGCCAAAT 359
Qy       1954 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2013
Db        360 GAGTTCAGTGCCCAGACTTTCTA--CGGCTTAGCCTACTATGCACAGTCAAGCAACACAG 417
Qy       2014 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2073
Db        418 GTGCCAA-TAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGC-AACCAA 475
Qy       2074 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCT 2129
Db        476 ATTAATACGGNACCCAAGCCAGCAGGCCCCACAANTTACAGTCTCCTCTCAGCTCT 531


RESULT 12
US-09-105-058C-26
; Sequence 26, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
;  APPLICANT:  Blanar, Michael A.
;  APPLICANT:  Dworetzky, Steven
;  APPLICANT:  Gribkoff, Valentin K.
;  APPLICANT:  Levesque, Paul C.
;  APPLICANT:  Little, Wayne A.
;  APPLICANT:  Neubauer, Michael G.
;  APPLICANT:  Yang, Wen-Pin
;  TITLE OF INVENTION:  KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
;  FILE REFERENCE:  3053-4052
;  CURRENT APPLICATION NUMBER: US/09/105,058C
;  CURRENT FILING DATE:  1998-06-26
;  PRIOR APPLICATION NUMBER:  US 60/055,599
;  PRIOR FILING DATE:  1997-08-12
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 26
;   LENGTH: 2565
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-105-058C-26

  Query Match           16.0%;  Score 427.2;  DB 3;  Length 2565;
  Best Local Similarity  56.7%;  Pred. No. 2.1e-119;
  Matches  923;  Conservative    0;  Mismatches  648;  Indels   57;  Gaps    5;

Qy         13 GAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGCGACGGCCTGCTA 72
Db         43 GCGGCGGCGGCCGGCGACGAGGAGCGGAAAGTGGGGCTGGCGCCCGGCGACGTGGAGCAA 102
Qy         73 CTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTGAGGGAGAGCCGC 132
Db        103 GTCACCTTGGCGCTCGGGGCCGGAGCCGACAAAGACGGGACCCTGCTGCTGGAGGGCGGC 162
Qy        133 CGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCTTACACGAGTAGC 192
Db        163 GGCCGCGACGAGGGGCAGCGGAGGACCCCGCAGGGCATCGGGCTCCTGGCCAAGACCCCG 222
Qy        193 CAGAGCTGCC---------GGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTGTAC 243
Db        223 CTGAGCCGCCCAGTCAAGAGAAACAACGCCAAGTACCGGCGCATCCAAACTTTGATCTAC 282

Qy        244 AACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTCCTT 303
Db        283 GACGCCCTGGAGAGACCGCGGGGCTGGGCGCTGCTTTACCACGCGTTGGTGTTCCTGATT 342
Qy        304 GTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTGGCC 363
Db        343 GTCCTGGGGTGCTTGATTCTGGCTGTCCTGACCACATTCAAGGAGTATGAGACTGTCTCG 402
Qy        364 TCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTCATC 423
Db        403 GGAGACTGGCTTCTGTTACTGGAGACATTTGCTATTTTCATCTTTGGAGCCGAGTTTGCT 462
Qy        424 ATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTGAGG 483
Db        463 TTGAGGATCTGGGCTGCTGGATGTTGCTGCCGATACAAAGGCTGGCGGGGCCGACTGAAG 522
Qy        484 TTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCAGTT 543
Db        523 TTTGCCAGGAAGCCCCTGTGCATGTTGGACATCTTTGTGCTGATTGCCTCTGTGCCAGTG 582
Qy        544 GTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGTTTC 603
Db        583 GTTGCTGTGGGAAACCAAGGCAATGTTCTGGCCACCT---CCCTGCGAAGCCTGCGCTTC 639
Qy        604 CTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTGGGT 663
Db        640 CTGCAGATCCTGCGCATGCTGCGGATGGACCGGAGAGGTGGCACCTGGAAGCTTCTGGGC 699
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Qy        874 CTTTCTGCAGGCTTTGCACTCCTTGGCATTTCTTTCTTTGCACTTCCTGCCGGCATTCTT 933
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Qy        934 GGCTCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAGAAACACTTTGAGAAAAGA 993
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Qy        994 AGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGTTACGCAGCTGATGAGAAA 1053
Db       1060 AGGAAGCCAGCTGCTGAGCTCATTCAGGCTGCCTGGAGGTATTATGCTACCAACCCCAAC 1119
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Qy       1225 ACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGC 1284
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Db       1420 ACAGGTGACCCCATGGC------GGAAGACAGGGGCTATGGGAATGACTTCCCCATCGAA 1473

Qy       1405 GACCTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTT 1464
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Qy       1465 GCAAAACGGAAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAA 1524
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Qy       1585 CAAATTCT 1592
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RESULT 13
US-09-177-650-6
; Sequence 6, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
;  APPLICANT: Leppert, Mark F.
;  APPLICANT: Singh, Nanda
;  APPLICANT: Charlier, Carole
;  TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
;  TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
;  TITLE OF INVENTION: AND OTHER EPILEPSIES
;  FILE REFERENCE: 2323-134
;  CURRENT APPLICATION NUMBER: US/09/177,650
;  CURRENT FILING DATE: 1998-10-23
;  EARLIER APPLICATION NUMBER: 60/063,147
;  EARLIER FILING DATE: 1997-10-24
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 2914
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (19)..(2634)
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: (840)
;   OTHER INFORMATION: The polymorphism of a T to a C at this position
;   OTHER INFORMATION: has appeared in one individual.
;   FEATURE:
;   NAME/KEY: mutation
;   LOCATION: (947)
;   OTHER INFORMATION: The missense mutation from a G to a T occurs at
;   OTHER INFORMATION: this position in a BFNC family.
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: (678)
;   OTHER INFORMATION: This position is polymorphic for C or T.
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: (750)
;   OTHER INFORMATION: This position is polymorphic for T or C.
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: (1089)
;   OTHER INFORMATION: This position is polymorphic for G or C.
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: (2598)
;   OTHER INFORMATION: This position is polymorphic for T or C.
US-09-177-650-6

  Query Match             16.0%;  Score 427.2;  DB 3;  Length 2914;
  Best Local Similarity   56.7%;  Pred. No. 2.4e-119;
  Matches  923;  Conservative    0;  Mismatches  648;  Indels   57;  Gaps    5;

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Qy        133 CGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCTTACACGAGTAGC 192
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Db        235 GGCCGCGACGAGGGGCAGCGGAGGACCCCGCAGGGCATCGGGCTCCTGGCCAAGACCCCG 294

Qy        193 CAGAGCTGCC---------GGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTGTAC 243
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Qy        244 AACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTCCTT 303
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Db        355 GACGCCCTGGAGAGACCGCGGGGCTGGGCGCTGCTTTACCACGCGTTGGTGTTCCTGATT 414

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Db        415 GTCCTGGGGTGCTTGATTCTGGCTGTCCTGACCACATTCAAGGAGTATGAGACTGTCTCG 474

Qy        364 TCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTCATC 423
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Qy        484 TTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCAGTT 543
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Db        772 TCAGCCATCTGTGCCCACAGCAAAGAACTCATCACGGCCTGGTACATCGGTTTCCTGACA 831

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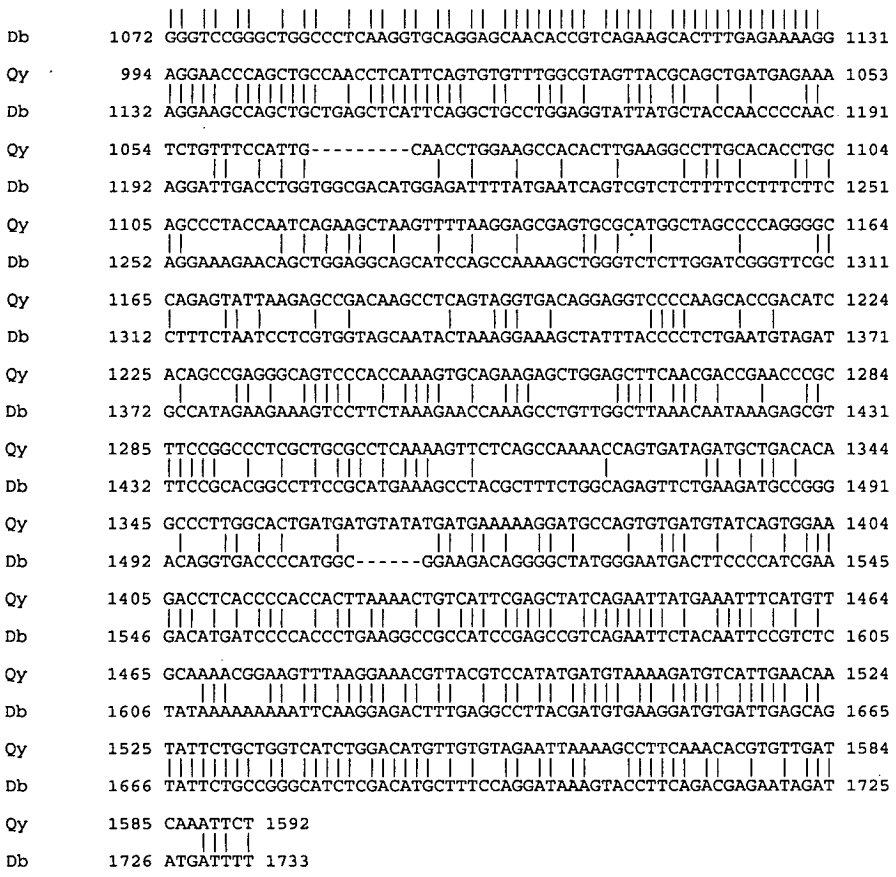
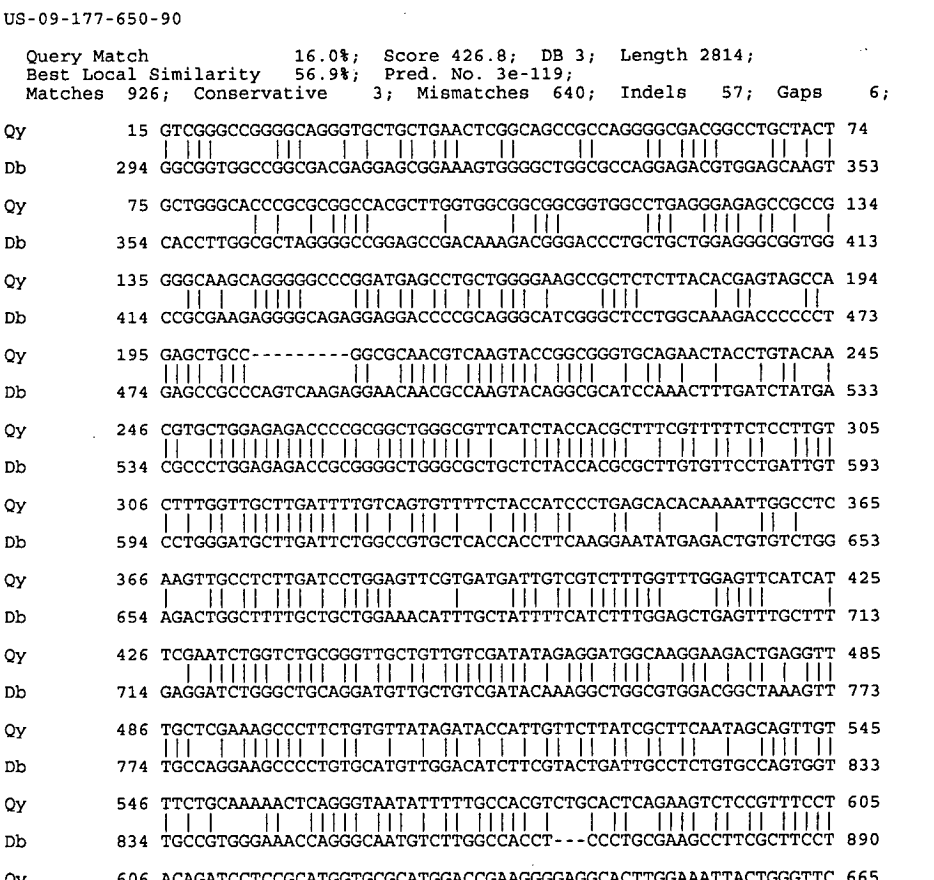
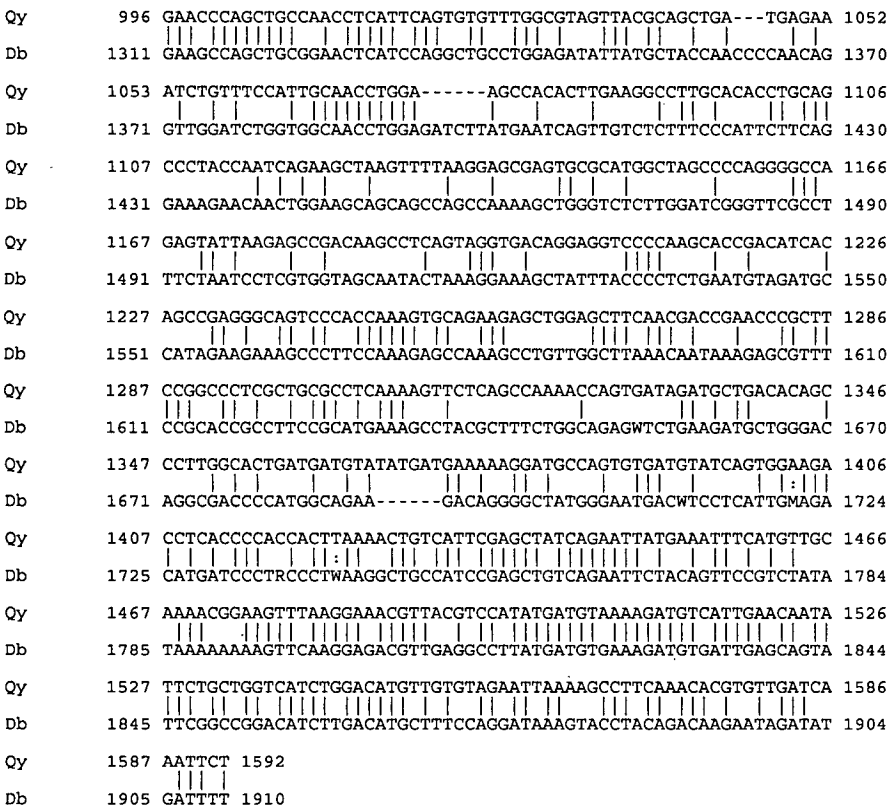


RESULT 14
US-09-177-650-90
; Sequence 90, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; TITLE OF INVENTION: AND OTHER EPILEPSIES
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 2814
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (202)..(2811)

US-09-177-650-90

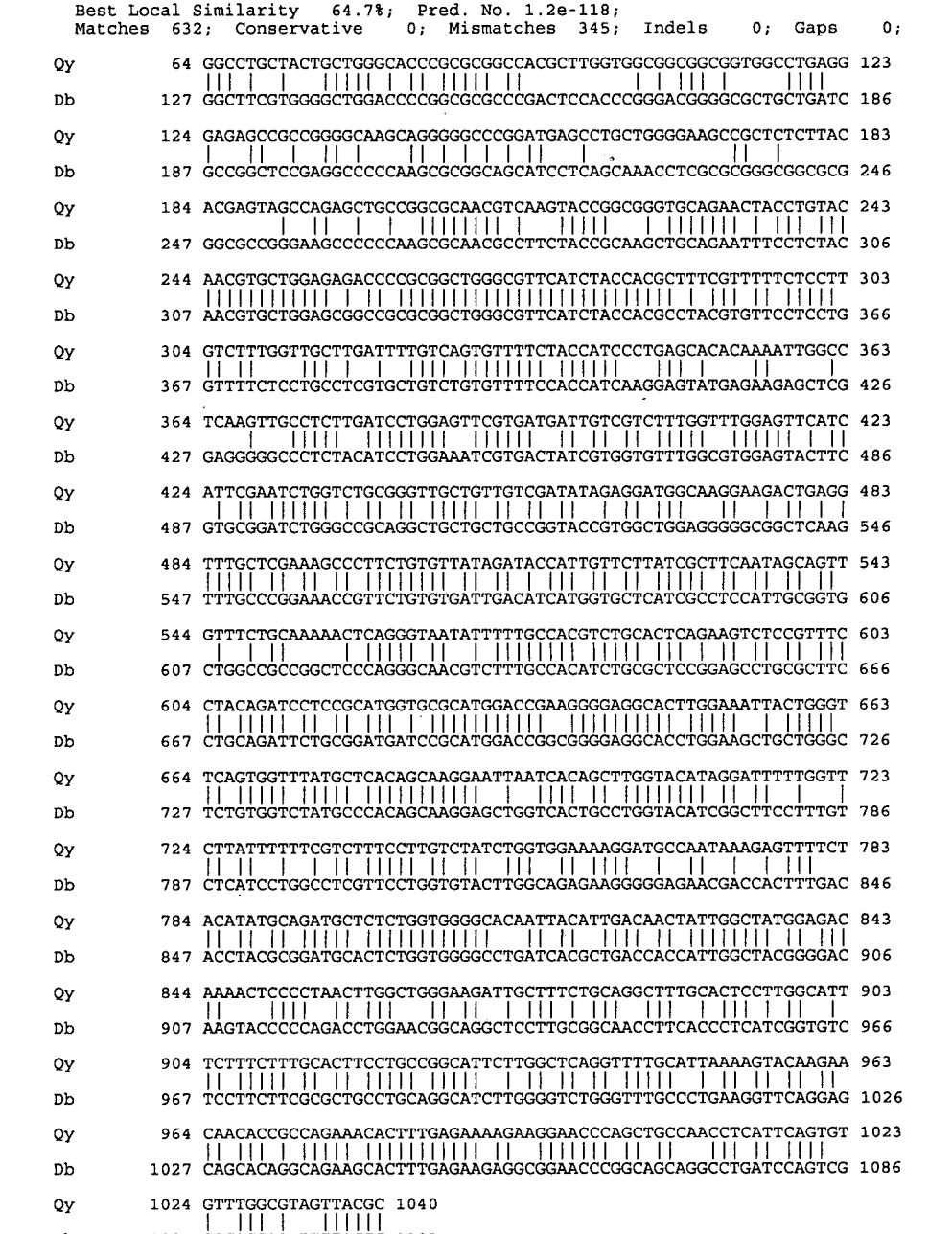
Query Match 16.0%; Score 426.8; DB 3; Length 2814;
Best Local Similarity 56.9%; Pred. No. 3e-119;
Matches 926; Conservative 3; Mismatches 640; Indels 57; Gaps 6;





RESULT 15
US-09-105-058C-19
; Sequence 19, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blanar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 3287
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-105-058C-19

Query Match 15.9%; Score 425; DB 3; Length 3287;



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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2662.2	99.8	3111	6	AX268476	AX268476 Sequence
5	2630	98.6	2694	6	AX322509	AX322509 Sequence
6	2625.2	98.4	3137	6	AR430568	AR430568 Sequence
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ALIGNMENTS

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DEFINITION Sequence 1 from patent US 6767736.
ACCESSION AR565635
VERSION AR565635.1 GI:53981668
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2772)
AUTHORS Hu,Y., Kieke,J.A., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B. and Sands,A.T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: US 6767736-A 1 27-JUL-2004;
FEATURES Location/Qualifiers
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ORIGIN

Query Match 99.8%; Score 2662.2; DB 6; Length 2772;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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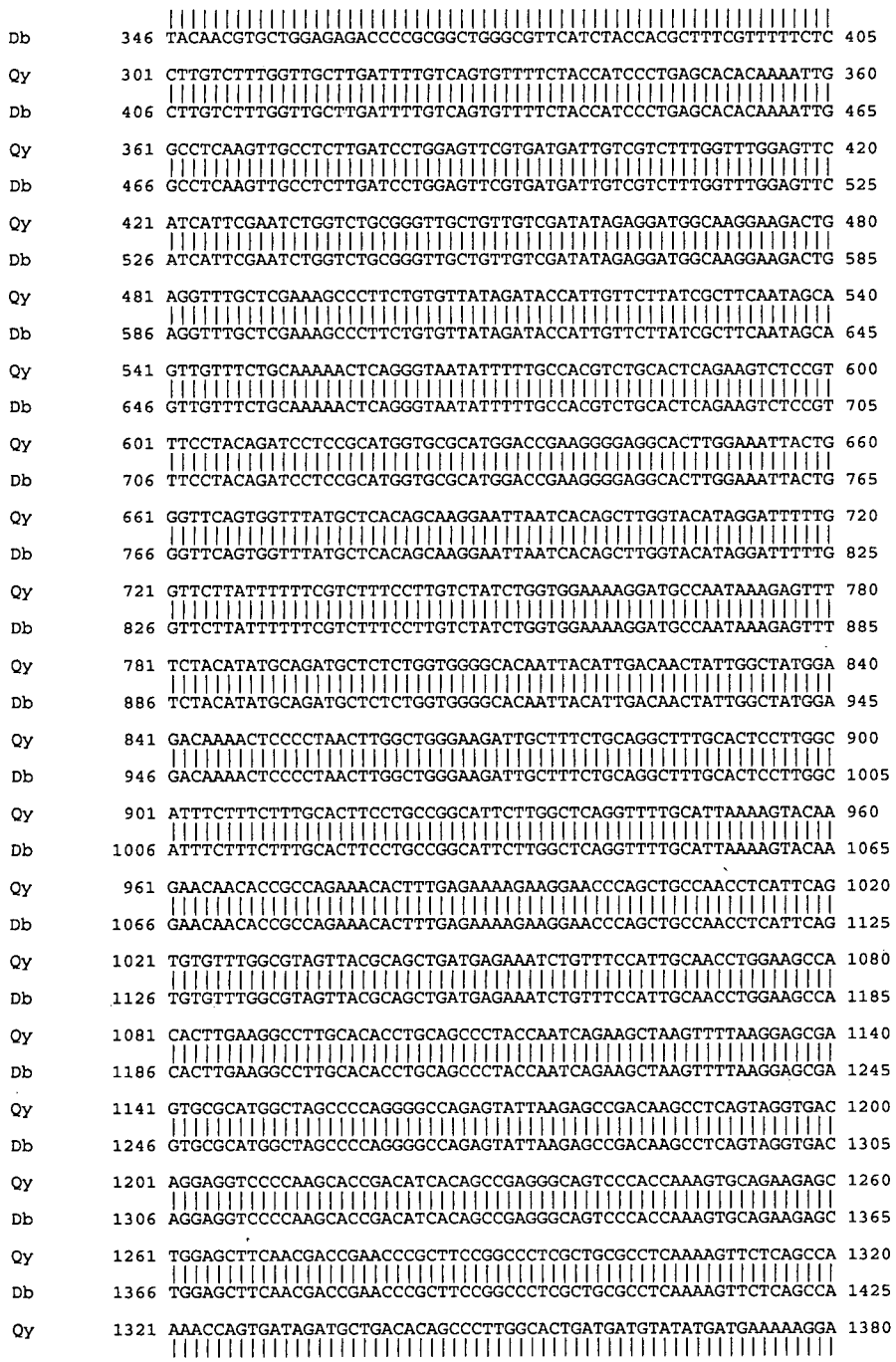
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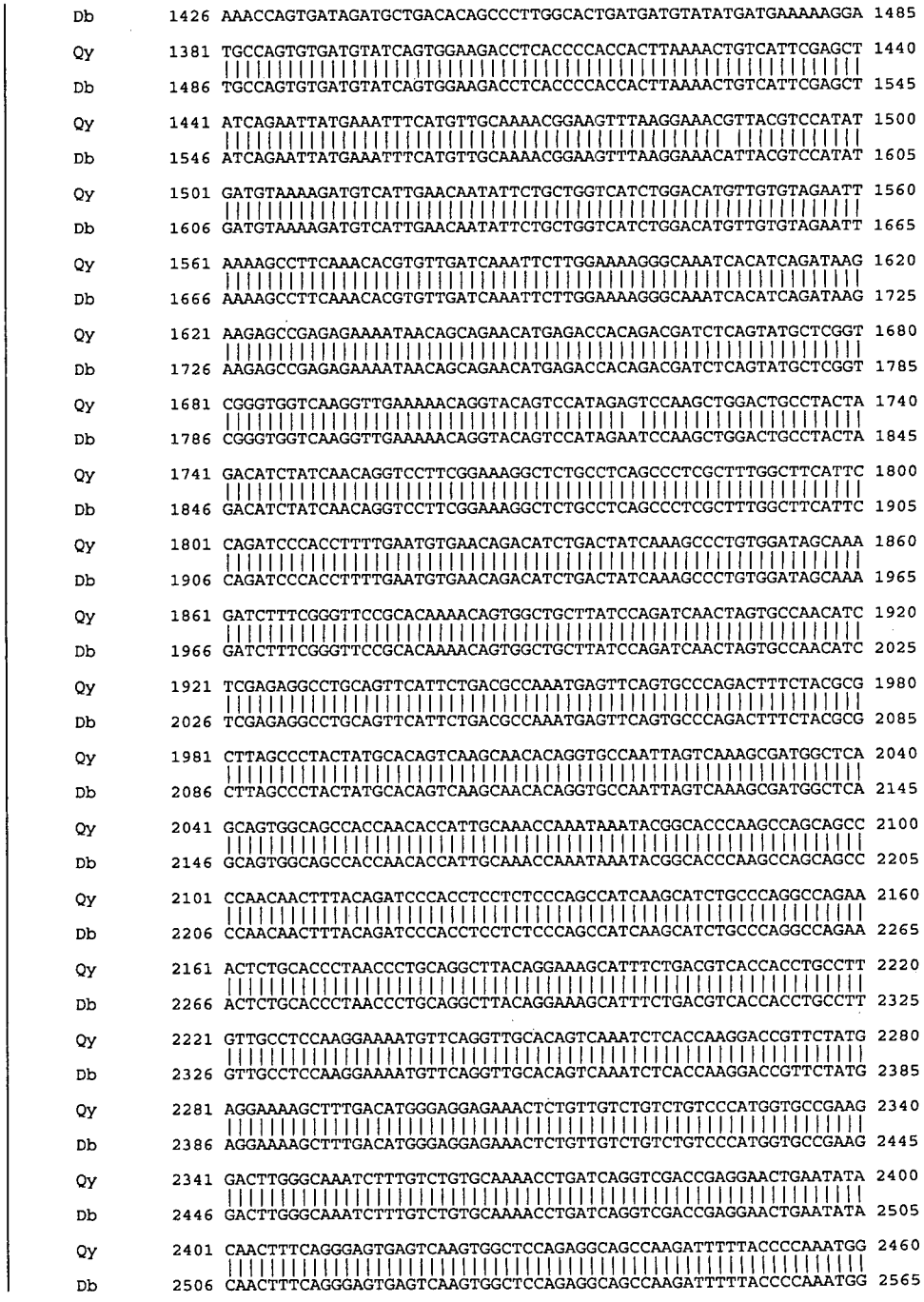
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RESULT 2
AX268474
LOCUS       AX268474               2772 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 1 from Patent WO0175108.
ACCESSION   AX268474
VERSION     AX268474.1  GI:16541652
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hu,Y., Kieke,J.A., Turner,A.C., Nehls,M.C., Friedrich,G.B.,
            Zambrowicz,B. and Sands,A.T.
  TITLE     Human ion channel protein and polynucleotides encoding the same
  JOURNAL   Patent: WO 0175108-A 1 11-OCT-2001;
            Lexicon Genetics Incorporated (US)
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ORIGIN

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Db        106 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 165

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
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Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
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Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
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Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
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Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
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Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
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Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
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Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
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Qy       1201 AGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGC 1260
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Qy       1321 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 1380
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Db       1606 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 1665

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RESULT 3
AR565636
LOCUS AR565636 3111 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 3 from patent US 6767736.
ACCESSION AR565636
VERSION AR565636.1 GI:53981669
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 3111)
AUTHORS Hu,Y., Kieke,J.A., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B. and Sands,A.T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: US 6767736-A 3 27-JUL-2004;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 99.8%; Score 2662.2; DB 6; Length 3111;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
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Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
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Qy      2101 CCAACAACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAA 2160
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Qy      2161 ACTCTGCACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTT 2220
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Qy      2221 GTTGCCTCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATG 2280
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Qy      2341 GACTTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATA 2400
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Qy      2521 ACTTTTGATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGG 2580
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Db      2745 ACTGGAAGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTC 2804

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RESULT 4
AX268476
LOCUS AX268476 3111 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 3 from Patent WO0175108.
ACCESSION AX268476

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VERSION     AX268476.1  GI:16541653
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hu,Y., Kieke,J.A., Turner,A.C., Nehls,M.C., Friedrich,G.B.,
            Zambrowicz,B. and Sands,A.T.
  TITLE     Human ion channel protein and polynucleotides encoding the same
  JOURNAL   Patent: WO 0175108-A 3 11-OCT-2001;
            Lexicon Genetics Incorporated (US)
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             99.8%;  Score 2662.2;  DB 6;  Length 3111;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2664;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 224

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        225 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTCGGTGGCGGCGGCGGTGGCCTG 284

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Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
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Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
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Db        405 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 464

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ACCESSION   AX322509
VERSION     AX322509.1  GI:18093555
KEYWORDS    .
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Dworetzky,S.I., Ramanathan,C.S., Trojnacki,J.T., Boissard,C.G. and
            Gribkoff,V.K.
  TITLE     Human kcnq5 potassium channel, methods and compositions thereof
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ORIGIN
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Query Match 98.6%; Score 2630; DB 6; Length 2694;
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Matches 2667; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

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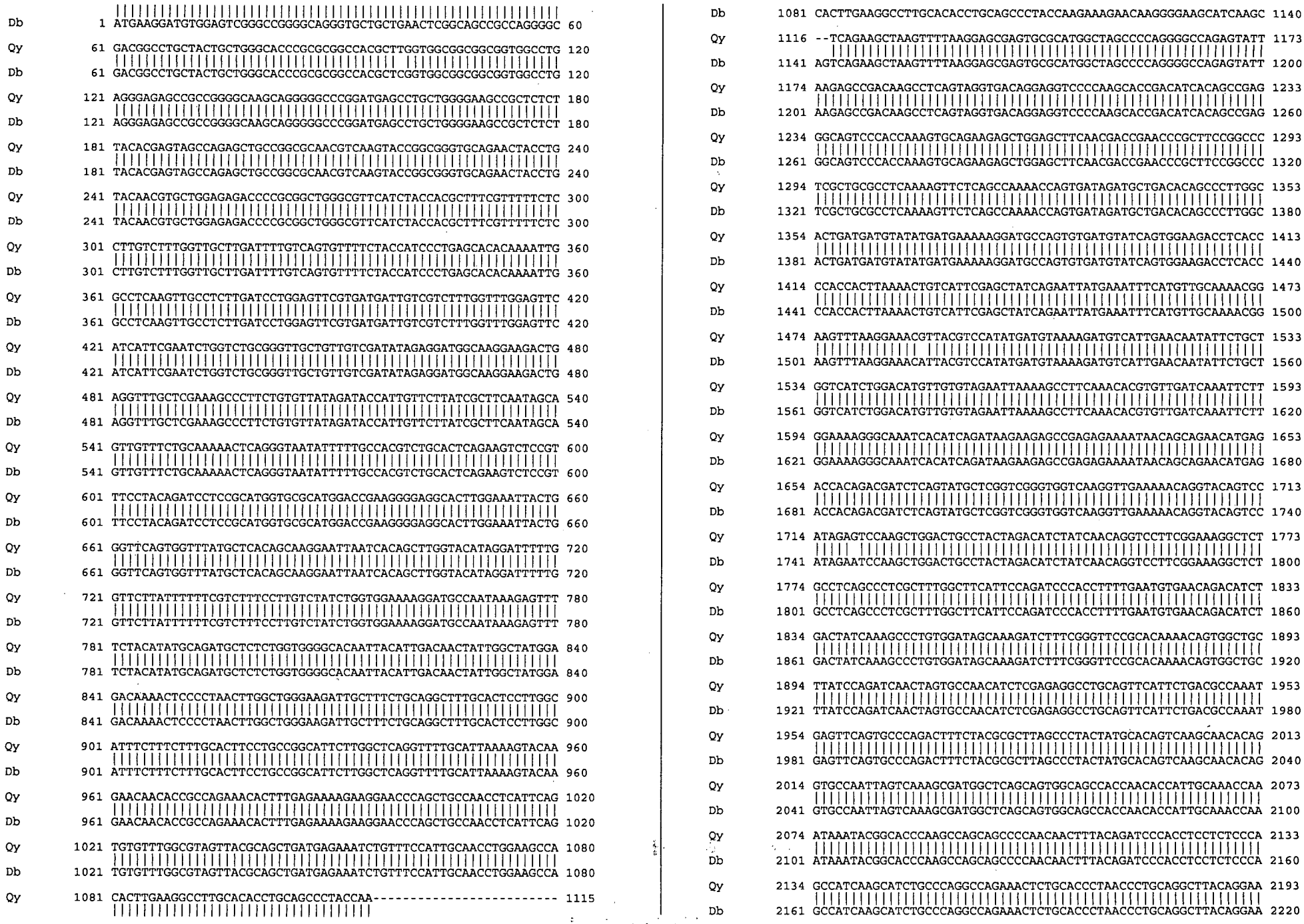
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Db 2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220

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Qy       2194 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2253
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Db       2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280

Qy       2254 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2313
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Qy       2314 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2373
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DEFINITION  Sequence 1 from Patent WO0077035.
ACCESSION   AX056817
VERSION     AX056817.1  GI:12309758
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jentsch,T.J.
  TITLE     Novel potassium channels and genes encoding these potassium
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  JOURNAL   Patent: WO 0077035-A 1 21-DEC-2000;
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ORIGIN
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  Matches 2664;  Conservative    0;  Mismatches    3;  Indels   27;  Gaps    1;

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Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
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Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
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Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
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Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660

Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
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Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
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Qy        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
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Db        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840

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Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
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Qy      1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAA---------------------------- 1115
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Qy      1116 --TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1173
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Qy      1234 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1293
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Qy      2254 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2313
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RESULT 8
AF202977

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DEFINITION  Homo sapiens potassium voltage-gated channel, KQT-like subfamily,
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ACCESSION   AF202977
VERSION     AF202977.1  GI:7798695
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3137)
  AUTHORS   Schroeder,B.C., Hechenberger,M., Weinreich,F., Kubisch,C. and
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  TITLE     KCNQ5, a novel potassium channel broadly expressed in brain,
            mediates M-type currents
  JOURNAL   J. Biol. Chem. 275 (31), 24089-24095 (2000)
  MEDLINE   20379054
   PUBMED   10816588
REFERENCE   2  (bases 1 to 3137)
  AUTHORS   Schroeder,B.C., Hechenberger,M., Weinreich,F., Kubisch,C. and
            Jentsch,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-NOV-1999) ZMNH, Hamburg University, Martinistrasse
            85, Hamburg 20246, Germany
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Query Match 98.4%; Score 2625.2; DB 9; Length 3137;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

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Qy       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAA---------------------------- 1115
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Qy       1116 --TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1173
Db       1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200

Qy       1174 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1233
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Qy       1294 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1353
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Db       1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440

Qy       1414 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1473
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Db       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340

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RESULT 9
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DEFINITION  Sequence 1 from patent US 6617131.
ACCESSION   AR393778
VERSION     AR393778.1  GI:40120748
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3074)
  AUTHORS   Steinmeyer,K., Lerche,C., Scherer,C., Seebohm,G. and Busch,A.E.
  TITLE     Nucleic acid molecule encoding the potassium channel protein, KCNQ5
  JOURNAL   Patent: US 6617131-A 1 09-SEP-2003;
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ORIGIN
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Query Match 98.1%; Score 2617.2; DB 6; Length 3074;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2659; Conservative 0; Mismatches 8; Indels 27; Gaps 1;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 274

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 334

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              |||||||||||||||||||||||||||||||||||||||||||||||| | | ||||||
Db        335 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGAAGCCGCCTCTCT 394

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
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Db        395 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 454

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Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
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Db        515 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 574

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Db        575 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 634

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
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Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
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Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
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Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
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Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
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Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
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Db       1175 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1234

Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
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RESULT 10
AX253254
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DEFINITION Sequence 1 from Patent WO0170811.
ACCESSION AX253254
VERSION AX253254.1 GI:16073802
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Lerche,C., Scherer,C., Seebohm,G., Busch,A. and Steinmeyer,K.
TITLE Potassium channel protein kcnq5, a target for diseases of central nervous system and cardiovascular system
JOURNAL Patent: WO 0170811-A 1 27-SEP-2001;

Aventis Pharma Deutschland GmbH (DE)

FEATURES Location/Qualifiers
source 1. .3074
/organism="Homo sapiens"
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ORIGIN

Query Match 98.1%; Score 2617.2; DB 6; Length 3074;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2659; Conservative 0; Mismatches 8; Indels 27; Gaps 1;

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Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
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Db        275 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 334

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
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Db        335 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGAAGCCGCCTCTCT 394

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
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Db        395 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 454

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
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Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
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Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
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RESULT 11
AX456864
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DEFINITION  Sequence 5 from Patent WO0232960.
ACCESSION   AX456864
VERSION     AX456864.1  GI:21715731
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Argentieri,T.M. and Sheldon,J.H.
  TITLE     Methods of selecting compounds for modulation of bladder function
  JOURNAL   Patent: WO 0232960-A 5 25-APR-2002;
            Wyeth (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           98.1%;  Score 2617.2;  DB 6;  Length 3074;
  Best Local Similarity   98.7%;  Pred. No. 0;
  Matches 2659;  Conservative    0;  Mismatches    8;  Indels   27;  Gaps    1;
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Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
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Db        215 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 274

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
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Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
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Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
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Qy       1954 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2013
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Qy       2014 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2073
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Qy       2074 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2133
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Qy       2134 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2193
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Db       2375 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2434

Qy       2194 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2253
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Qy       2254 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2313
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Qy       2314 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2373
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Qy       2434 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2493
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Qy       2494 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2553
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Qy       2554 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2613
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Qy       2614 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2667
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RESULT 12
AF249278
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DEFINITION  Homo sapiens voltage-gated potassium channel (KCNQ5) mRNA, complete
            cds.
ACCESSION   AF249278
VERSION     AF249278.1  GI:9651966
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3074)
  AUTHORS   Lerche,C., Scherer,C.R., Seebohm,G., Derst,C., Wei,A.D., Busch,A.E.
            and Steinmeyer,K.
  TITLE     Molecular cloning and functional expression of KCNQ5, a potassium
            channel subunit that may contribute to neuronal M-current diversity
  JOURNAL   J. Biol. Chem. 275 (29), 22395-22400 (2000)
  MEDLINE   20357367
   PUBMED   10787416
REFERENCE   2  (bases 1 to 3074)
  AUTHORS   Lerche,C., Scherer,C.R., Seebohm,G., Derst,C., Wei,A.D., Busch,A.E.
            and Steinmeyer,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAR-2000) Cardiovascular Diseases, Aventis Pharma
            Deutschland GmbH, Building H824, Frankfurt a. M. 65926, Germany
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ORIGIN

  Query Match          98.1%;  Score 2617.2;  DB 9;  Length 3074;
  Best Local Similarity  98.7%;  Pred. No. 0;
  Matches 2659;  Conservative    0;  Mismatches    8;  Indels   27;  Gaps    1;

Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
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Db        215 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 274

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
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Db        275 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 334

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
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Db        335 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGAAGCCGCCTCTCT 394

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Db        395 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 454

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
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Db        455 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTCCTC 514

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
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Db        515 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 574

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
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Db        575 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 634

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
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Db        635 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 694

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
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Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
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Db        755 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 814

Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
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Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
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Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
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Qy        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
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Db       1055 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 1114

Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
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Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
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Db       1175 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1234

Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
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Db       1235 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1294

Qy       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAA---------------------------- 1115
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Db       1355 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1414

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Qy       1774 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1833
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RESULT 13
BD275572
LOCUS       BD275572               3718 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Novel Human Voltage-Gated Potassium Channel.
ACCESSION   BD275572
VERSION     BD275572.1  GI:33085340
KEYWORDS    JP 2002543768-A/2.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3718)
  AUTHORS   Metzker,M.L., Li,W., Petrukhin,K. and Caskey,T.C.
  TITLE     Novel Human Voltage-Gated Potassium Channel
  JOURNAL   Patent: JP 2002543768-A 2 24-DEC-2002;
            Merck and Co Inc
COMMENT     OS   Homo Sapiens
            PN   JP 2002543768-A/2
            PD   24-DEC-2002
            PF   10-APR-2000 JP 2000611548
            PR   14-APR-1999 US    60/129274
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            CC
            FH   Key             Location/Qualifiers.
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ORIGIN
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Query Match 94.5%; Score 2521; DB 6; Length 3718;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 2564; Conservative 0; Mismatches 10; Indels 27; Gaps 1;

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Db         78 ACTGCTGAGGACTGCGGCGGTGGCCTGAGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGG 137

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Qy        214 AAGTACCGGCGGGTGCAGAACTACCTGTACAACGTGCTGGAGAGACCCCGCGGCTGGGCG 273
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Db        198 AAGTACCGGCGGGTGCAGAACTACCTGTACAACGTGCTGGAGAGACCCCGCGGCTGGGCG 257

Qy        274 TTCATCTACCACGCTTTCGTTTTTCTCCTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTT 333
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Qy        334 TCTACCATCCCTGAGCACACAAAATTGGCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTG 393
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Qy        394 ATGATTGTCGTCTTTGGTTTGGAGTTCATCATTCGAATCTGGTCTGCGGGTTGCTGTTGT 453
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Db        378 ATGATTGTCGTCTTTGGTTTGGAGTTCATCATTCGAATCTGGTCTGCGGGTTGCTGTTGT 437

Qy        454 CGATATAGAGGATGGCAAGGAAGACTGAGGTTTGCTCGAAAGCCCTTCTGTGTTATAGAT 513
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Qy        514 ACCATTGTTCTTATCGCTTCAATAGCAGTTGTTTCTGCAAAAACTCAGGGTAATATTTTT 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 ACCATTGTTCTTATCGCTTCAATAGCAGTTGTTTCTGCAAAAACTCAGGGTAATATTTTT 557

Qy        574 GCCACGTCTGCACTCAGAAGTCTCCGTTTCCTACAGATCCTCCGCATGGTGCGCATGGAC 633
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Qy        694 ATCACAGCTTGGTACATAGGATTTTTGGTTCTTATTTTTTCGTCTTTCCTTGTCTATCTG 753
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Db       2658 CCTCATGTCAAACTGAAATAA 2678
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RESULT 14
AF263835
LOCUS       AF263835               2832 bp    mRNA    linear   PRI 01-JUN-2000
DEFINITION  Homo sapiens voltage-gated potassium channel KCNQ5 (KCNQ5) mRNA,
            partial cds.
ACCESSION   AF263835
VERSION     AF263835.1  GI:8132996
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2832)
  AUTHORS   Kniazeva,M. and Han,M.
  TITLE     A new gene of the voltage-gated potassium channel KCNQ family,
            KCNQ5, is a candidate gene for retinal disorders
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2832)
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  AUTHORS   Kniazeva,M. and Han,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder,
            Porter Biosciences Bldg., Boulder, CO 80309, USA
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ORIGIN

  Query Match           94.0%;  Score 2507.6;  DB 9;  Length 2832;
  Best Local Similarity  98.6%;  Pred. No. 0;
  Matches 2550;  Conservative    0;  Mismatches    9;  Indels   27;  Gaps    1;

Qy        109 GGCGGTGGCCTGAGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGG 168
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Qy        709 ATAGGATTTTTGGTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCC 768
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Qy        889 GCACTCCTTGGCATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCA 948
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Qy        949 TTAAAAGTACAAGAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCC 1008
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Db       2161 CAGGTTGCACAGTCAAATCTACCCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGA 2220

Qy       2302 GGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCT 2361
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Db       2221 GGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCT 2280

Qy       2362 GTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCA 2421
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Qy       2542 CCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCT 2601
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Qy       2602 CAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTG 2661
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Qy       2662 AAATAA 2667
             ||||||
Db       2581 AAATAA 2586
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RESULT 15
AF263836
LOCUS       AF263836               3108 bp    mRNA    linear   ROD 01-JUN-2000
DEFINITION  Mus musculus voltage-gated potassium channel KCNQ5 (Kcnq5) mRNA,
            partial cds.
ACCESSION   AF263836
VERSION     AF263836.1  GI:8132998
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3108)
  AUTHORS   Kniazeva,M. and Han,M.
  TITLE     A new gene of the voltage-gated potassium channel KCNQ family,
            KCNQ5, is a candidate gene for retinal disorders
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3108)
  AUTHORS   Kniazeva,M. and Han,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder,
            Porter Biosciences Bldg., Boulder, CO 80309, USA
FEATURES             Location/Qualifiers
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     gene            <1. .3108
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     CDS             <1. .2638
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ORIGIN

  Query Match           80.8%;  Score 2155;  DB 10;  Length 3108;
  Best Local Similarity  89.0%;  Pred. No. 0;
  Matches 2348;  Conservative    0;  Mismatches  263;  Indels   27;  Gaps    1;

Qy         57 GGGCGACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGG 116
              ||||||||||||||  |||| ||||||||||||||  |||| || || |||||||| ||
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Qy        117 CCTGAGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCT 176
              | |||| ||||||||||||||||||||||||||| ||||||||||||||||||||||||
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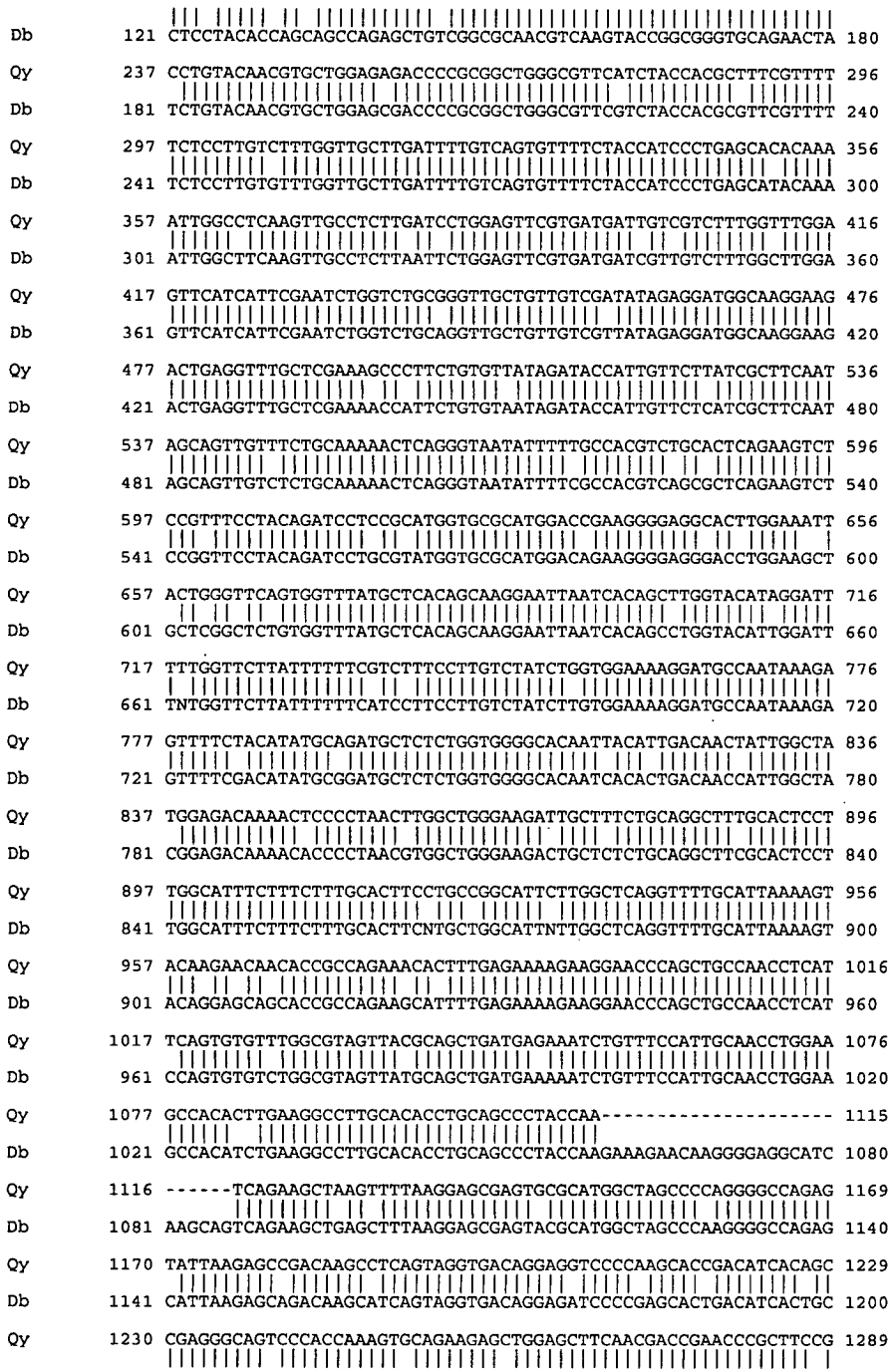
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Qy 357 ATTGGCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGA 416
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Qy 657 ACTGGGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATT 716
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Qy 717 TTTGGTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGA 776
Db 661 TNTGGTTCTTATTTTTTCATCCTTCCTTGTCTATCTTGTGGAAAAGGATGCCAATAAAGA 720
Qy 777 GTTTTCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTA 836
Db 721 GTTTTCGACATATGCGGATGCTCTCTGGTGGGGCACAATCACACTGACAACCATTGGCTA 780
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Db 781 CGGAGACAAAACACCCCTAACGTGGCTGGGAAGACTGCTCTCTGCAGGCTTCGCACTCCT 840
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Qy 1017 TCAGTGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAA 1076
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Qy 1116 ------TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAG 1169
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Qy 1710 GTCCATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGG 1769
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Qy 1950 AAATGAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAAC 2009
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Qy 2070 CCAAATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCT 2129
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Qy       2370 CCTGATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTC 2429
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Db       2341 CCTGATCAGGTCGACAGAAGAACTGAACTTACAGTTTTCAGGCAGCGAGTCAAGCGGCTC 2400

Qy       2430 CAGAGGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGA 2489
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Qy       2490 AGAGGTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAG 2549
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Db       2461 GGAGGTCGGTGCCGAAGAGACAGAAACAGATACTTTTGACGGCACCCCACCGCCTGCGGG 2520

Qy       2550 GGAAGCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCAT 2609
             ||| ||||| ||  |||||||||||||||||||||||||||||||| |||||||||| |||
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Qy       2610 TTGTAAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2667
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Db       2581 TTGTAAGACAGGAGACAGTACAGACGCCCTCAGTTTGCCTCACGTCAAACTGAACTAA 2638
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Search completed: April 11, 2005, 16:49:54
Job time : 13218.7 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 08:07:42 ; Search time 1365.59 Seconds
(without alignments)
11561.287 Million cell updates/sec

Title: US-09-810-796-3
Perfect score: 2667
Sequence: 1 atgaaggatgtggagtcggg.....ctcatgtcaaactgaaataa 2667

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
2: geneseqn1990s:*
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4: geneseqn2001as:*
5: geneseqn2001bs:*
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13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2667	100.0	2667	4	AAS14653	Aas14653 Human cDN
2	2662.2	99.8	2772	5	AAH43633	Aah43633 Human ion
3	2662.2	99.8	3111	5	AAH43634	Aah43634 Human ion
4	2630	98.6	2694	4	AAS14652	Aas14652 Human cDN
5	2630	98.6	2694	6	AAD27192	Aad27192 Human pot
6	2626.4	98.5	3071	4	AAS14651	Aas14651 Human cDN
7	2625.2	98.4	3137	4	AAC85414	Aac85414 Human KCN
8	2617.2	98.1	3074	4	AAH49499	Aah49499 Human KCN
9	2615.6	98.1	3074	10	ADB78684	Adb78684 Human pot
10	2521	94.5	3718	3	AAC64371	Aac64371 Human KCN
11	963.4	36.1	125910	3	AAC64370	Aac64370 Human KCN
12	509.8	19.1	582	8	ACA04855	Aca04855 cDNA enco
13	492	18.4	2335	3	AAA47618	Aaa47618 KCNQ4 Pot
14	492	18.4	2335	10	ADE31698	Ade31698 Human 323
15	489.2	18.3	2273	2	AAX57140	Aax57140 Mouse KCN
16	475.6	17.8	2169	2	AAX26588	Aax26588 Nucleotid
17	472.2	17.7	7407	10	ADB78688	Adb78688 Human pot
18	472.2	17.7	7407	10	ADB78686	Adb78686 Human pot
19	472.2	17.7	7407	10	ADB78683	Adb78683 Human pot
20	472.2	17.7	7407	10	ADB78687	Adb78687 Human pot
21	472.2	17.7	7411	10	ADD29557	Add29557 Human tum
22	472.2	17.7	7420	11	ADN38963	Adn38963 Cancer/an
23	472.2	17.7	7420	11	ADP65810	Adp65810 Human mRN
24	472.2	17.7	7420	11	ADP65731	Adp65731 Human pot
25	472.2	17.7	7420	12	ADL06495	Adl06495 Human tum
26	472.2	17.7	7863	10	ADJ56529	Adj56529 Human cDN
27	470.6	17.6	7407	10	ADB78685	Adb78685 Human pot
28	465	17.4	548	6	ABA90234	Aba90234 Human ORF
29	452.2	17.0	7413	5	AAS74832	Aas74832 DNA encod
30	452	16.9	575	8	ACA04857	Aca04857 cDNA enco
31	447	16.8	2565	2	AAX81548	Aax81548 Human bra
32	447	16.8	3195	5	AAS74831	Aas74831 DNA encod
33	445.2	16.7	5595	13	ADS17851	Ads17851 Rattus no
34	436.6	16.4	3029	2	AAX81547	Aax81547 Human bra
35	427.4	16.0	1848	12	ADH51119	Adh51119 Potassium
36	427.4	16.0	1848	12	ADM77995	Adm77995 KCNQ2-15b
37	427.2	16.0	2565	2	AAX26596	Aax26596 Nucleotid
38	427.2	16.0	2914	2	AAX57059	Aax57059 Human KCN
39	427.2	16.0	2926	10	ADB78690	Adb78690 Human pot
40	427.2	16.0	2926	10	ADB78682	Adb78682 Human pot
41	427.2	16.0	2926	10	ADB78691	Adb78691 Human pot
42	426.8	16.0	2814	2	AAX57141	Aax57141 Mouse KCN
43	425.6	16.0	2926	10	ADB78689	Adb78689 Human pot
44	425.4	16.0	2766	13	ADS17849	Ads17849 Rattus no
45	425	15.9	3287	2	AAX26587	Aax26587 Nucleotid

ALIGNMENTS

RESULT 1
AAS14653
ID AAS14653 standard; cDNA; 2667 BP.
XX
AC AAS14653;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human cDNA encoding a voltage gated potassium channel hKVNQ5-2.
XX
KW Human; ss; voltage-gated potassium channel; KCNQ5-2; nootropic;
KW cerebroprotective; neurotropic; analgesic; vision disorder;
KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder; stroke;
KW pain; gene therapy; splice variant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .2967
FT /*tag= a
FT /product= "hKCNQ5-2"
XX
PN WO200170759-A1.
XX
PD 27-SEP-2001.
XX
PF 20-MAR-2001; 2001WO-US009328.
XX
PR 21-MAR-2000; 2000US-0190954P.
XX
PA (ICAG-) ICAGEN INC.
XX
PI Jegla TJ;
XX
DR WPI; 2001-611467/70.
DR P-PSDB; AAU09021.
XX
PT Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT identifying a compound modulating ion flux in eukaryotic cell or cell
PT membrane expressing the protein, comprises KCNQ approximatelya- subunits.
XX
PS Claim 5; Page 63-64; 78pp; English.

XX
CC The invention relates to an isolated polypeptide comprising an alpha-
CC subunit of a KCNQ potassium channel, with a subsequence having 65%
CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
CC and forms a KCNQ potassium channel having the characteristic of voltage-
CC gating with at least an additional KCNQ alpha-subunit. Also included in
CC the scope of the invention are the nucleic acids encoding hKCNQ5
CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
CC vectors encoding them, antibodies against them, the use of 3-dimensional
CC computer modelling to identify molecules that bind to a KCNQ containing
CC potassium channel and modulate ion flux through the channel. The KCNQ
CC polypeptide is useful for identifying a compound that increases or
CC decreases ion flux through a potassium channel expressed in an eukaryotic
CC host cell or cell membrane. The compound (and the KCNQ nucleic acid when
CC used in gene therapy)is useful as a pharmaceutical agent for treating
CC diseases involving abnormal ion flux, such as disorders of the central
CC nervous system, such as epilepsy, migraines, hearing and vision problems,
CC psychotic disorders, seizures, learning and memory disorders, stroke and
CC pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
CC human tissue and the use of a nucleotide sequence of KCNQ5 to search
CC computer databases to find variants of the sequence which are associated
CC with disease states, is useful for screening mutations of KCNQ5. The
CC present sequence is a splice variant of hKCNQ5 encoding hKCNQ5-2
XX
SQ Sequence 2667 BP; 701 A; 667 C; 660 G; 639 T; 0 U; 0 Other;

Query Match 100.0%; Score 2667; DB 4; Length 2667;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540

Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600

Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660

Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
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Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
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Qy        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
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Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
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Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
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Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
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Qy       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAATCAGAAGCTAAGTTTTAAGGAGCGA 1140
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Qy       1201 AGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1261 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 1320

Qy       1321 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1381 TGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1441 ATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATAT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1501 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 1560
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Qy       1561 AAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1621 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGT 1680
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Db       1621 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGT 1680

Qy       1681 CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGCTGGACTGCCTACTA 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1741 GACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1800
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Db       1741 GACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1800

Qy       1801 CAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAA 1860
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Db       1801 CAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAA 1860

Qy       1861 GATCTTTCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATC 1920
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Qy       1921 TCGAGAGGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCG 1980
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Qy       1981 CTTAGCCCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCA 2040
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Qy       2101 CCAACAACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAA 2160
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Qy       2161 ACTCTGCACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTT 2220
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Qy       2281 AGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAG 2340
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Db       2581 ACTGGAAGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTC 2640

Qy       2641 AGCTTGCCTCATGTCAAACTGAAATAA 2667
             |||||||||||||||||||||||||||
Db       2641 AGCTTGCCTCATGTCAAACTGAAATAA 2667


RESULT 2
AAH43633
ID   AAH43633 standard; cDNA; 2772 BP.
XX
AC   AAH43633;
XX
DT   21-JAN-2002  (first entry)
XX
DE   Human ion-channel forming protein ORF.
XX
KW   Ion-channel forming protein; voltage-gated potassium channel; fetal;
KW   brain; thymus; prostate; heart; skeletal muscle; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175108-A1.
XX
PD   11-OCT-2001.
XX
PF   03-APR-2001; 2001WO-US010875.
XX
PR   03-APR-2000; 2000US-0194255P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;
PI   Sands AT;
XX
DR   WPI; 2001-656987/75.
DR   P-PSDB; AAB47678.
XX
PT   New human ion channel protein and polynucleotides encoding the protein,
PT   useful in diagnosing or treating diseases, in drug screening, and in
PT   clinical trial monitoring.
XX
PS   Claim 1; Page 34-35; 41pp; English.
XX
CC   The sequences in AAH43633-34 encode a novel ion-channel forming protein.
CC   The protein shares structural similarity with mammalian ion channel
CC   proteins, particularly voltage-gated potassium channel proteins. The
CC   protein is expressed in many human cell lines including fetal brain,
CC   brain, thymus,prostate, heart and skeletal muscle. The novel protein can
CC   be used in the diagnosis or treatment of diseases, in drug screening, and
CC   in clinical trial monitoring. The oligonucleotides may be used as
CC   hybridization probes for screening libraries, and assessing gene
CC   expression patterns (particularly using a micro array or high throughput
CC   chip format). The nucleic acids and novel protein can also be used in the
CC   identification, selection and validation of novel molecular targets for
CC   drug discovery, to screen collections of genetic material from patients
CC   who have a particular medical condition, to identify mutations associated
CC   with a particular disease, as a diagnostic or prognostic assay, and to
CC   screen for drugs which can be used to treat symptomatic or phenotypic
CC   manifestations of perturbing the normal function of novel human protein.
CC   The polypeptides are further used in generating antibodies
XX
SQ   Sequence 2772 BP; 715 A; 700 C; 713 G; 644 T; 0 U; 0 Other;

  Query Match            99.8%;  Score 2662.2;  DB 5;  Length 2772;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 2664;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        166 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTCGGTGGCGGCGGCGGTGGCCTG 225

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
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Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 405
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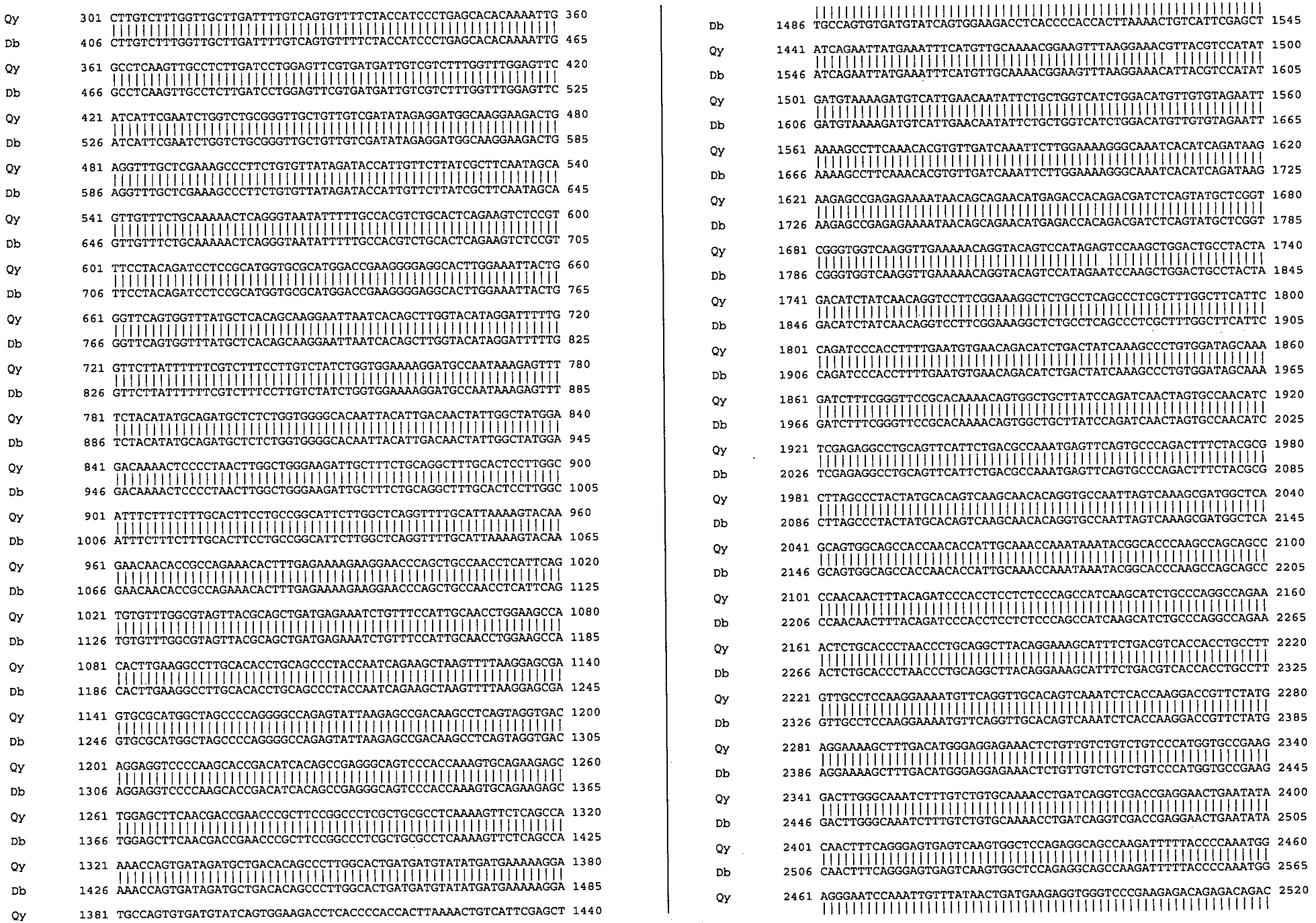
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Db 406 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 465
Qy 361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
Db 466 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 525
Qy 421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
Db 526 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 585
Qy 481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
Db 586 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 645
Qy 541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
Db 646 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 705
Qy 601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
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Qy 661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
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Db 946 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 1005
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Qy 1321 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 1380
Db 1426 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 1485
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Qy 1441 ATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATAT 1500
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Qy 1501 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 1560
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Db 1666 AAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAG 1725
Qy 1621 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGT 1680
Db 1726 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGT 1785
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Db 1786 CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAATCCAAGCTGGACTGCCTACTA 1845
Qy 1741 GACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1800
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Db 2026 TCGAGAGGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCG 2085
Qy 1981 CTTAGCCCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCA 2040
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Db 2326 GTTGCCTCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATG 2385
Qy 2281 AGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAG 2340
Db 2386 AGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAG 2445
Qy 2341 GACTTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATA 2400
Db 2446 GACTTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATA 2505
Qy 2401 CAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGG 2460
Db 2506 CAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGG 2565
Qy 2461 AGGGAATCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGAC 2520

```
Db       2566 AGGGAATCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGAC 2625

Qy       2521 ACTTTTGATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGG 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2626 ACTTTTGATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGG 2685

Qy       2581 ACTGGAAGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTC 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2686 ACTGGAAGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTC 2745

Qy       2641 AGCTTGCCTCATGTCAAACTGAAATAA 2667
             ||||||||||||||||||||||||||||
Db       2746 AGCTTGCCTCATGTCAAACTGAAATAA 2772


RESULT 3
AAH43634
ID   AAH43634 standard; cDNA; 3111 BP.
XX
AC   AAH43634;
XX
DT   21-JAN-2002  (first entry)
XX
DE   Human ion-channel forming protein coding sequence.
XX
KW   Ion-channel forming protein; voltage-gated potassium channel; fetal;
KW   brain; thymus; prostate; heart; skeletal muscle; probe; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             59. .2831
FT                   /*tag= a
FT                   /product= "Human ion-channel forming protein"
XX
PN   WO200175108-A1.
XX
PD   11-OCT-2001.
XX
PF   03-APR-2001; 2001WO-US010875.
XX
PR   03-APR-2000; 2000US-0194255P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Hu Y,  Kieke JA,  Turner AC,  Nehls MC,  Friedrich G,  Zambrowicz B;
PI   Sands AT;
XX
DR   WPI; 2001-656987/75.
DR   P-PSDB; AAB47678.
XX
PT   New human ion channel protein and polynucleotides encoding the protein,
PT   useful in diagnosing or treating diseases, in drug screening, and in
PT   clinical trial monitoring.
XX
PS   Disclosure; Page 37-38; 41pp; English.
XX
CC   The sequences in AAH43633-34 encode a novel ion-channel forming protein.
CC   The protein shares structural similarity with mammalian ion channel
CC   proteins, particularly voltage-gated potassium channel proteins. The
CC   protein is expressed in many human cell lines including fetal brain,
CC   brain, thymus,prostate, heart and skeletal muscle. The novel protein can
CC   be used in the diagnosis or treatment of diseases, in drug screening, and
CC   in clinical trial monitoring. The oligonucleotides may be used as
CC   hybridization probes for screening libraries, and assessing gene
CC   expression patterns (particularly using a micro array or high throughput
CC   chip format). The nucleic acids and novel protein can also be used in the
CC   identification, selection and validation of novel molecular targets for
CC   drug discovery, to screen collections of genetic material from patients
CC   who have a particular medical condition, to identify mutations associated
CC   with a particular disease, as a diagnostic or prognostic assay, and to
CC   screen for drugs which can be used to treat symptomatic or phenotypic
CC   manifestations of perturbing the normal function of novel human protein.
CC   The polypeptides are further used in generating antibodies
XX
SQ   Sequence 3111 BP; 814 A; 771 C; 789 G; 737 T; 0 U; 0 Other;

  Query Match            99.8%;  Score 2662.2;  DB 5;  Length 3111;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 2664;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 224

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTCGGTGGCGGCGGCGGTGGCCTG 284

Qy        121 AGGGAGAGCCGCCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 344

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 404

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 464

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 524

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 584

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 644

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 704

Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        705 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 764

Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 824

Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        825 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 884

Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        885 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 944

Qy        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        945 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 1004

Qy        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1005 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 1064

Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1065 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 1124

Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
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Db       1125 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1184
Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Db       1185 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1244
Qy       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAATCAGAAGCTAAGTTTTAAGGAGCGA 1140
Db       1245 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAATCAGAAGCTAAGTTTTAAGGAGCGA 1304
Qy       1141 GTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGAC 1200
Db       1305 GTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGAC 1364
Qy       1201 AGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGC 1260
Db       1365 AGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGC 1424
Qy       1261 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 1320
Db       1425 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 1484
Qy       1321 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 1380
Db       1485 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 1544
Qy       1381 TGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCT 1440
Db       1545 TGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCT 1604
Qy       1441 ATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATAT 1500
Db       1605 ATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACATTACGTCCATAT 1664
Qy       1501 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 1560
Db       1665 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 1724
Qy       1561 AAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAG 1620
Db       1725 AAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAG 1784
Qy       1621 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGT 1680
Db       1785 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGT 1844
Qy       1681 CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGCTGGACTGCCTACTA 1740
Db       1845 CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAATCCAAGCTGGACTGCCTACTA 1904
Qy       1741 GACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1800
Db       1905 GACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1964
Qy       1801 CAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAA 1860
Db       1965 CAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAA 2024
Qy       1861 GATCTTTCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATC 1920
Db       2025 GATCTTTCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATC 2084
Qy       1921 TCGAGAGGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCG 1980
Db       2085 TCGAGAGGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCG 2144
Qy       1981 CTTAGCCCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCA 2040
Db       2145 CTTAGCCCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCA 2204
Qy       2041 GCAGTGGCAGCCACCAACACCATTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCC 2100
Db       2205 GCAGTGGCAGCCACCAACACCATTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCC 2264
Qy       2101 CCAACAACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAA 2160
Db       2265 CCAACAACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAA 2324
Qy       2161 ACTCTGCACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTT 2220
Db       2325 ACTCTGCACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTT 2384
Qy       2221 GTTGCCTCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATG 2280
Db       2385 GTTGCCTCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATG 2444
Qy       2281 AGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAG 2340
Db       2445 AGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAG 2504
Qy       2341 GACTTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATA 2400
Db       2505 GACTTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATA 2564
Qy       2401 CAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGG 2460
Db       2565 CAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGG 2624
Qy       2461 AGGGAATCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGAC 2520
Db       2625 AGGGAATCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGAC 2684
Qy       2521 ACTTTTGATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGG 2580
Db       2685 ACTTTTGATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGG 2744
Qy       2581 ACTGGAAGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTC 2640
Db       2745 ACTGGAAGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTC 2804
Qy       2641 AGCTTGCCTCATGTCAAACTGAAATAA 2667
Db       2805 AGCTTGCCTCATGTCAAACTGAAATAA 2831
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RESULT 4
AAS14652
ID   AAS14652 standard; cDNA; 2694 BP.
XX
AC   AAS14652;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human cDNA encoding a voltage gated potassium channel hKVNQ5-1.
XX
KW   Human; ss; voltage-gated potassium channel; hKCNQ5-1; nootropic;
KW   cerebroprotective; neurotropic; analgesic; vision disorder;
KW   central nervous system disorder; epilepsy; migraine; hearing disorder;
KW   psychotic disorder; seizure; learning disorder; memory disorder; stroke;
KW   pain; gene therapy; splice variant.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2994
FT                   /*tag=  a
FT                   /product= "hKCNQ5-1"
XX
PN   WO200170759-A1.
XX
PD   27-SEP-2001.
XX
PF   20-MAR-2001; 2001WO-US009328.
XX
PR   21-MAR-2000; 2000US-0190954P.
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XX
PA (ICAG-) ICAGEN INC.
XX
PI Jegla TJ;
XX
DR WPI; 2001-611467/70.
DR P-PSDB; AAU09020.
XX
PT Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT identifying a compound modulating ion flux in eukaryotic cell or cell
PT membrane expressing the protein, comprises KCNQ approximatelya- subunits.
XX
PS Claim 5; Page 62-63; 78pp; English.
XX
CC The invention relates to an isolated polypeptide comprising an alpha-
CC subunit of a KCNQ potassium channel, with a subsequence having 65%
CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
CC and forms a KCNQ potassium channel having the characteristic of voltage-
CC gating with at least an additional KCNQ alpha-subunit. Also included in
CC the scope of the invention are the nucleic acids encoding hKCNQ5
CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
CC vectors encoding them, antibodies against them, the use of 3-dimensional
CC computer modelling to identify molecules that bind to a KCNQ containing
CC potassium channel and modulate ion flux through the channel. The KCNQ
CC polypeptide is useful for identifying a compound that increases or
CC decreases ion flux through a potassium channel expressed in an eukaryotic
CC host cell or cell membrane. The compound (and the KCNQ nucleic acid when
CC used in gene therapy)is useful as a pharmaceutical agent for treating
CC diseases involving abnormal ion flux, such as disorders of the central
CC nervous system, such as epilepsy, migraines, hearing and vision problems,
CC psychotic disorders, seizures, learning and memory disorders, stroke and
CC pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
CC human tissue and the use of a nucleotide sequence of KCNQ5 to search
CC computer databases to find variants of the sequence which are associated
CC with disease states, is useful for screening mutations of KCNQ5. The
CC present sequence is a splice variant of hKCNQ5 encoding hKCNQ5-1
XX
SQ Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 U; 0 Other;

Query Match 98.6%; Score 2630; DB 4; Length 2694;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2667; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

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Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540

Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600

Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660

Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720

Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780

Qy        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840

Qy        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900

Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960

Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020

Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080

Qy       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAA---------------------------- 1115
              ||||||||||||||||||||||||||||||||||
Db       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140

Qy       1116 --TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1173
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200

Qy       1174 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260

Qy       1234 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320

Qy       1294 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380

Qy       1354 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440

Qy       1414 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500

Qy       1474 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560
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Qy       1534 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1593
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620

Qy       1594 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAAATAACAGCAGAACATGAG 1653
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680

Qy       1654 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1713
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740

Qy       1714 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1773
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800

Qy       1774 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1833
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860

Qy       1834 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1893
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920

Qy       1894 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1953
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980

Qy       1954 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2013
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040

Qy       2014 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2073
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100

Qy       2074 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2133
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160

Qy       2134 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2193
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220

Qy       2194 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2253
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280

Qy       2254 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2313
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340

Qy       2314 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2373
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400

Qy       2374 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2433
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460

Qy       2434 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2493
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520

Qy       2494 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2553
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580

Qy       2554 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2613
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640

Qy       2614 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2667
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
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RESULT 5
AAD27192
ID AAD27192 standard; cDNA; 2694 BP.
XX
AC AAD27192;
XX
DT 09-APR-2002 (first entry)
XX
DE Human potassium channel polypeptide, KCNQ5 cDNA.
XX
KW Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;
KW dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis; ALS;
KW multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
KW anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
KW addiction; myokymia; Alzheimer's disease; age-associated memory loss;
KW learning deficiency; cognitive disorder; motor disease; neuron disease;
KW neurophysiological disorder; neuropsychological disorder; asthma;
KW neuron cell death; brain tumour; gene therapy; antisense therapy;
KW synaptic transmission; electrical excitability; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .2694
FT /*tag= a
FT /product= "Human KCNQ5 protein"
XX
PN WO200192526-A1.
XX
PD 06-DEC-2001.
XX
PF 24-MAY-2001; 2001WO-US017314.
XX
PR 26-MAY-2000; 2000US-0207389P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Dworetzky SI, Ramanathan CS, Trojnacki JT, Boissard CG;
PI Gribkoff VK;
XX
DR WPI; 2002-122069/16.
DR P-PSDB; AAE16599.
XX
PT Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding
PT it, for diagnosing, treating and identifying modulators useful in
PT treating neurological, neurophysiological and neuropsychological
PT diseases.
XX
PS Claim 3; Fig 1; 128pp; English.
XX
CC The invention relates to potassium channel polypeptides referred to as
CC KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5
CC polypeptides are useful for identifying compounds that modulate their
CC biological activity. The compounds identified and KCNQ5 polynucleotides
CC are useful for treating acute and chronic pain, migraine, acute stroke,
CC dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis (ALS),
CC multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety disorders,
CC depression, bipolar disorders, sleep disorders, eating disorders,
CC addiction, myokymia, Alzheimer's disease, age-associated memory loss,
CC learning deficiencies, cognitive disorders and motor neuron diseases. The
CC nucleic acid molecules of the invention are further useful for treating
CC neurophysiological, neuropsychological disorders, asthma, neuron cell
CC death and brain tumours. They are also used in gene therapy and antisense
CC therapy. KCNQ5 polypeptides modulate synaptic transmission and electrical
CC excitability in the brain and are useful for generating antibodies. They
CC are also useful to affinity purify biological effectors from biological
CC materials e.g. disease tissues or cells. The present sequence is human
CC KCNQ5 cDNA

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XX
SQ   Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 U; 0 Other;

  Query Match            98.6%;  Score 2630;  DB 6;  Length 2694;
  Best Local Similarity  99.0%;  Pred. No. 0;
  Matches 2667;  Conservative    0;  Mismatches    0;  Indels   27;  Gaps    1;

Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540

Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600

Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660

Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720

Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780

Qy        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840

Qy        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900

Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960

Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020

Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080

Qy       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAA---------------------------- 1115
              ||||||||||||||||||||||||||||||||||
Db       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140

Qy       1116 --TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1173
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200

Qy       1174 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260

Qy       1234 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320

Qy       1294 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380

Qy       1354 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440

Qy       1414 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500

Qy       1474 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1533
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Db       1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560

Qy       1534 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1594 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680

Qy       1654 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740

Qy       1714 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800

Qy       1774 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860

Qy       1834 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1893
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920

Qy       1894 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1953
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980

Qy       1954 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2013
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040

Qy       2014 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2073
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
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Qy       2074 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2133
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2134 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2193
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220

Qy       2194 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2253
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280

Qy       2254 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2313
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340

Qy       2314 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2373
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400

Qy       2374 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2433
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460

Qy       2434 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2493
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520

Qy       2494 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2553
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580

Qy       2554 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2613
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640

Qy       2614 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2667
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
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RESULT 6
AAS14651
ID AAS14651 standard; cDNA; 3071 BP.
XX
AC AAS14651;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human cDNA for voltage gated potassium channel hKVNQ5.
XX
KW Human; ss; voltage-gated potassium channel; hKCNQ5; nootropic;
KW cerebroprotective; neurotropic; analgesic; vision disorder;
KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder; stroke;
KW pain; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200170759-A1.
XX
PD 27-SEP-2001.
XX
PF 20-MAR-2001; 2001WO-US009328.
XX
PR 21-MAR-2000; 2000US-0190954P.
XX
PA (ICAG-) ICAGEN INC.
XX
PI Jegla TJ;
XX
DR WPI; 2001-611467/70.
XX
PT Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT identifying a compound modulating ion flux in eukaryotic cell or cell
PT membrane expressing the protein, comprises KCNQ approximatelya- subunits.
XX
PS Claim 5; Page 61-62; 78pp; English.
XX
CC The invention relates to an isolated polypeptide comprising an alpha-
CC subunit of a KCNQ potassium channel, with a subsequence having 65%
CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
CC and forms a KCNQ potassium channel having the characteristic of voltage-
CC gating with at least an additional KCNQ alpha-subunit. Also included in
CC the scope of the invention are the nucleic acids encoding hKCNQ5
CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
CC vectors encoding them, antibodies against them, the use of 3-dimensional
CC computer modelling to identify molecules that bind to a KCNQ containing
CC potassium channel and modulate ion flux through the channel. The KCNQ
CC polypeptide is useful for identifying a compound that increases or
CC decreases ion flux through a potassium channel expressed in an eukaryotic
CC host cell or cell membrane. The compound (and the KCNQ nucleic acid when
CC used in gene therapy)is useful as a pharmaceutical agent for treating
CC diseases involving abnormal ion flux, such as disorders of the central
CC nervous system, such as epilepsy, migraines, hearing and vision problems,
CC psychotic disorders, seizures, learning and memory disorders, stroke and
CC pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
CC human tissue and the use of a nucleotide sequence of KCNQ5 to search
CC computer databases to find variants of the sequence which are associated
CC with disease states, is useful for screening mutations of KCNQ5. The
CC present sequence is a representative cDNA for hKCNQ5
XX
SQ Sequence 3071 BP; 849 A; 734 C; 737 G; 750 T; 0 U; 1 Other;

Query Match 98.5%; Score 2626.4; DB 4; Length 3071;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 1; Mismatches 2; Indels 27; Gaps 1;

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Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
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Db         10 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 69

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 129

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 189

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 249

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
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Db        250 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 309

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 369

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 429

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 489

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 549

Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
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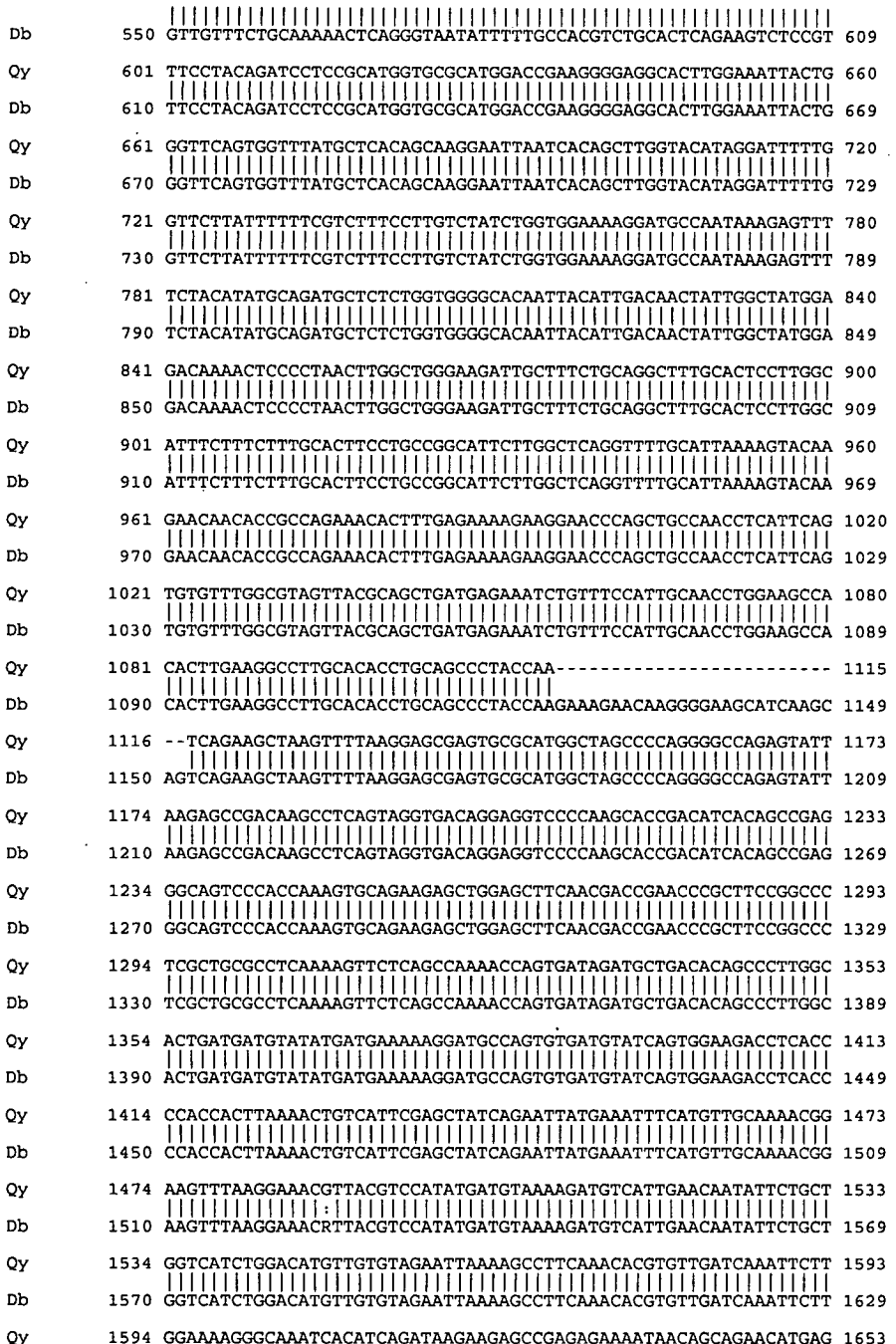

RESULT 7
AAC85414

```
ID   AAC85414 standard; cDNA; 3137 BP.
XX
AC   AAC85414;
XX
DT   20-APR-2001  (first entry)
XX
DE   Human KCNQ5 potassium channel subunit coding sequence.
XX
KW   Human; KCNQ5; heteromeric channel; chromosome 6; Parkinson's disease;
KW   central nervous system; CNS; Alzheimer's disease; anxiety; ataxia;
KW   CNS damage; trauma; stroke; neurodegenerative illness; schizophrenia;
KW   compulsive behaviour; dementia; depression; Huntington's disease; mania;
KW   memory impairment; memory dysfunction; spinal cord damage; phobia;
KW   pick's disease; psychosis; stroke; tremor; seizure; convulsion; epilepsy;
KW   ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2694
FT                   /*tag=  a
FT                   /product= "KCNQ5 subunit"
XX
PN   WO200077035-A2.
XX
PD   21-DEC-2000.
XX
PF   29-MAY-2000; 2000WO-DK000289.
XX
PR   11-JUN-1999;   99DK-00000828.
XX
PA   (NEUR-) NEUROSEARCH AS.
XX
PI   Jentsch TJ;
XX
DR   WPI; 2001-080678/09.
DR   P-PSDB; AAB47046.
XX
PT   Novel genes encoding KCNQ5 potassium channel subunits, useful for
PT   treating Alzheimer's disease, anxiety, ataxia, stroke, dementia,
PT   depression, Huntington's disease, schizophrenia and Parkinson's disease.
XX
PS   Claim 2; Page 44-48; 50pp; English.
XX
CC   This sequence encodes the human KCNQ5 protein. The KCNQ5 protein forms
CC   heteromeric channels with other KCNQ channel subunits, in particular
CC   KCNQ3 and KCNQ4. The KCNQ5 gene has been localised to the long arm of
CC   chromosome 6 (6q14). Chemicals which have the ability to bind to KCNQ5
CC   are useful for diagnosis, treatment, prevention or alleviation of
CC   diseases related to diseases or adverse conditions of the central nervous
CC   system (CNS), including affective disorders, Alzheimer's disease,
CC   anxiety, ataxia, CNS damage caused by trauma, stroke or neurodegenerative
CC   illness, cognitive deficits, compulsive behavior, dementia, depression,
CC   Huntington's disease, mania, memory impairment, memory disorders, memory
CC   dysfunction, motion disorders, motor disorders, neurodegenerative
CC   diseases, Parkinson's disease and Parkinson-like motor disorders,
CC   phobias, pick's disease, psychosis, schizophrenia, spinal cord damage,
CC   stroke, tremor, seizures, convulsions and epilepsy
XX
SQ   Sequence 3137 BP; 865 A; 749 C; 745 G; 778 T; 0 U; 0 Other;

  Query Match             98.4%;  Score 2625.2;  DB 4;  Length 3137;
  Best Local Similarity   98.9%;  Pred. No. 0;
  Matches 2664;  Conservative    0;  Mismatches    3;  Indels   27;  Gaps    1;

Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
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Db          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTCGGTGGCGGCGGCGGTGGCCTG 120

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
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Db        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540

Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
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Db        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600

Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
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Db        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660

Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
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Db        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720

Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780

Qy        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840

Qy        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900

Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960

Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020

Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080

Qy       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAA---------------------------- 1115
              ||||||||||||||||||||||||||||||||||
Db       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140

Qy       1116 --TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1173
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200

Qy       1174 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1233
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Db       1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260

Qy       1234 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1293
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Db       1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320

Qy       1294 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1353
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Db       1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380

Qy       1354 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1413
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Db       1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440

Qy       1414 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1473
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Db       1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500

Qy       1474 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1533
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Db       1501 AAGTTTAAGGAAACATTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560

Qy       1534 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1593
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Qy       1654 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1713
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Db       1741 ATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800

Qy       1774 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1833
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Db       1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860

Qy       1834 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1893
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Qy       1894 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1953
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Qy       1954 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2013
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Qy       2014 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2073
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Qy       2074 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2133
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Qy       2134 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2193
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Qy       2194 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2253
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Qy       2254 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2313
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340

Qy       2314 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2373
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400

Qy       2374 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2433
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460

Qy       2434 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2493
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Db       2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520

Qy       2494 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2553
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Db       2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580

Qy       2554 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2613
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Db       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640

Qy       2614 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2667
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Db       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
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RESULT 8
AAH49499
ID AAH49499 standard; DNA; 3074 BP.
XX
AC AAH49499;
XX
DT 11-DEC-2001 (first entry)
XX
DE Human KCNQ5 DNA.
XX
KW KCNQ5; potassium channel protein; human; neurological; cardiovascular;
KW anticonvulsant; excitablilty modulator; membrane potential; neuron;
KW voltage-dependent KCNQ5 potassium channel; cardiomyocyte; epilepsy;
KW screening; central nervous system disease; cardiovascular disease; ds.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   110. .2908
FT   /*tag= a
FT   /product= "KCNQ5"
XX
PN DE10013732-A1.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2000; 2000DE-01013732.
XX
PR 21-MAR-2000; 2000DE-01013732.
XX
PA (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI Steinmeyer K, Lerche C, Scherer C, Seebohm G, Busch AE;
XX
DR WPI; 2001-571700/65.
DR P-PSDB; AAB86979.
XX
PT New DNA sequence encoding potassium channel KCNQ5, useful in screening
PT for specific modulators, potential agents for treating central nervous
PT system and cardiovascular diseases.
XX
PS Claim 2a; Page 9-10; 20pp; German.
XX
CC This invention describes a novel DNA sequence (I) encoding: (i) a
CC polypeptide (II) with potassium channel KCNQ5 activity; (ii) a
CC polypeptide with the amino acid (aa) sequence of KCNQ5. The products of

CC the invention have neurological, cardiovascular and anticonvulsant
CC activity and act as modulators of the voltage-dependent KCNQ5 potassium
CC channel, a key regulator of membrane potential and modulator of
CC excitability of electrically activated cells such as neurons and
CC cardiomyocytes. KCNQ5 may be implicated in some forms of epilepsy. (II)
CC are used to screen for compounds that modulate the activity of KCNQ5,
CC potentially useful for treating central nervous system (e.g. epilepsy)
CC and cardiovascular diseases. This sequence encodes the human potassium
CC channel KCNQ5 protein described in the invention
XX
SQ Sequence 3074 BP; 788 A; 784 C; 789 G; 713 T; 0 U; 0 Other;

Query Match 98.1%; Score 2617.2; DB 4; Length 3074;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2659; Conservative 0; Mismatches 8; Indels 27; Gaps 1;

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Qy        1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
Db      215 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 274

Qy       61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
Db      275 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 334

Qy      121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
Db      335 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGAAGCCGCCTCTCT 394

Qy      181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
Db      395 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 454

Qy      241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
Db      455 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTCCTC 514

Qy      301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
Db      515 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 574

Qy      361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
Db      575 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 634

Qy      421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
Db      635 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 694

Qy      481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
Db      695 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 754

Qy      541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
Db      755 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 814

Qy      601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
Db      815 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 874

Qy      661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
Db      875 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 934

Qy      721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
Db      935 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 994

Qy      781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
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Qy     1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Db     1235 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1294

Qy     1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAA---------- 1115
Db     1295 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1354

Qy     1116 --TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1173
Db     1355 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1414

Qy     1174 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1233
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Qy     1234 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1293
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Qy     1474 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1533
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Qy     1534 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1593
Db     1775 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1834

Qy     1594 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1653
Db     1835 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1894

Qy     1654 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1713
Db     1895 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1954

Qy     1714 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1773
Db     1955 ATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 2014

Qy     1774 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1833
Db     2015 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 2074

Qy     1834 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1893
Db     2075 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 2134

Qy     1894 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1953
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Db       2135 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 2194

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Db       2195 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2254

Qy       2014 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2073
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Qy       2074 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2133
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Qy       2254 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2313
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Qy       2314 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2555 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2614

Qy       2374 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2433
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Db       2615 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2674

Qy       2434 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2675 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2734

Qy       2494 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2553
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2735 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2794

Qy       2554 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2613
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2795 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2854

Qy       2614 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2667
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Db       2855 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2908
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RESULT 9
ADB78684
ID   ADB78684 standard; cDNA; 3074 BP.
XX
AC   ADB78684;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human potassium channel subunit mutant cDNA SEQ ID NO:55.
XX
KW   ss; gene; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW   neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW   antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW   nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW   ion channel dysfunction; human.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003008574-A1.
XX
PD   30-JAN-2003.
XX
PF   08-JUL-2002; 2002WO-AU000910.
XX
PR   18-JUL-2001; 2001AU-00006452.
PR   05-MAR-2002; 2002AU-00000910.
PR   13-MAY-2002; 2002AU-00002292.
XX
PA   (BION-) BIONOMICS LTD.
PA   (WALL/) WALLACE R W.
XX
PI   Mulley JC,  Harkin LA,  Dibbens LM,  Phillips HA,  Heron SE;
PI   Berkovic SF,  Scheffer IE;
XX
DR   WPI; 2003-239332/23.
XX
PT   Identifying predisposition to an ion channel dysfunction, such as
PT   periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT   schizophrenia, anxiety and depression, by detecting encoding-gene
PT   mutation events.
XX
PS   Claim 6; SEQ ID NO 55; 106pp; English.
XX
CC   The invention relates to a novel method for identifying a subject
CC   predisposed to a disorder associated with ion channel dysfunction. The
CC   method comprises ascertaining if at least one of the genes encoding ion
CC   channel subunits (ICS) has undergone a mutation event so that a cDNA
CC   derived from the subject has any of 134 nucleotide sequences. The method
CC   of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC   antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC   neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC   ophthalmological activity. A polynucleotide of the invention acts as an
CC   ion channel agonist, or ion channel antagonist. The methods, isolated
CC   nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC   modulator of an ion channel, cells and genetically modified non-human
CC   animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC   disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC   kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC   myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC   disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC   depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC   pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC   Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC   fibrosis, congenital stationary night blindness and total colour
CC   blindness. The present sequence represents a mutant cDNA of the
CC   invention. The sequence data for this patent is not represented in the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ   Sequence 3074 BP; 787 A; 784 C; 789 G; 714 T; 0 U; 0 Other;

  Query Match             98.1%;  Score 2615.6;  DB 10;  Length 3074;
  Best Local Similarity   98.7%;  Pred. No. 0;
  Matches 2658;  Conservative    0;  Mismatches    9;  Indels   27;  Gaps    1;

Qy         1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       215 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 274

Qy        61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       275 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 334

Qy       121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
             |||||||||||||||||||||||||||||||||||||||||||||| |  |  ||||||
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Qy       241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
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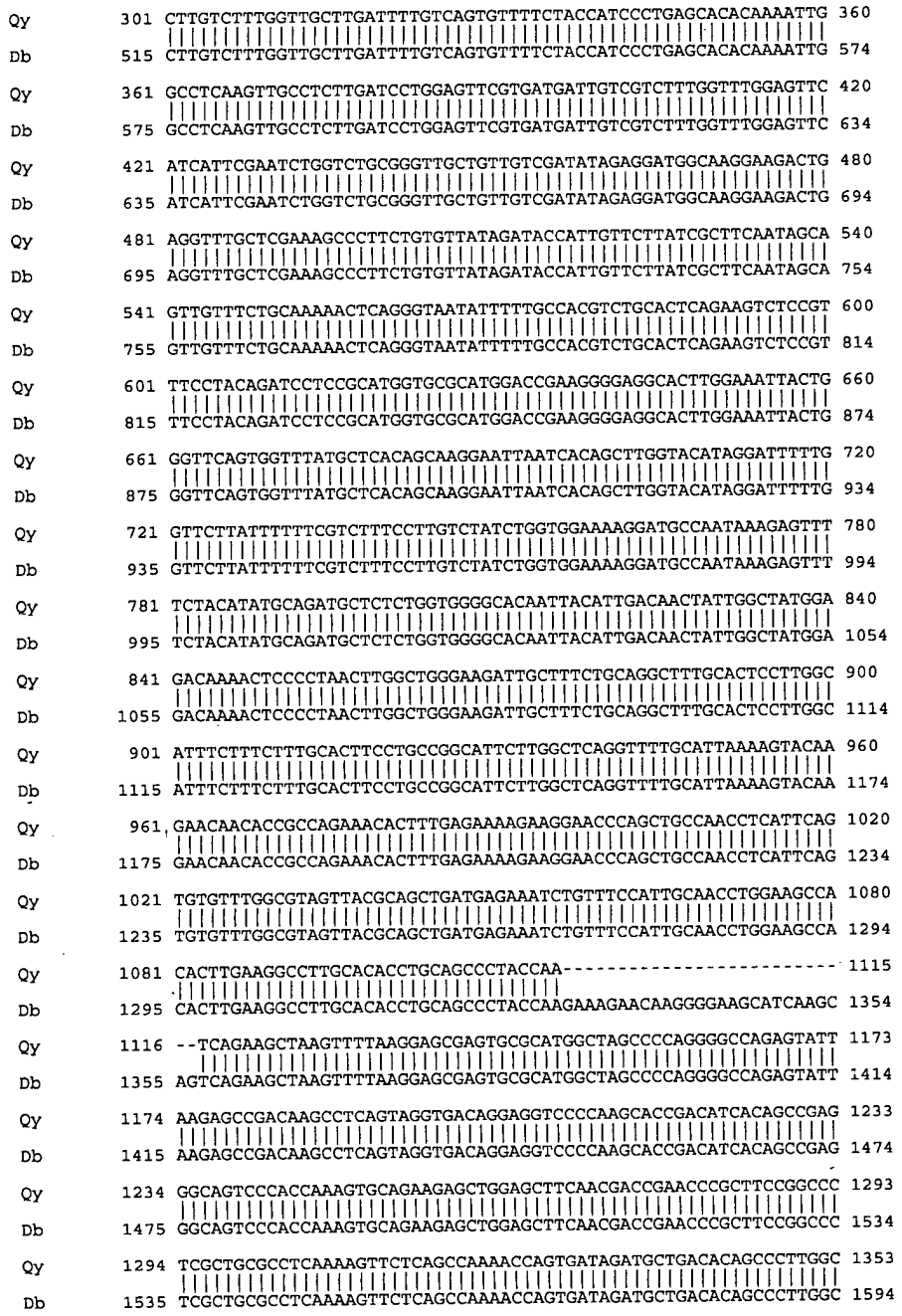
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Db 515 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 574
Qy 361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
Db 575 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 634
Qy 421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
Db 635 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 694
Qy 481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
Db 695 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 754
Qy 541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
Db 755 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 814
Qy 601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
Db 815 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 874
Qy 661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
Db 875 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 934
Qy 721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
Db 935 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 994
Qy 781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
Db 995 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 1054
Qy 841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
Db 1055 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 1114
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Db 1355 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1414
Qy 1174 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1233
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Db 1895 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1954
Qy 1714 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1773
Db 1955 ATAGAATCCAAGCTGGACTGCCTTCTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 2014
Qy 1774 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1833
Db 2015 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 2074
Qy 1834 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1893
Db 2075 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 2134
Qy 1894 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1953
Db 2135 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 2194
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Qy 2194 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2253
Db 2435 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2494
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Qy 2434 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2493

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Qy       2554 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2613
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 10
AAC64371
ID   AAC64371 standard; cDNA; 3718 BP.
XX
AC   AAC64371;
XX
DT   07-FEB-2001  (first entry)
XX
DE   Human KCNQ5 (KCN6q) cDNA sequence SEQ ID NO:2.
XX
KW   Human; KCNQ5; KCN6q; chromosome 6; voltage-gated potassium channel;
KW   Stargardt-like macular dystrophy; cone-rod macular dystrophy;
KW   Salla disease; ophthalmological; auditory; central nervous system;
KW   cardioactive; anticonvulsant; gastrointestinal; muscular active;
KW   age-related macular degeneration; macular degeneration; deafness;
KW   epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
KW   gastrointestinal disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061606-A1.
XX
PD   19-OCT-2000.
XX
PF   10-APR-2000; 2000WO-US009587.
XX
PR   14-APR-1999;   99US-0129274P.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Petrukhin K,  Caskey CT,  Li W,  Metzker ML;
XX
DR   WPI; 2000-647417/62.
DR   P-PSDB; AAB24241.
XX
PT   Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
PT   inhibitors and activators which can treat e.g. Stargardt-like macular
PT   dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy.
XX
PS   Claim 3; Fig 2; 99pp; English.
XX
CC   The present sequence encodes the human KCNQ5 (also called KCN6q) protein,
CC   which is a voltage-gated potassium channel protein. Human KCNQ5 has
CC   ophthalmological, auditory, central nervous system (CNS), cardioactive,
CC   anticonvulsant, gastrointestinal and muscular active activities.
CC   Sequences and methods from the present invention are useful for
CC   identifying activators or inhibitors of KCNQ5 protein. These activators
CC   and inhibitors are useful for treating Stargardt-like macular dystrophy,
CC   cone-rod dystrophy, Salla disease, age-related macular degeneration,
CC   other forms of macular degeneration, deafness, epilepsy, and different
CC   forms of neuropsychiatric, heart, gastrointestinal, and muscle disorders.
CC   Stargardt-like macular dystrophy and cone-rod dystrophies are located at
CC   chromosome 6q
XX
SQ   Sequence 3718 BP; 1054 A; 845 C; 866 G; 953 T; 0 U; 0 Other;

  Query Match             94.5%;  Score 2521;  DB 3;  Length 3718;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches 2564;  Conservative    0;  Mismatches   10;  Indels   27;  Gaps    1;

Qy         94 ACGCTTGGTGGCGGCGGCGGTGGCCTGAGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGG 153
              ||  ||  | | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 ACTGCTGAGGACTGCGGCGGTGGCCTGAGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGG 137

Qy        154 ATGAGCCTGCTGGGGAAGCCGCTCTCTTACACGAGTAGCCAGAGCTGCCGGCGCAACGTC 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 ATGAGCCTGCTGGGGAAGCCGCTCTCTTACACGAGTAGCCAGAGCTGCCGGCGCAACGTC 197

Qy        214 AAGTACCGGCGGGTGCAGAACTACCTGTACAACGTGCTGGAGAGACCCCGCGGCTGGGCG 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 AAGTACCGGCGGGTGCAGAACTACCTGTACAACGTGCTGGAGAGACCCCGCGGCTGGGCG 257

Qy        274 TTCATCTACCACGCTTTCGTTTTTCTCCTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTT 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TTCATCTACCACGCTTTCGTTTTTCTCCTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTT 317

Qy        334 TCTACCATCCCTGAGCACACAAAATTGGCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTG 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 TCTACCATCCCTGAGCACACAAAATTGGCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTG 377

Qy        394 ATGATTGTCGTCTTTGGTTTGGAGTTCATCATTCGAATCTGGTCTGCGGGTTGCTGTTGT 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 ATGATTGTCGTCTTTGGTTTGGAGTTCATCATTCGAATCTGGTCTGCGGGTTGCTGTTGT 437

Qy        454 CGATATAGAGGATGGCAAGGAAGACTGAGGTTTGCTCGAAAGCCCTTCTGTGTTATAGAT 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 CGATATAGAGGATGGCAAGGAAGACTGAGGTTTGCTCGAAAGCCCTTCTGTGTTATAGAT 497

Qy        514 ACCATTGTTCTTATCGCTTCAATAGCAGTTGTTTCTGCAAAAACTCAGGGTAATATTTTT 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 ACCATTGTTCTTATCGCTTCAATAGCAGTTGTTTCTGCAAAAACTCAGGGTAATATTTTT 557

Qy        574 GCCACGTCTGCACTCAGAAGTCTCCGTTTCCTACAGATCCTCCGCATGGTGCGCATGGAC 633
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 GCCACGTCTGCACTCAGAAGTCTCCGTTTCCTACAGATCCTCCGCATGGTGCGCATGGAC 617

Qy        634 CGAAGGGGAGGCACTTGGAAATTACTGGGTTCAGTGGTTTATGCTCACAGCAAGGAATTA 693
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 CGAAGGGGAGGCACTTGGAAATTACTGGGTTCAGTGGTTTATGCTCACAGCAAGGAATTA 677

Qy        694 ATCACAGCTTGGTACATAGGATTTTTGGTTCTTATTTTTTCGTCTTTCCTTGTCTATCTG 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 ATCACAGCTTGGTACATAGGATTTTTGGTTCTTATTTTTTCGTCTTTCCTTGTCTATCTG 737

Qy        754 GTGGAAAAGGATGCCAATAAAGAGTTTTCTACATATGCAGATGCTCTCTGGTGGGGCACA 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        738 GTGGAAAAGGATGCCAATAAAGAGTTTTCTACATATGCAGATGCTCTCTGGTGGGGCACA 797

Qy        814 ATTACATTGACAACTATTGGCTATGGAGACAAAACTCCCCTAACTTGGCTGGGAAGATTG 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        798 ATTACATTGACAACTATTGGCTATGGAGACAAAACTCCCCTAACTTGGCTGGGAAGATTG 857

Qy        874 CTTTCTGCAGGCTTTGCACTCCTTGGCATTTCTTTCTTTGCACTTCCTGCCGGCATTCTT 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        858 CTTTCTGCAGGCTTTGCACTCCTTGGCATTTCTTTCTTTGCACTTCCTGCCGGCATTCTT 917

Qy        934 GGCTCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAGAAACACTTTGAGAAAAGA 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        918 GGCTCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAGAAACACTTTGAGAAAAGA 977

Qy        994 AGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGTTACGCAGCTGATGAGAAA 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        978 AGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGTTACGCAGCTGATGAGAAA 1037

Qy       1054 TCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGCACACCTGCAGCCCTACC 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1038 TCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGCACACCTGCAGCCCTACC 1097

Qy       1114 AA---------------------------TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGC 1146
              ||                           ||||||||||||||||||||||||||||||||
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Db       1098 AAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGC 1157

Qy       1147 ATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGG 1206

Db       1158 ATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGG 1217

Qy       1207 TCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGC 1266

Db       1218 TCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGC 1277

Qy       1267 TTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCA 1326

Db       1278 TTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCA 1337

Qy       1327 GTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAG 1386

Db       1338 GTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAG 1397

Qy       1387 TGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGA 1446

Db       1398 TGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGA 1457

Qy       1447 ATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATATGATGTA 1506

Db       1458 ATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACATTACGTCCATATGATGTA 1517

Qy       1507 AAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGC 1566

Db       1518 AAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGC 1577

Qy       1567 CTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGC 1626

Db       1578 CTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGC 1637

Qy       1627 CGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGTCGGGTG 1686

Db       1638 CGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGTCGGGTG 1697

Qy       1687 GTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGCTGGACTGCCTACTAGACATC 1746

Db       1698 GTCAAGGTTGAAAAACAGGTACAGTCCATAGAATCCAAGCTGGACTGCCTACTAGACATC 1757

Qy       1747 TATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTCCAGATC 1806

Db       1758 TATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTCCAGATC 1817

Qy       1807 CCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAAGATCTT 1866

Db       1818 CCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAAGATCTT 1877

Qy       1867 TCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATCTCGAGA 1926

Db       1878 TCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATCTCGAGA 1937

Qy       1927 GGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCGCTTAGC 1986

Db       1938 GGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCGCTTAGC 1997

Qy       1987 CCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCAGCAGTG 2046

Db       1998 CCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCAGCAGTG 2057

Qy       2047 GCAGCCACCAACACCATTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCCCCAACA 2106

Db       2058 GCAGCCACCAACACCATTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCCCCAACA 2117

Qy       2107 ACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAAACTCTG 2166

Db       2118 ACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAAACTCTG 2177

Qy       2167 CACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTTGTTGCC 2226

Db       2178 CACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTTGTTGCC 2237

Qy       2227 TCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATGAGGAAA 2286

Db       2238 TCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATGAGGAAA 2297

Qy       2287 AGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAGGACTTG 2346

Db       2298 AGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAGGACTTG 2357

Qy       2347 GGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATACAACTT 2406

Db       2358 GGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATACAACTT 2417

Qy       2407 TCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGGAGGGAA 2466

Db       2418 TCAGGGAGTGAGTCAAGTGCCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGGAGGGAA 2477

Qy       2467 TCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGACACTTTT 2526

Db       2478 TCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGACACTTTT 2537

Qy       2527 GATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGGACTGGA 2586

Db       2538 GATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGGACTGGA 2597

Qy       2587 AGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTCAGCTTG 2646

Db       2598 AGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTCAGCTTG 2657

Qy       2647 CCTCATGTCAAACTGAAATAA 2667

Db       2658 CCTCATGTCAAACTGAAATAA 2678
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RESULT 11
AAC64370
ID AAC64370 standard; DNA; 125910 BP.
XX
AC AAC64370;
XX
DT 07-FEB-2001 (first entry)
XX
DE Human KCNQ5 (KCN6q) gene sequence SEQ ID NO:1.
XX
KW Human; KCNQ5; KCN6q; chromosome 6; voltage-gated potassium channel;
KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;
KW Salla disease; ophthalmological; auditory; central nervous system;
KW cardioactive; anticonvulsant; gastrointestinal; muscular active;
KW age-related macular degeneration; macular degeneration; deafness;
KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
KW gastrointestinal disorder; ds.
XX
OS Homo sapiens.
XX
PN WO200061606-A1.
XX
PD 19-OCT-2000.
XX
PF 10-APR-2000; 2000WO-US009587.
XX
PR 14-APR-1999; 99US-0129274P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Petrukhin K, Caskey CT, Li W, Metzker ML;
XX
DR WPI; 2000-647417/62.
DR P-PSDB; AAB24241.
XX
PT Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
PT inhibitors and activators which can treat e.g. Stargardt-like macular
PT dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy.
XX

PS Claim 3; Fig 1; 99pp; English.
XX
CC The present sequence represents the human KCNQ5 (also called KCN6q) gene,
CC which encodes a voltage-gated potassium channel protein. Human KCNQ5 has
CC ophthalmological, auditory, central nervous system (CNS), cardioactive,
CC anticonvulsant, gastrointestinal and muscular active activities.
CC Sequences and methods from the present invention are useful for
CC identifying activators or inhibitors of KCNQ5 protein. These activators
CC and inhibitors are useful for treating Stargardt-like macular dystrophy,
CC cone-rod dystrophy, Salla disease, age-related macular degeneration,
CC other forms of macular degeneration, deafness, epilepsy, and different
CC forms of neuropsychiatric, heart, gastrointestinal, and muscle disorders.
CC Stargardt-like macular dystrophy and cone-rod dystrophies are located at
CC chromosome 6q
XX
SQ Sequence 125910 BP; 40132 A; 24180 C; 23166 G; 38360 T; 0 U; 72 Other;

Query Match 36.1%; Score 963.4; DB 3; Length 125910;
Best Local Similarity 99.9%; Pred. No. 6.6e-272;
Matches 964; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1703 AGGTACAGTCCATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTC 1762
             ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db     123624 AGGTACAGTCCATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTC 123683

Qy       1763 GGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTG 1822
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123684 GGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTG 123743

Qy       1823 AACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAA 1882
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123744 AACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAA 123803

Qy       1883 ACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTC 1942
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123804 ACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTC 123863

Qy       1943 TGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTC 2002
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123864 TGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTC 123923

Qy       2003 AAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCA 2062
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123924 AAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCA 123983

Qy       2063 TTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCAC 2122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123984 TTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCAC 124043

Qy       2123 CTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAG 2182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124044 CTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAG 124103

Qy       2183 GCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTC 2242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124104 GCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTC 124163

Qy       2243 AGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAG 2302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124164 AGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAG 124223

Qy       2303 GAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTG 2362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124224 GAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTG 124283

Qy       2363 TGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAA 2422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124284 TGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAA 124343

Qy       2423 GTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAA 2482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124344 GTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAA 124403

Qy       2483 CTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGC 2542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124404 CTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGC 124463

Qy       2543 CTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTC 2602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124464 CTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTC 124523

Qy       2603 AGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGA 2662
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124524 AGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGA 124583

Qy       2663 AATAA 2667
             |||||
Db     124584 AATAA 124588
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RESULT 12
ACA04855
ID ACA04855 standard; cDNA; 582 BP.
XX
AC ACA04855;
XX
DT 28-MAY-2003 (first entry)
XX
DE cDNA encoding human membrane associated protein fragment #303.
XX
KW Human; ss; gene; microarray; membrane-associated protein; neuropathology;
KW immunopathology; pancreatic disease; cancer; diabetes; hyperlipidaemia;
KW pancreatic cholera; Alzheimer's disease; Huntington's disease; sarcoma;
KW fibrocystic disease; leukaemia; adenocarcinoma; AIDS; allergy; anaemia;
KW asthma; gout; dementia.
XX
OS Homo sapiens.
XX
PN US6492505-B1.
XX
PD 10-DEC-2002.
XX
PF 31-JAN-2000; 2000US-00495050.
XX
PR 01-FEB-1999; 99US-0118318P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Reddy R, Guegler KJ, Au-Young J;
XX
DR WPI; 2003-327324/31.
XX
PT Combination for research/diagnostic applications and for monitoring
PT treatment of e.g., cancer, comprises polynucleotides comprising a
PT fragment of gene encoding membrane-associated proteins, receptors or ion
PT channels.
XX
PS Claim 1; Fig 2; 147pp; English.
XX
CC The invention relates to a combination comprising several polynucleotide
CC sequences comprising a fragment of gene encoding membrane-associated
CC proteins, receptors or ion channels. The combination is useful as a
CC probe, for research and diagnostic applications, for monitoring the
CC expression of several expressed polynucleotides, in the diagnosis and
CC monitoring of treatment of pancreatic disease, cancer, immunopathology or
CC neuropathology, for investigating an individual's predisposition to the
CC above disease, in genetic or gene expression analysis of polynucleotide
CC sequences, to investigate cellular responses to infection or drug
CC treatment, as hybridisable array elements in a microarray, to purify a
CC subpopulation of mRNAs, cDNAs or genomic fragments in a sample, in
CC diagnostics, prognostics and treatment regimens, in drug discovery and
CC development, in toxicological and carcinogenicity studies, and in
CC forensics or pharmacogenomics, to monitor the progression of disease, to
CC monitor the efficacy of treatment, to diagnose the conditions of the
CC pancreas e.g. diabetes, pancreatic cholera, hyperlipidaemia or
CC fibrocystic disease, to diagnose a cancer e.g. leukaemia, adenocarcinoma

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CC   or sarcoma, to diagnose immunopathologies e.g. AIDS, allergies, anaemia,
CC   asthma or gout, to diagnose neuropathologies e.g. Alzheimer's disease,
CC   dementia or Huntington's disease, to rapidly screen large numbers of
CC   candidate drug molecules and as query sequences against GenBank,
CC   SwissProt, BLOCKS and PRINTS databases. The combination is employed to
CC   fine tune the treatment regimen and thus the expression patterns
CC   associated with undesirable side effects are avoided. The present
CC   sequence represents a cDNA encoding a fragment of gene encoding human
CC   membrane-associated proteins, receptors or ion channels
XX
SQ   Sequence 582 BP; 180 A; 157 C; 125 G; 120 T; 0 U; 0 Other;

  Query Match             19.1%;  Score 509.8;  DB 8;  Length 582;
  Best Local Similarity   99.4%;  Pred. No. 2.4e-139;
  Matches  522;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy       1594 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1653
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 60

Qy       1654 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1713
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 120

Qy       1714 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1773
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 180

Qy       1774 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1833
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 240

Qy       1834 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1893
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 300

Qy       1894 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1953
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 360

Qy       1954 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2013
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 420

Qy       2014 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2073
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 480

Qy       2074 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATC 2118
             |||||||||||||| ||||||||| |||||||||||||||||||
Db        481 ATAAATACGGCACCAAAGCCAGCAG-CCCAACAACTTTACAGATC 524


RESULT 13
AAA47618
ID   AAA47618 standard; cDNA; 2335 BP.
XX
AC   AAA47618;
XX
DT   08-NOV-2000  (first entry)
XX
DE   KCNQ4 Potassium channel gene.
XX
KW   KCNQ4; potassium channel; cardiac arrhythmia; neonatal epilepsy;
KW   deafness; probes; treatment; therapy; transgenic animal; antibody;
KW   agonist; antagonist; tinnitus; hearing loss; neonatal deafness;
KW   presbyacusis; affective disorder, Alzheimer's disease; anxiety; ataxia;
KW   cognitive deficits; compulsive behavior; dementia; depression;
KW   Huntington's disease; mania; memory impairment; motor disorders;
KW   neurodegenerative disease; Parkinson's disease; Pick's disease;
KW   psychosis; schizophrenia; spinal cord damage; stroke; tremor; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             83. .2170
FT                   /*tag=  a
FT                   /product= "KCNQ4 Potassium channel polypeptide"
XX
PN   WO200044786-A1.
XX
PD   03-AUG-2000.
XX
PF   19-JAN-2000; 2000WO-DK000024.
XX
PR   26-JAN-1999;   99DK-00000076.
PR   19-MAY-1999;   99DK-00000693.
XX
PA   (NEUR-) NEUROSEARCH AS.
XX
PI   Jentsch TJ;
XX
DR   WPI; 2000-548813/50.
DR   P-PSDB; AAB01476.
XX
PT   Nucleic acids encoding the novel KCNQ4 potassium channel subunit, useful
PT   e.g. for treating tinnitus, deafness, Alzheimer's and Parkinson's
PT   diseases.
XX
PS   Claim 1; Page 43-48; 65pp; English.
XX
CC   Mutations in 3 known genes of the KCNQ branch of the potassium channel
CC   gene family underlie inherited cardiac arrhythmia's, neonatal epilepsy
CC   and in some cases associated with deafness. KCNQ4 has been mapped to the
CC   DFNA2 locus for autosomal dominant hearing loss, and a dominant negative
CC   KCNQ4 mutation that causes deafness in a DFNA2 pedigree has been
CC   identified. KCNQ4 is the first potassium channel gene underlying non-
CC   syndromic deafness. KCNQ4 forms heteromeric channels with other KCNQ
CC   channel subunits, especially KCNQ3. Nucleotides encoding the KCNQ4
CC   protein and the protein itself may be used in the prevention, treatment
CC   and diagnosis of diseases associated with inappropriate KCNQ4 expression.
CC   The nucleotides may also be used as DNA probes in diagnostic assays (e.g.
CC   polymerase chain reactions (PCR)) to detect and quantitate the presence
CC   of similar nucleic acid sequences in samples and to identify mutations
CC   within them, and hence which patients may be in need of restorative
CC   therapy. They may also be used to study the expression and function of
CC   KCNQ4 polypeptides and their role in metabolism, for example through the
CC   production of transgenic animals. The KCNQ4 polypeptides may be used as
CC   antigens in the production of antibodies and to identify modulators
CC   (agonists and antagonists) of KCNQ4 expression and activity. The anti-
CC   KCNQ4 antibodies and KCNQ4 antagonists may also be used to down regulate
CC   KCNQ4 expression and activity. They may be used in this way to treat
CC   tinnitus, loss of hearing (especially progressive hearing loss, neonatal
CC   deafness and presbyacusis (deafness of the elderly)) and disease or
CC   adverse conditions of the central nervous system (CNS) such as affective
CC   disorder, Alzheimer's disease, anxiety, ataxia, CNS damage caused by
CC   trauma, stroke or neurodegenerative illness, cognitive deficits,
CC   compulsive behavior, dementia, depression, Huntington's disease, mania,
CC   memory impairment, memory disorders and dysfunctions, motion disorders,
CC   motor disorders, neurodegenerative diseases, Parkinson's disease,
CC   Parkinson-like motor disorders, phobias, Pick's disease, psychosis,
CC   schizophrenia, spinal cord damage, stroke and/or tremor. Conversely,
CC   antisense nucleic acid molecules may be administered to down regulate
CC   KCNQ4 expression by binding with the cells own KCNQ4 genes and preventing
CC   their expression
XX
SQ   Sequence 2335 BP; 396 A; 812 C; 719 G; 408 T; 0 U; 0 Other;

  Query Match             18.4%;  Score 492;  DB 3;  Length 2335;
  Best Local Similarity   59.3%;  Pred. No. 1e-133;
  Matches 1087;  Conservative    0;  Mismatches  555;  Indels  192;  Gaps    7;

Qy        217 TACCGGCGGGTGCAGAACTACCTGTACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTC 276
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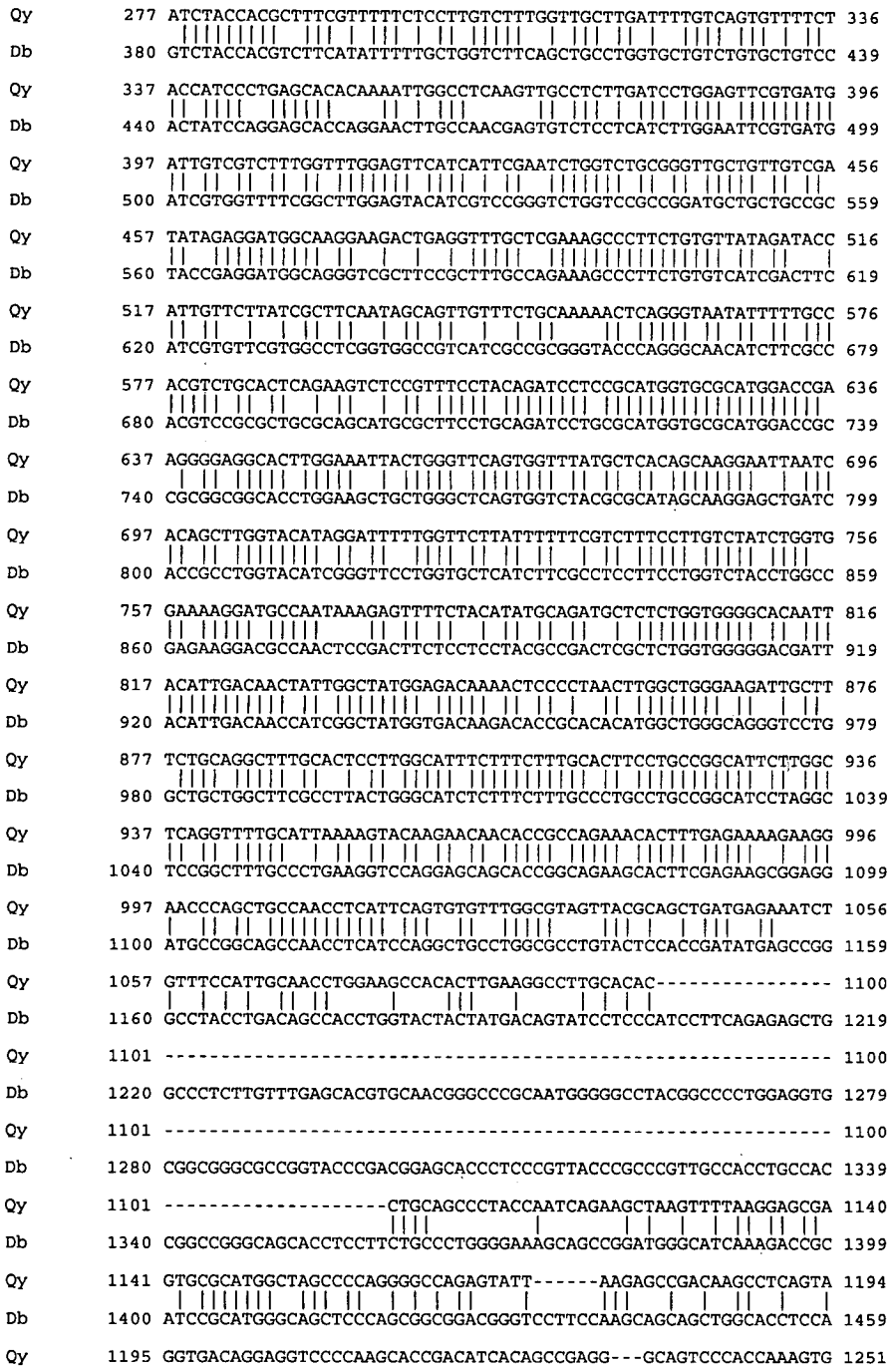
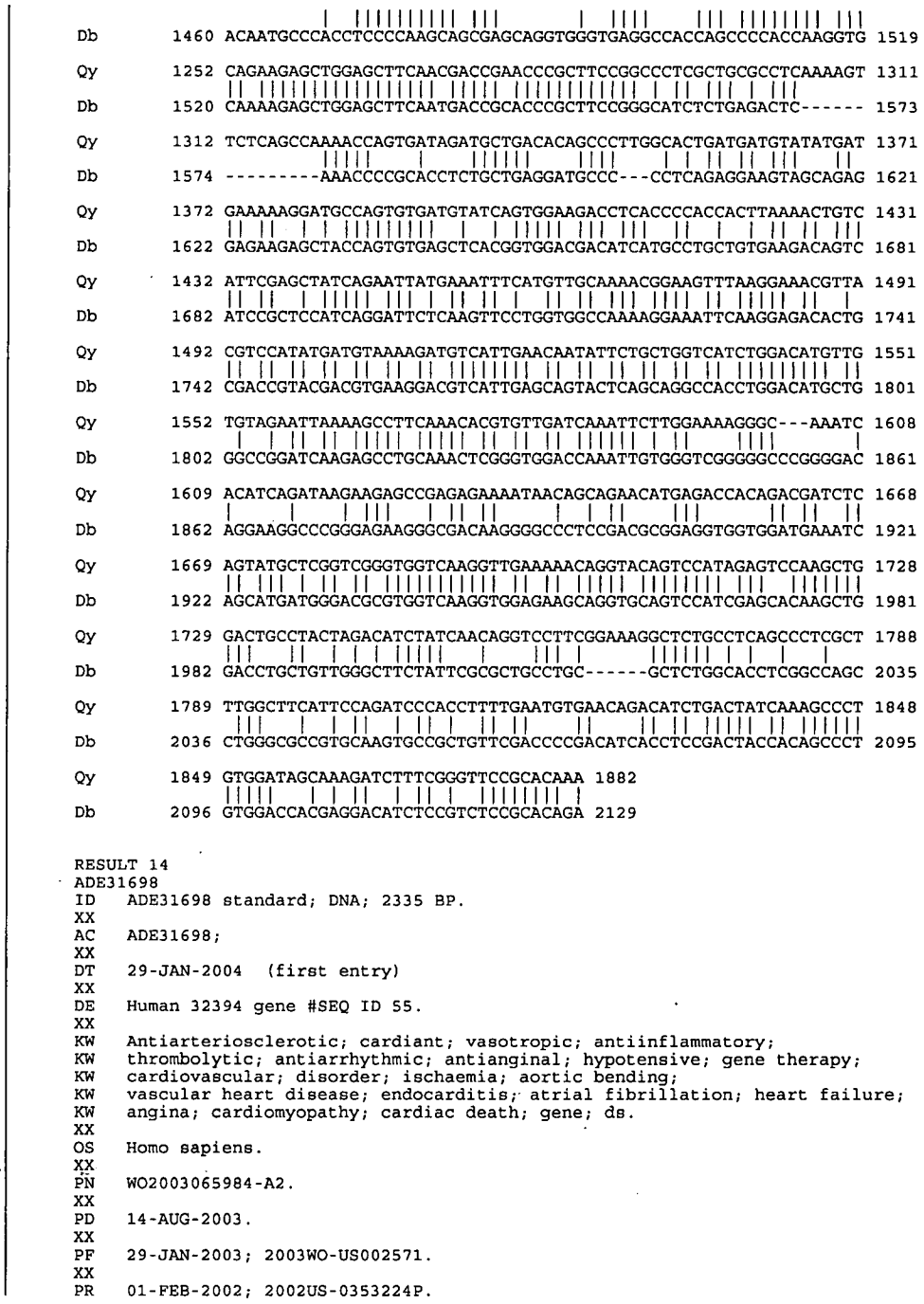
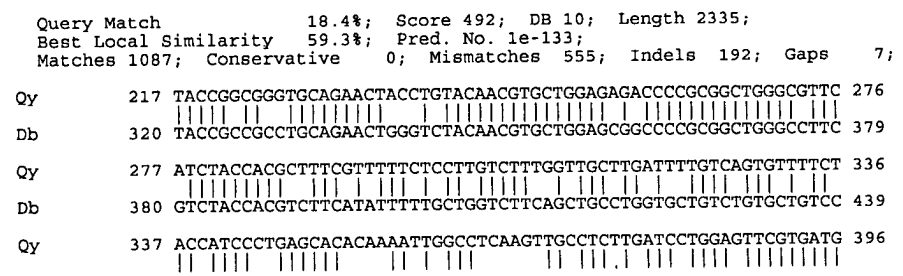


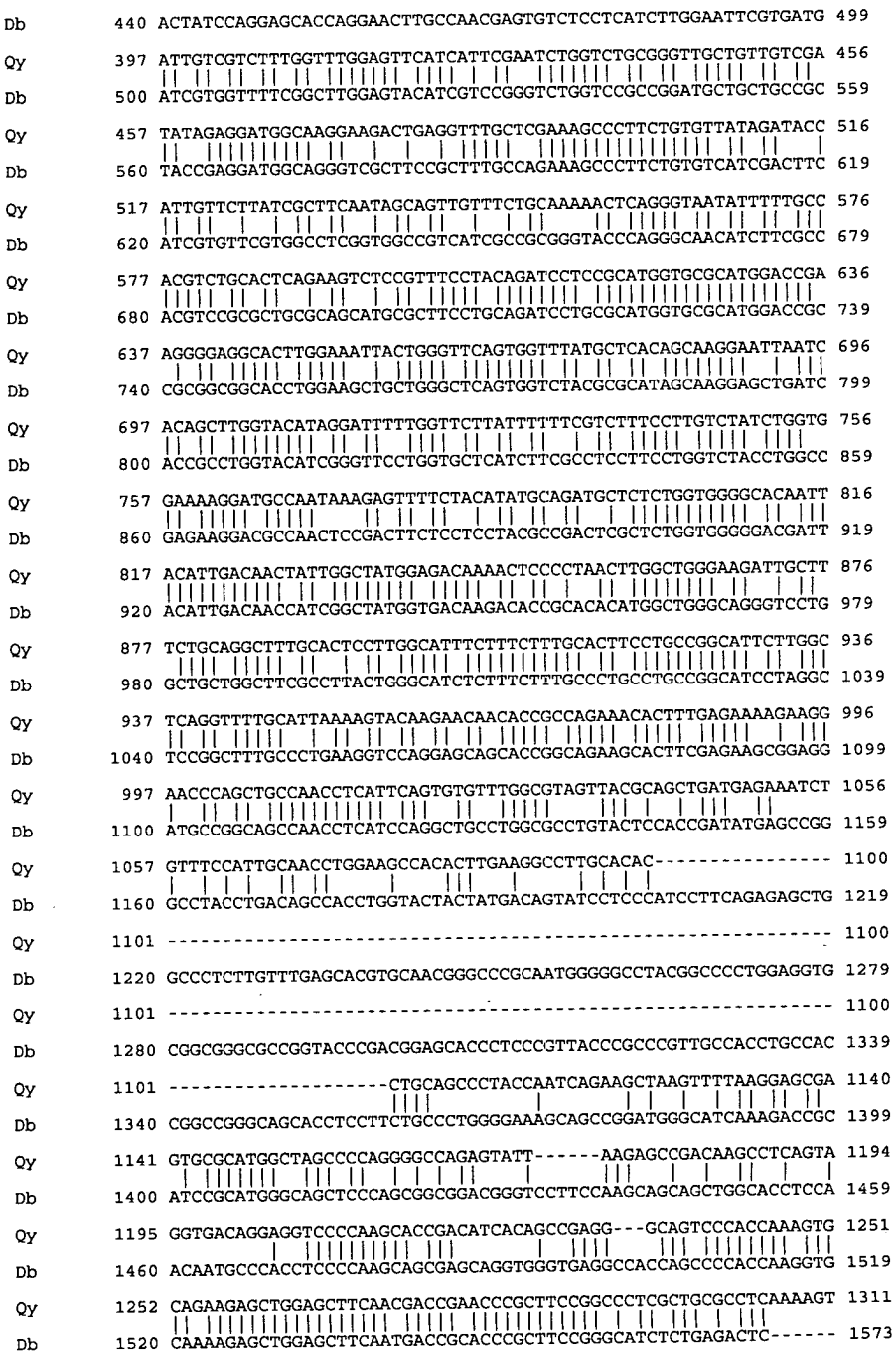


RESULT 14
ADE31698
ID ADE31698 standard; DNA; 2335 BP.
XX
AC ADE31698;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 32394 gene #SEQ ID 55.
XX
KW Antiarteriosclerotic; cardiant; vasotropic; antiinflammatory;
KW thrombolytic; antiarrhythmic; antianginal; hypotensive; gene therapy;
KW cardiovascular; disorder; ischaemia; aortic bending;
KW vascular heart disease; endocarditis; atrial fibrillation; heart failure;
KW angina; cardiomyopathy; cardiac death; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003065984-A2.
XX
PD 14-AUG-2003.
XX
PF 29-JAN-2003; 2003WO-US002571.
XX
PR 01-FEB-2002; 2002US-0353224P.

PR 15-MAR-2002; 2002US-0364529P.
PR 19-APR-2002; 2002US-0373861P.
PR 29-APR-2002; 2002US-0376287P.
PR 12-JUN-2002; 2002US-0388080P.
PR 24-JUN-2002; 2002US-0390971P.
PR 03-JUL-2002; 2002US-0394130P.
PR 10-JUL-2002; 2002US-0394797P.
PR 21-AUG-2002; 2002US-0404904P.
PR 23-AUG-2002; 2002US-0405450P.
PR 04-SEP-2002; 2002US-0408070P.
PR 06-NOV-2002; 2002US-0424300P.
PR 05-DEC-2002; 2002US-0431042P.
PR 05-DEC-2002; 2002US-0431079P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Logan TJ, Chun M, Galvin KM, Healy A, Acton SL, Donaghue M;
PI Stagliano N, Perodin J, Rodrigue-Way A;
XX
DR WPI; 2003-731468/69.
DR P-PSDB; ADE31699.
XX
PT Identifying a compound capable of treating a cardiovascular disorder
PT (e.g. atherosclerosis) comprises assaying the ability of the compound to
PT modulate the expression or activity of e.g. 1682, 6169 or 6193
PT polypeptide or nucleic acid.
XX
PS Disclosure; SEQ ID NO 55; 328pp; English.
XX
CC The invention relates to a method for identifying a compound capable of
CC treating a cardiovascular disorder. The present invention identifies the
CC differential expression of 1682, 6169, 6193, 7771, 14395, 29002, 33216,
CC 43726, 69292, 21656, 32427, 2402, 7747, 1720, 9151, 60491, 1371, 7077,
CC 33207, 1419, 18036, 16105, 38650, 14245, 58848, 1870, 25856, 32394, 3484,
CC 345, 9252, 9135, 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912,
CC 2868, 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914, 51130,
CC 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474, 9792, 15400, 1452 or
CC 6585 genes in cardiovascular disease states. The methods are useful in
CC diagnosing, preventing and treating cardiovascular disorders, such as
CC atherosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury,
CC restenosis, arterial inflammation, vascular wall remodeling, coronary
CC microembolism, tachycardia, bradycardia, pressure overload, aortic
CC bending, coronary artery ligation, vascular heart disease, valvular
CC disease, including but not limited to, valvular degeneration caused by
CC calcification, rheumatic heart disease, endocarditis, or complications of
CC artificial valves; atrial fibrillation, long-QT syndrome, congestive
CC heart failure, sinus node dysfunction, angina, heart failure,
CC hypertension, atrial fibrillation, atrial flutter, pericardial disease,
CC including but not limited to, pericardial effusion and pericarditis;
CC cardiomyopathies, e.g. dilated cardiomyopathy or idiopathic
CC cardiomyopathy, myocardial infarction, coronary artery disease, coronary
CC artery spasm, ischaemic disease, arrhythmia, sudden cardiac death and
CC cardiovascular developmental disorders. The methods may also be used for
CC identifying compounds that modulate cardiovascular disorders. Sequences
CC given in ADE31644-ADE31769 represent the genes and proteins that may be
CC regulated by a compound of the invention.
XX
SQ Sequence 2335 BP; 396 A; 812 C; 719 G; 408 T; 0 U; 0 Other;

Query Match 18.4%; Score 492; DB 10; Length 2335;
Best Local Similarity 59.3%; Pred. No. 1e-133;
Matches 1087; Conservative 0; Mismatches 555; Indels 192; Gaps 7;





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Qy       1372 GAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTC 1431
Db       1622 GAGAAGAGCTACCAGTGTGAGCTCACGGTGGACGACATCATGCCTGCTGTGAAGACAGTC 1681

Qy       1432 ATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTA 1491
Db       1682 ATCCGCTCCATCAGGATTCTCAAGTTCCTGGTGGCCAAAAGGAAATTCAAGGAGACACTG 1741

Qy       1492 CGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTG 1551
Db       1742 CGACCGTACGACGTGAAGGACGTCATTGAGCAGTACTCAGCAGGCCACCTGGACATGCTG 1801

Qy       1552 TGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGC---AAATC 1608
Db       1802 GGCCGGATCAAGAGCCTGCAAACTCGGGTGGACCAAATTGTGGGTCGGGGGCCCGGGGAC 1861

Qy       1609 ACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTC 1668
Db       1862 AGGAAGGCCCGGGAGAAGGGCGACAAGGGGCCCTCCGACGCGGAGGTGGTGGATGAAATC 1921

Qy       1669 AGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGCTG 1728
Db       1922 AGCATGATGGGACGCGTGGTCAAGGTGGAGAAGCAGGTGCAGTCCATCGAGCACAAGCTG 1981

Qy       1729 GACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCT 1788
Db       1982 GACCTGCTGTTGGGCTTCTATTCGCGCTGCCTGC------GCTCTGGCACCTCGGCCAGC 2035

Qy       1789 TTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCT 1848
Db       2036 CTGGGCGCCGTGCAAGTGCCGCTGTTCGACCCCGACATCACCTCCGACTACCACAGCCCT 2095

Qy       1849 GTGGATAGCAAAGATCTTTCGGGTTCCGCACAAA 1882
Db       2096 GTGGACCACGAGGACATCTCCGTCTCCGCACAGA 2129
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RESULT 15
AAX57140
ID AAX57140 standard; DNA; 2273 BP.
XX
AC AAX57140;
XX
DT 22-JUL-1999 (first entry)
XX
DE Mouse KCNQ2 cDNA.
XX
KW KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
KW benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy; JME;
KW rolandic epilepsy; mutant; treatment; screening; epilepsy; detection;
KW gene therapy; drug screening; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 1. .2273
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FT /note= "Partial sequence, no stop codon given"
XX
PN WO9921875-A1.
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PD 06-MAY-1999.
XX
PF 23-OCT-1998; 98WO-US022375.
XX
PR 24-OCT-1997; 97US-0063147P.
XX
PA (UTAH) UNIV UTAH RES FOUND.
XX
PI Singh NA, Leppert MF, Charlier C;
XX
DR WPI; 1999-312938/26.
DR P-PSDB; AAY08345.
XX
PT Nucleic acid encoding potassium channels KCNQ2 and 3.
XX
PS Claim 1; Page 153-156; 195pp; English.
XX
CC This invention describes novel human and mouse potassium channel proteins
CC KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
CC KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
CC prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic
CC epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)
CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
CC in cell-free form) are used to screen for agents that can be used to
CC treat or prevent these forms of epilepsy. Fragments of the encoding
CC nucleic acids are used as probes or primers, either for detecting
CC mutations or for isolation of related sequences, while the complete
CC sequences may be used in gene therapy to provide wild-type protein.
CC Antibodies specific for mutant or wild-type proteins are used as
CC diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
CC useful in rational design of drugs and therapeutically (in replacement
CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and
CC 3 sequences can now be diagnosed early (before symptoms are manifest),
CC and better treatment options will be available
XX
SQ Sequence 2273 BP; 486 A; 670 C; 653 G; 448 T; 0 U; 16 Other;

Query Match 18.3%; Score 489.2; DB 2; Length 2273;
Best Local Similarity 57.0%; Pred. No. 6.9e-133;
Matches 1020; Conservative 2; Mismatches 667; Indels 99; Gaps 4;

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Db         67 GGCTTCGTGGGGCTGGACCCCGGCGNGCCCGANTCCACACGCGACGGCNCNCTACTCATC 126

Qy        124 GAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCTTAC 183
Db        127 GCGGGCTCCGAGGCCCCCAAGCGCGGCANCNTNTTGAGCAAGCCGCGGACGGGCGGCGCG 186

Qy        184 ACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTGTAC 243
Db        187 GGANCCGGGAAGCCCCCNAANCGCAACGCCTTCTACCGCAAGCTGCAGAATTTCCTCTAC 246

Qy        244 AACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTCCTT 303
Db        247 AACGTGCTAGAGCGGCCCCGCGGCTNGGCGTTCATCTACCACGCCTACGTGTTCCTCCTG 306

Qy        304 GTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTGGCC 363
Db        307 GTTTTCTCCTGCCTTGTGCTTTCTGTGTTTTCCACCATCAAGGAGTACGAGAAGAGCTCT 366

Qy        364 TCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTCATC 423
Db        367 GAGGGGGCCCTCTACATCTTGGAAATCGTGACTATCGTGGTATTCGGTGTTGAGTACTTT 426

Qy        424 ATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTGAGG 483
Db        427 GTGAGGATCTGGGCTGCAGGCTGCTGTTGCCGGTATCGAGGCTGGAGGGGCAGGCTCAAG 486

Qy        484 TTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCAGTT 543
Db        487 TTTGCCAGGAAGCCGTTCTGTGTGATTGATATCATGGTGCTGATTGCCTCCATTGCTGTG 546

Qy        544 GTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGTTTC 603
Db        547 CTGGCTGCTGGTTCCCAGGGCAATGTCTTTGCCACATCTGCGCTTCGGAGCTTGCGGTTC 606

Qy        604 CTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTGGGT 663
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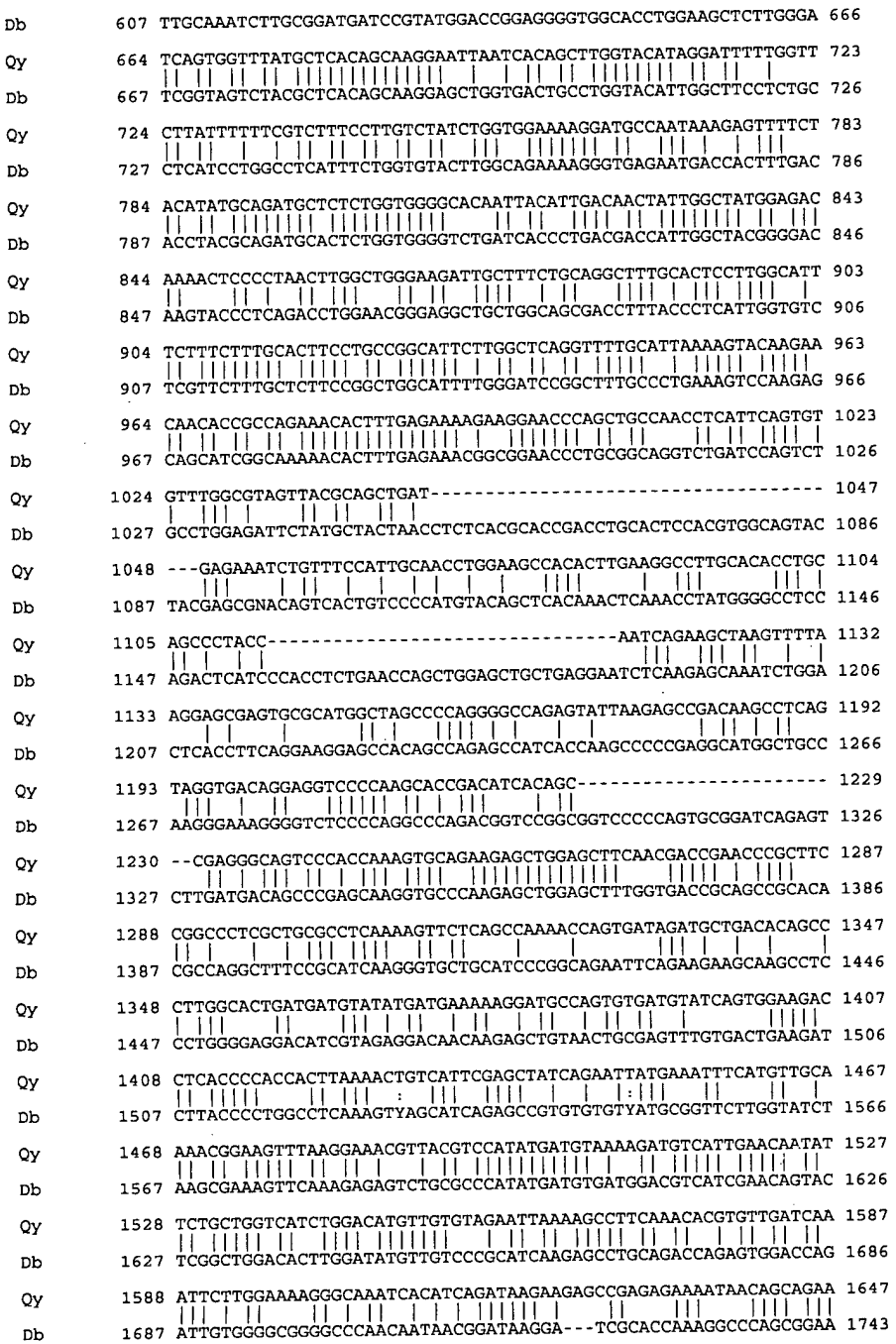

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SUMMARIES

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7	2630	98.6	2694	9	US-09-810-796-2	Sequence 2, Appli
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9	2626.4	98.5	3071	9	US-09-810-796-1	Sequence 1, Appli
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11	2617.2	98.1	3074	9	US-09-813-148-1	Sequence 1, Appli
12	509.8	19.1	582	15	US-10-313-542-303	Sequence 303, App
13	492	18.4	2335	17	US-10-353-690-55	Sequence 55, Appl
14	492	18.4	2335	19	US-10-850-928-1	Sequence 1, Appli
15	489.2	18.3	2273	16	US-10-096-578-88	Sequence 88, Appl
16	475.6	17.8	2169	13	US-10-128-870-22	Sequence 22, Appl
17	475.6	17.8	2169	14	US-10-131-685-22	Sequence 22, Appl
18	472.2	17.7	7411	18	US-10-335-053-6	Sequence 6, Appli
19	472.2	17.7	7420	17	US-10-295-027-281	Sequence 281, App
20	472.2	17.7	7420	18	US-10-643-795A-75	Sequence 75, Appl
21	472.2	17.7	7420	19	US-10-948-518-75	Sequence 75, Appl
22	472.2	17.7	7863	15	US-10-084-817-335	Sequence 335, App
23	465.4	17.5	896	13	US-10-128-870-1	Sequence 1, Appli
24	465.4	17.5	896	14	US-10-131-685-1	Sequence 1, Appli
25	465	17.4	548	10	US-09-826-734-269	Sequence 269, App
26	452	16.9	575	15	US-10-313-542-305	Sequence 305, App
27	445.2	16.7	5595	18	US-10-820-307-8	Sequence 8, Appli
28	427.4	16.0	1848	18	US-10-744-796-5	Sequence 5, Appli
29	427.2	16.0	2565	13	US-10-128-870-26	Sequence 26, Appl
30	427.2	16.0	2565	14	US-10-131-685-26	Sequence 26, Appl
31	427.2	16.0	2914	16	US-10-096-578-6	Sequence 6, Appli
32	426.8	16.0	2814	16	US-10-096-578-90	Sequence 90, Appl
33	425.4	16.0	455	17	US-10-242-535A-25396	Sequence 25396, A
34	425.4	16.0	455	17	US-10-085-783A-25396	Sequence 25396, A
35	425.4	16.0	2766	18	US-10-820-307-6	Sequence 6, Appli
36	425	15.9	3287	13	US-10-128-870-19	Sequence 19, Appl
37	425	15.9	3287	14	US-10-131-685-19	Sequence 19, Appl
38	424.2	15.9	4512	15	US-10-084-817-334	Sequence 334, App
39	423.8	15.9	2755	18	US-10-820-307-4	Sequence 4, Appli
40	423.4	15.9	1425	10	US-09-960-706-511	Sequence 511, App
41	423.4	15.9	1425	10	US-09-873-319-313	Sequence 313, App
42	423.4	15.9	1425	16	US-10-116-712-662	Sequence 662, App
43	423.4	15.9	1878	18	US-10-744-796-3	Sequence 3, Appli
44	423.4	15.9	1932	18	US-10-744-796-1	Sequence 1, Appli
45	423.4	15.9	2619	15	US-10-345-680-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-810-796-3
; Sequence 3, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAgen, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-2 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(2667)
; OTHER INFORMATION: KCNQ5-2
US-09-810-796-3

Query Match 100.0%; Score 2667; DB 9; Length 2667;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60

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Qy        61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
Db        61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120

Qy       121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
Db       121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180

Qy       181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
Db       181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240

Qy       241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
Db       241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300

Qy       301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
Db       301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360

Qy       361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
Db       361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420

Qy       421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
Db       421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480

Qy       481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
Db       481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540

Qy       541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
Db       541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600

Qy       601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
Db       601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660

Qy       661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
Db       661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720

Qy       721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
Db       721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780

Qy       781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
Db       781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840

Qy       841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
Db       841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900

Qy       901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
Db       901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960

Qy       961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
Db       961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020

Qy      1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Db      1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080

Qy      1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAATCAGAAGCTAAGTTTTAAGGAGCGA 1140
Db      1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAATCAGAAGCTAAGTTTTAAGGAGCGA 1140

Qy      1141 GTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGAC 1200
Db      1141 GTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGAC 1200

Qy      1201 AGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGC 1260
Db      1201 AGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGC 1260

Qy      1261 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 1320
Db      1261 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 1320

Qy      1321 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 1380
Db      1321 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 1380

Qy      1381 TGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCT 1440
Db      1381 TGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCT 1440

Qy      1441 ATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATAT 1500
Db      1441 ATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATAT 1500

Qy      1501 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 1560
Db      1501 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 1560

Qy      1561 AAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAG 1620
Db      1561 AAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAG 1620

Qy      1621 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGT 1680
Db      1621 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGT 1680

Qy      1681 CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGCTGGACTGCCTACTA 1740
Db      1681 CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGCTGGACTGCCTACTA 1740

Qy      1741 GACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1800
Db      1741 GACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1800

Qy      1801 CAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAA 1860
Db      1801 CAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAA 1860

Qy      1861 GATCTTTCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATC 1920
Db      1861 GATCTTTCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATC 1920

Qy      1921 TCGAGAGGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCG 1980
Db      1921 TCGAGAGGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCG 1980

Qy      1981 CTTAGCCCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCA 2040
Db      1981 CTTAGCCCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCA 2040

Qy      2041 GCAGTGGCAGCCACCAACACCATTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCC 2100
Db      2041 GCAGTGGCAGCCACCAACACCATTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCC 2100

Qy      2101 CCAACAACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAA 2160
Db      2101 CCAACAACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAA 2160

Qy      2161 ACTCTGCACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTT 2220
Db      2161 ACTCTGCACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTT 2220

Qy      2221 GTTGCCTCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATG 2280
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Db       2221 GTTGCCTCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATG 2280

Qy       2281 AGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 AGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAG 2340

Qy       2341 GACTTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATA 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 GACTTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATA 2400

Qy       2401 CAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGG 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 CAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGG 2460

Qy       2461 AGGGAATCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGAC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 AGGGAATCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGAC 2520

Qy       2521 ACTTTTGATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGG 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 ACTTTTGATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGG 2580

Qy       2581 ACTGGAAGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTC 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 ACTGGAAGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTC 2640

Qy       2641 AGCTTGCCTCATGTCAAACTGAAATAA 2667
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Db       2641 AGCTTGCCTCATGTCAAACTGAAATAA 2667
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RESULT 2
US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-1

Query Match 99.8%; Score 2662.2; DB 9; Length 2772;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db        106 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 165

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        166 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTCGGTGGCGGCGGCGGTGGCCTG 225

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        226 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 285

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 345

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
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Db        346 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 405

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 465

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
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Db        466 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 525

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
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Db        526 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 585

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
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Db        586 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 645

Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 705

Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 765

Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 825

Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 885

Qy        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
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Db        886 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 945

Qy        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 1005

Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
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Db       1006 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 1065

Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
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Db       1066 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1125

Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1185

Qy       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAATCAGAAGCTAAGTTTTAAGGAGCGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAATCAGAAGCTAAGTTTTAAGGAGCGA 1245

Qy       1141 GTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1246 GTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGAC 1305

Qy       1201 AGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 AGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGC 1365
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Qy       1261 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 1320
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Db       1366 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 1425

Qy       1321 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 1380
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Db       1426 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 1485

Qy       1381 TGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCT 1440
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Db       1486 TGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCT 1545

Qy       1441 ATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATAT 1500
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Db       1546 ATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACATTACGTCCATAT 1605

Qy       1501 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 1560
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Db       1606 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 1665

Qy       1561 AAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAG 1620
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Db       1666 AAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAG 1725

Qy       1621 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1726 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGT 1785

Qy       1681 CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGCTGGACTGCCTACTA 1740
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1786 CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAATCCAAGCTGGACTGCCTACTA 1845

Qy       1741 GACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1800
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Db       1846 GACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1905

Qy       1801 CAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAA 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1906 CAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAA 1965

Qy       1861 GATCTTTCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATC 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1966 GATCTTTCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATC 2025

Qy       1921 TCGAGAGGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCG 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2026 TCGAGAGGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCG 2085

Qy       1981 CTTAGCCCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCA 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2086 CTTAGCCCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCA 2145

Qy       2041 GCAGTGGCAGCCACCAACACCATTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCC 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2146 GCAGTGGCAGCCACCAACACCATTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCC 2205

Qy       2101 CCAACAACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAA 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2206 CCAACAACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAA 2265

Qy       2161 ACTCTGCACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTT 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2266 ACTCTGCACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTT 2325

Qy       2221 GTTGCCTCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2326 GTTGCCTCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATG 2385

Qy       2281 AGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2386 AGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAG 2445
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Qy       2341 GACTTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATA 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2446 GACTTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATA 2505

Qy       2401 CAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGG 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2506 CAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGG 2565

Qy       2461 AGGGAATCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGAC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2566 AGGGAATCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGAC 2625

Qy       2521 ACTTTTGATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGG 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2626 ACTTTTGATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGG 2685

Qy       2581 ACTGGAAGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTC 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2686 ACTGGAAGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTC 2745

Qy       2641 AGCTTGCCTCATGTCAAACTGAAATAA 2667
             ||||||||||||||||||||||||||||
Db       2746 AGCTTGCCTCATGTCAAACTGAAATAA 2772
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RESULT 3
US-10-803-268-1
; Sequence 1, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-1

Query Match 99.8%; Score 2662.2; DB 18; Length 2772;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 165

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        166 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTCGGTGGCGGCGGCGGTGGCCTG 225

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 285

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 345
```

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Qy       241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
Db       346 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 405

Qy       301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
Db       406 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 465

Qy       361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
Db       466 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 525

Qy       421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
Db       526 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 585

Qy       481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
Db       586 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 645

Qy       541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
Db       646 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 705

Qy       601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
Db       706 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 765

Qy       661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
Db       766 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 825

Qy       721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
Db       826 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 885

Qy       781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
Db       886 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 945

Qy       841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
Db       946 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 1005

Qy       901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
Db      1006 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 1065

Qy       961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
Db      1066 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1125

Qy      1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Db      1126 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1185

Qy      1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAATCAGAAGCTAAGTTTTAAGGAGCGA 1140
Db      1186 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAATCAGAAGCTAAGTTTTAAGGAGCGA 1245

Qy      1141 GTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGAC 1200
Db      1246 GTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGAC 1305

Qy      1201 AGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGC 1260
Db      1306 AGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGC 1365

Qy      1261 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 1320
Db      1366 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 1425
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Qy      1321 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 1380
Db      1426 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 1485

Qy      1381 TGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCT 1440
Db      1486 TGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCT 1545

Qy      1441 ATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATAT 1500
Db      1546 ATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACATTACGTCCATAT 1605

Qy      1501 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 1560
Db      1606 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 1665

Qy      1561 AAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAG 1620
Db      1666 AAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAG 1725

Qy      1621 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGT 1680
Db      1726 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGT 1785

Qy      1681 CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGCTGGACTGCCTACTA 1740
Db      1786 CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAATCCAAGCTGGACTGCCTACTA 1845

Qy      1741 GACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1800
Db      1846 GACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1905

Qy      1801 CAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAA 1860
Db      1906 CAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAA 1965

Qy      1861 GATCTTTCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATC 1920
Db      1966 GATCTTTCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATC 2025

Qy      1921 TCGAGAGGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCG 1980
Db      2026 TCGAGAGGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCG 2085

Qy      1981 CTTAGCCCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCA 2040
Db      2086 CTTAGCCCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCA 2145

Qy      2041 GCAGTGGCAGCCACCAACACCATTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCC 2100
Db      2146 GCAGTGGCAGCCACCAACACCATTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCC 2205

Qy      2101 CCAACAACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAA 2160
Db      2206 CCAACAACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAA 2265

Qy      2161 ACTCTGCACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTT 2220
Db      2266 ACTCTGCACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTT 2325

Qy      2221 GTTGCCTCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATG 2280
Db      2326 GTTGCCTCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATG 2385

Qy      2281 AGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAG 2340
Db      2386 AGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAG 2445

Qy      2341 GACTTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATA 2400
Db      2446 GACTTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATA 2505

Qy      2401 CAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGG 2460
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2506 CAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGG 2565

Qy       2461 AGGGAATCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGAC 2520
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2566 AGGGAATCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGAC 2625

Qy       2521 ACTTTTGATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGG 2580
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2626 ACTTTTGATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGG 2685

Qy       2581 ACTGGAAGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTC 2640
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2686 ACTGGAAGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTC 2745

Qy       2641 AGCTTGCCTCATGTCAAACTGAAATAA 2667
                 ||||||||||||||||||||||||||||
Db       2746 AGCTTGCCTCATGTCAAACTGAAATAA 2772


RESULT 4
US-09-825-147-3
; Sequence 3, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
;  APPLICANT: Hu, Yi
;  APPLICANT:  Kieke, James Alvin
;  APPLICANT:  Turner, C. Alexander Jr.
;  APPLICANT:  Nehls, Michael C.
;  APPLICANT:  Friedrich, Glenn
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
;  TITLE OF INVENTION:  Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0160-USA
;  CURRENT APPLICATION NUMBER: US/09/825,147
;  CURRENT FILING DATE:  2001-04-03
;  PRIOR APPLICATION NUMBER: US 60/194,255
;  PRIOR FILING DATE: 2000-04-03
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 3111
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-825-147-3

  Query Match             99.8%;  Score 2662.2;  DB 9;  Length 3111;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2664;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 224

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        225 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTCGGTGGCGGCGGCGGTGGCCTG 284

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 344

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 404

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 464

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 524

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 584

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 644

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 704

Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        705 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 764

Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 824

Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        825 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 884

Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        885 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 944

Qy        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        945 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 1004

Qy        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1005 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 1064

Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1065 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 1124

Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1125 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1184

Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1185 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1244

Qy       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAATCAGAAGCTAAGTTTTAAGGAGCGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1245 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAATCAGAAGCTAAGTTTTAAGGAGCGA 1304

Qy       1141 GTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1305 GTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGAC 1364

Qy       1201 AGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1365 AGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGC 1424

Qy       1261 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1425 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 1484

Qy       1321 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1485 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 1544

Qy       1381 TGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1545 TGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCT 1604
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Qy       1441 ATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATAT 1500
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1605 ATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACATTACGTCCATAT 1664

Qy       1501 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 1560
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Db       1665 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 1724

Qy       1561 AAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAG 1620
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Db       1725 AAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAG 1784

Qy       1621 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGT 1680
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Db       1785 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGT 1844

Qy       1681 CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGCTGGACTGCCTACTA 1740
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Db       1845 CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAATCCAAGCTGGACTGCCTACTA 1904

Qy       1741 GACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1800
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Db       1905 GACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1964

Qy       1801 CAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAA 1860
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Db       1965 CAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAA 2024

Qy       1861 GATCTTTCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATC 1920
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Db       2025 GATCTTTCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATC 2084

Qy       1921 TCGAGAGGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCG 1980
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Db       2085 TCGAGAGGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCG 2144

Qy       1981 CTTAGCCCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCA 2040
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2145 CTTAGCCCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCA 2204

Qy       2041 GCAGTGGCAGCCACCAACACCATTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCC 2100
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2205 GCAGTGGCAGCCACCAACACCATTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCC 2264

Qy       2101 CCAACAACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAA 2160
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2265 CCAACAACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAA 2324

Qy       2161 ACTCTGCACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTT 2220
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2325 ACTCTGCACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTT 2384

Qy       2221 GTTGCCTCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATG 2280
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2385 GTTGCCTCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATG 2444

Qy       2281 AGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAG 2340
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2445 AGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAG 2504

Qy       2341 GACTTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATA 2400
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2505 GACTTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATA 2564

Qy       2401 CAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGG 2460
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2565 CAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGG 2624

Qy       2461 AGGGAATCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGAC 2520
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2625 AGGGAATCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGAC 2684

Qy       2521 ACTTTTGATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGG 2580
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2685 ACTTTTGATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGG 2744

Qy       2581 ACTGGAAGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTC 2640
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2745 ACTGGAAGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTC 2804

Qy       2641 AGCTTGCCTCATGTCAAACTGAAATAA 2667
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Db       2805 AGCTTGCCTCATGTCAAACTGAAATAA 2831
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RESULT 5
US-10-803-268-3
; Sequence 3, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-3

Query Match 99.8%; Score 2662.2; DB 18; Length 3111;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        225 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTCGGTGGCGGCGGCGGTGGCCTG 284

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 344

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 404

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 464

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 524

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 584
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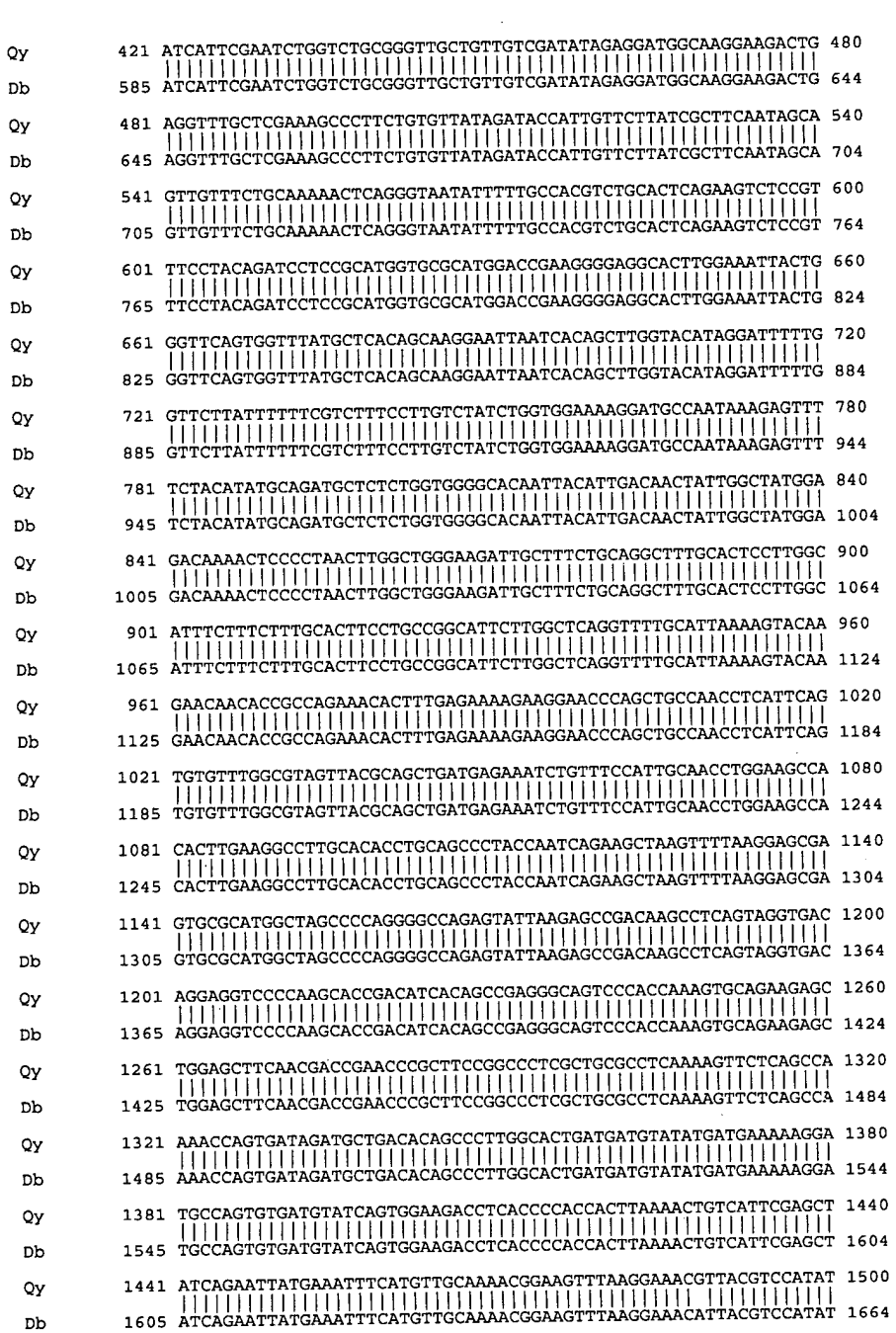
Qy 421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
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Qy 481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
Db 645 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 704
Qy 541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
Db 705 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 764
Qy 601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
Db 765 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 824
Qy 661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
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Qy 721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
Db 885 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 944
Qy 781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
Db 945 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 1004
Qy 841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
Db 1005 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 1064
Qy 901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
Db 1065 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 1124
Qy 961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
Db 1125 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1184
Qy 1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Db 1185 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1244
Qy 1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAATCAGAAGCTAAGTTTTAAGGAGCGA 1140
Db 1245 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAATCAGAAGCTAAGTTTTAAGGAGCGA 1304
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Qy 1201 AGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGC 1260
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Qy 1261 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 1320
Db 1425 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 1484
Qy 1321 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 1380
Db 1485 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 1544
Qy 1381 TGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCT 1440
Db 1545 TGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCT 1604
Qy 1441 ATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATAT 1500
Db 1605 ATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACATTACGTCCATAT 1664
Qy 1501 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 1560
Db 1665 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 1724
Qy 1561 AAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAG 1620
Db 1725 AAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAG 1784
Qy 1621 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGT 1680
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Qy 1681 CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGCTGGACTGCCTACTA 1740
Db 1845 CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAATCCAAGCTGGACTGCCTACTA 1904
Qy 1741 GACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1800
Db 1905 GACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1964
Qy 1801 CAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAA 1860
Db 1965 CAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAA 2024
Qy 1861 GATCTTTCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATC 1920
Db 2025 GATCTTTCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATC 2084
Qy 1921 TCGAGAGGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCG 1980
Db 2085 TCGAGAGGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCG 2144
Qy 1981 CTTAGCCCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCA 2040
Db 2145 CTTAGCCCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCA 2204
Qy 2041 GCAGTGGCAGCCACCAACACCATTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCC 2100
Db 2205 GCAGTGGCAGCCACCAACACCATTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCC 2264
Qy 2101 CCAACAACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAA 2160
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Qy 2161 ACTCTGCACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTT 2220
Db 2325 ACTCTGCACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTT 2384
Qy 2221 GTTGCCTCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATG 2280
Db 2385 GTTGCCTCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATG 2444
Qy 2281 AGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAG 2340
Db 2445 AGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAG 2504
Qy 2341 GACTTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATA 2400
Db 2505 GACTTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATA 2564
Qy 2401 CAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGG 2460
Db 2565 CAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGG 2624
Qy 2461 AGGGAATCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGAC 2520
Db 2625 AGGGAATCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGAC 2684
Qy 2521 ACTTTTGATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGG 2580
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Db       2745 ACTGGAAGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTC 2804

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RESULT 6
US-09-866-020-1
; Sequence 1, Application US/09866020
; Publication No. US20020040000A1
; GENERAL INFORMATION:
;  APPLICANT: DWORETZKY, STEVEN I
;  APPLICANT:  RAMANATHAN, CHANDRA S
;  APPLICANT:  TROJNACKI, JOANNE T
;  APPLICANT:  BOISSARD, CHRISTOPHER G
;  APPLICANT:  GRIBKOFF, VALENTIN K
;  TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 3053-4091US1
;  CURRENT APPLICATION NUMBER: US/09/866,020
;  CURRENT FILING DATE:  2001-05-24
;  PRIOR APPLICATION NUMBER: 60/207,389
;  PRIOR FILING DATE: 2000-05-26
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 2694
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-020-1

  Query Match             98.6%;  Score 2630;  DB 9;  Length 2694;
  Best Local Similarity   99.0%;  Pred. No. 0;
  Matches 2667;  Conservative    0;  Mismatches    0;  Indels   27;  Gaps    1;

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Db           1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60

Qy          61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
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Db          61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120

Qy         121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180

Qy         181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
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Db         181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240

Qy         241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
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Qy         361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
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Db         361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420

Qy         421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480

Qy         481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
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Db         481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540

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Db         781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840

Qy         841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900

Qy         901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960

Qy         961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
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Qy        1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080

Qy        1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAA---------------------------- 1115
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Db        1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140

Qy        1116 --TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1173
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Db        1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200

Qy        1174 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1233
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260

Qy        1234 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1293
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320

Qy        1294 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1353
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Db        1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380

Qy        1354 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1413
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Db        1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440

Qy        1414 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1473
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Qy        1534 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1593
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Db        1561 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620

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Qy       1654 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1713
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Db       1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740

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Db       1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800

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Db       1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860

Qy       1834 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1893
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1954 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2013
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Qy       2014 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2073
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2194 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2253
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Qy       2254 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2313
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Qy       2314 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2373
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Db       2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400

Qy       2374 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2433
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460

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Qy       2554 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2613
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640

Qy       2614 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2667
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Db       2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
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RESULT 7

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US-09-810-796-2
; Sequence 2, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
;  APPLICANT: Jegla, Timothy James
;  APPLICANT:  ICAgen, Inc.
;  TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
;  FILE REFERENCE: 018512-005010US
;  CURRENT APPLICATION NUMBER: US/09/810,796
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: US 60/190,954
;  PRIOR FILING DATE: 2000-03-21
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 2694
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: human outwardly-rectifying, voltage-gated
;   OTHER INFORMATION: potassium channel KCNQ5-1 coding sequence
;   NAME/KEY: CDS
;   LOCATION: (1)..(2694)
;   OTHER INFORMATION: KCNQ5-1
US-09-810-796-2

  Query Match             98.6%;  Score 2630;  DB 9;  Length 2694;
  Best Local Similarity   99.0%;  Pred. No. 0;
  Matches 2667;  Conservative    0;  Mismatches    0;  Indels   27;  Gaps    1;

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Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
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Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
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Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
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Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
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Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
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Db        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
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Db        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
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Db        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
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Db        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
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Qy       661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
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Qy       961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
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Db      1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080

Qy      1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAA---------------------------- 1115
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Qy      1174 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1233
Db      1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260

Qy      1234 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1293
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Qy      1354 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1413
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Qy      1414 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1473
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Qy      1474 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1533
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Qy      1534 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1593
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Qy      1714 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1773
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Db      1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920

Qy      1894 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1953
Db      1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980

Qy      1954 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2013
Db      1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040

Qy      2014 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2073
Db      2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100

Qy      2074 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2133
Db      2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160

Qy      2134 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2193
Db      2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220

Qy      2194 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2253
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Qy      2254 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2313
Db      2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340

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Qy      2434 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2493
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RESULT 8
US-10-948-493-1
; Sequence 1, Application US/10948493
; Publication No. US20050064491A1
; GENERAL INFORMATION:
; APPLICANT: DWORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T

```
;  APPLICANT:  BOISSARD, CHRISTOPHER G
;  APPLICANT:  GRIBKOFF, VALENTIN K
;  TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: D0023 DIV
;  CURRENT APPLICATION NUMBER: US/10/948,493
;  CURRENT FILING DATE:  2004-09-23
;  PRIOR APPLICATION NUMBER: 60/207,389
;  PRIOR FILING DATE: 2000-05-26
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 2694
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-948-493-1

  Query Match             98.6%;  Score 2630;  DB 19;  Length 2694;
  Best Local Similarity   99.0%;  Pred. No. 0;
  Matches 2667;  Conservative    0;  Mismatches    0;  Indels   27;  Gaps    1;

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Db          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
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Db        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
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Db        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540

Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600

Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660

Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720

Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780

Qy        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840

Qy        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
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Db        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900

Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960

Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020

Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080

Qy       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAA---------------------------- 1115
              ||||||||||||||||||||||||||||||||||
Db       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140

Qy       1116 --TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1173
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200

Qy       1174 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260

Qy       1234 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1320

Qy       1294 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1380

Qy       1354 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1440

Qy       1414 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500

Qy       1474 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1560

Qy       1534 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1593
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Db       1561 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1620

Qy       1594 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1680

Qy       1654 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740

Qy       1714 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800

Qy       1774 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1833
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Db       1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1860

Qy       1834 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1893
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Db     1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920

Qy     1894 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1953
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980

Qy     1954 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2013
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040

Qy     2014 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2073
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100

Qy     2074 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2133
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160

Qy     2134 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2193
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220

Qy     2194 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2253
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2221 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2280

Qy     2254 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2313
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2281 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2340

Qy     2314 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2373
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2341 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2400

Qy     2374 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2433
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460

Qy     2434 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2493
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2461 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2520

Qy     2494 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2553
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2521 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2580

Qy     2554 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2613
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2581 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640

Qy     2614 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2667
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2641 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
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RESULT 9
US-09-810-796-1
; Sequence 1, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAgen, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3071
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-1
; NAME/KEY: CDS
; LOCATION: (10)..(2703)
; OTHER INFORMATION: KCNQ5-1
US-09-810-796-1

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  Query Match             98.5%;  Score 2626.4;  DB 9;  Length 3071;
  Best Local Similarity   98.9%;  Pred. No. 0;
  Matches 2664;  Conservative    1;  Mismatches    2;  Indels   27;  Gaps    1;

Qy        1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       10 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 69

Qy       61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       70 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 129

Qy      121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
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Db      130 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 189

Qy      181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
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Db      190 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 249

Qy      241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
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Db      250 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 309

Qy      301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
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Db      310 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 369

Qy      361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      370 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 429

Qy      421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      430 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 489

Qy      481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      490 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 549

Qy      541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      550 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 609

Qy      601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      610 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 669

Qy      661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      670 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 729

Qy      721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      730 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 789

Qy      781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
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Db      790 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 849

Qy      841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
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Qy       901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
Db       910 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 969

Qy       961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
Db       970 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1029

Qy      1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Db      1030 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1089

Qy      1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAA---------------------------- 1115
Db      1090 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1149

Qy      1116 --TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1173
Db      1150 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1209

Qy      1174 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1233
Db      1210 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1269

Qy      1234 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1293
Db      1270 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1329

Qy      1294 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1353
Db      1330 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1389

Qy      1354 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1413
Db      1390 ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACC 1449

Qy      1414 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1473
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Qy      1474 AAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1533
Db      1510 AAGTTTAAGGAAACRTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCT 1569

Qy      1534 GGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAATTCTT 1593
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Qy      1594 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1653
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Qy      1654 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1713
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Qy      1714 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1773
Db      1750 ATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1809

Qy      1774 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1833
Db      1810 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGTTCCCACCTTTTGAATGTGAACAGACATCT 1869

Qy      1834 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1893
Db      1870 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1929

Qy      1894 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1953
Db      1930 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1989

Qy      1954 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2013
Db      1990 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2049

Qy      2014 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2073
Db      2050 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2109

Qy      2074 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2133
Db      2110 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2169

Qy      2134 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2193
Db      2170 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2229

Qy      2194 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2253
Db      2230 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2289

Qy      2254 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2313
Db      2290 TCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2349

Qy      2314 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2373
Db      2350 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2409

Qy      2374 ATCAGGTCGACCGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2433
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Qy      2434 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2493
Db      2470 GGCAGCCAAGATTTTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAG 2529

Qy      2494 GTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAA 2553
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Qy      2554 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2613
Db      2590 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2649

Qy      2614 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2667
Db      2650 AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2703
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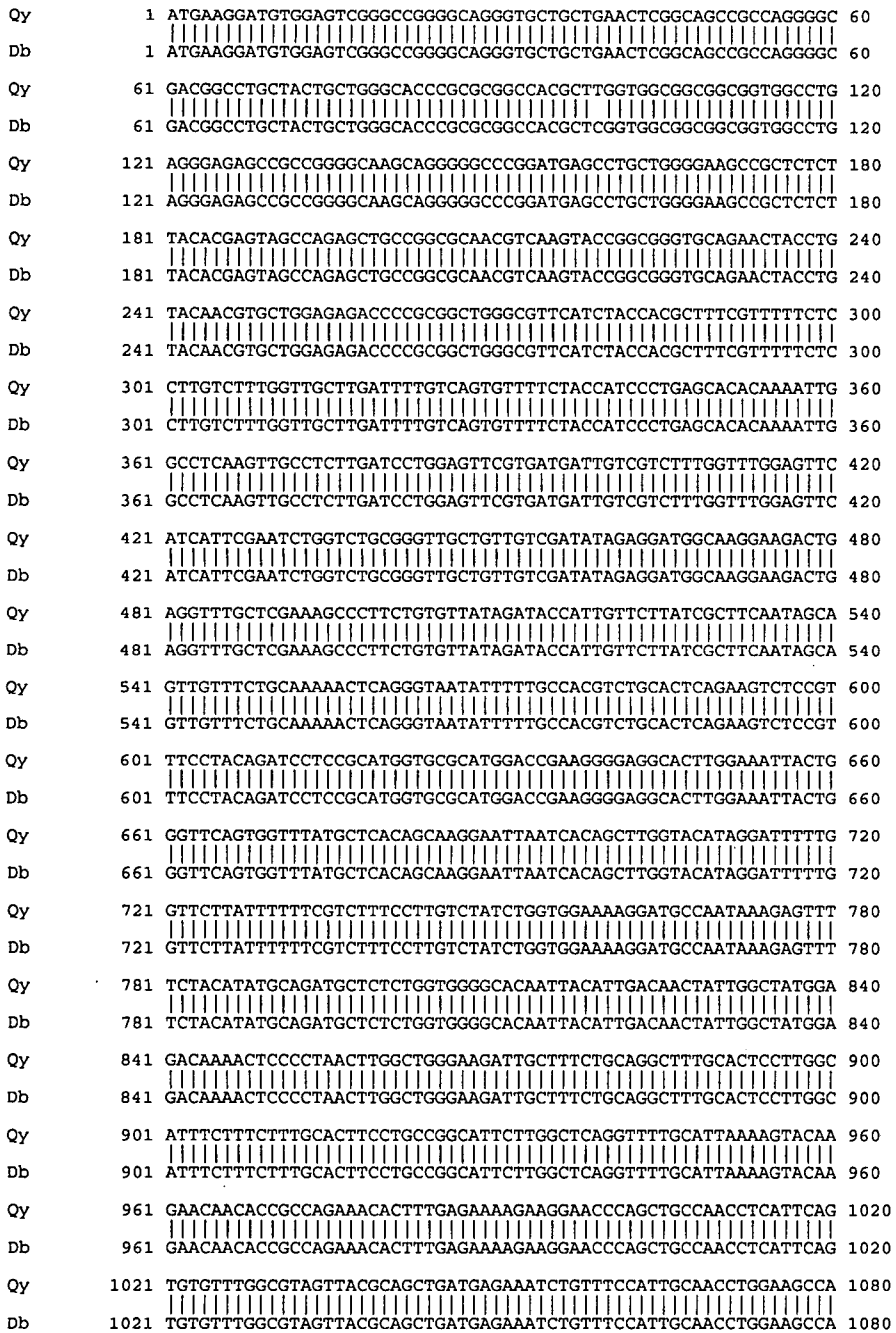
RESULT 10
US-10-661-629-1
; Sequence 1, Application US/10661629
; Publication No. US20040180405A1
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANN
; FILE REFERENCE: 2815-0236P
; CURRENT APPLICATION NUMBER: US/10/661,629
; CURRENT FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2691)
US-10-661-629-1

Query Match 98.4%; Score 2625.2; DB 18; Length 3137;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;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Qy 61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
Db 61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTCGGTGGCGGCGGCGGTGGCCTG 120
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Db 121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
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Db 901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
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Db 1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGC 1140
Qy 1116 --TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1173
Db 1141 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
Qy 1174 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1233
Db 1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1260
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Qy 1414 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1473
Db 1441 CCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGG 1500
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Qy 1834 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1893
Db 1861 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1920
Qy 1894 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1953
Db 1921 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1980
Qy 1954 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2013
Db 1981 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
Qy 2014 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2073
Db 2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2100
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Db 2101 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCA 2160
Qy 2134 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2193

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Db       2161 GCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAA 2220

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RESULT 11
US-09-813-148-1
; Sequence 1, Application US/09813148
; Patent No. US20020076809A1
; GENERAL INFORMATION:
; APPLICANT: STEINMEYER, Klaus
; APPLICANT: LERCHE, Christian
; APPLICANT: SCHERER, Constanze
; APPLICANT: SEEBOHM, Guiscard
; APPLICANT: BUSCH, Andreas E.
; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN
; TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
; FILE REFERENCE: 38005-119
; CURRENT APPLICATION NUMBER: US/09/813,148
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: DE 100 13 732.6
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/194,041
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-148-1

Query Match 98.1%; Score 2617.2; DB 9; Length 3074;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2659; Conservative 0; Mismatches 8; Indels 27; Gaps 1;

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Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120

Db        275 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 334

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Qy       1116 --TCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1173

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Db       1415 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1474

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Db       1475 GGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1534

Qy       1294 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1353
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Db       1535 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGC 1594

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Db       1895 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1954

Qy       1714 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1773
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Db       1955 ATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 2014

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Qy       2194 AGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAG 2253
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Qy       2314 TTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTG 2373
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RESULT 12
US-10-313-542-303
; Sequence 303, Application US/10313542
; Publication No. US20030120057A1
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/10/313,542
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: US/09/495,050
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 303
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030120057A1 4970006CT1
US-10-313-542-303

Query Match 19.1%; Score 509.8; DB 15; Length 582;
Best Local Similarity 99.4%; Pred. No. 1.7e-146;
Matches 522; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy       1594 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1653
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 60

Qy       1654 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1713
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Db         61 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 120

Qy       1714 ATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1773
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Db        121 ATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 180

Qy       1774 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1833
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Db        181 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 240

Qy       1834 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1893

Db        241 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 300

Qy       1894 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1953

Db        301 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 360

Qy       1954 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2013

Db        361 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 420

Qy       2014 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2073

Db        421 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 480

Qy       2074 ATAAATACGGCACCCAAGCCAGCAGCCCCAACAACTTTACAGATC 2118

Db        481 ATAAATACGGCACCAAAGCCAGCAG-CCCAACAACTTTACAGATC 524
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RESULT 13
US-10-353-690-55
; Sequence 55, Application US/10353690
; Publication No. US20030215840A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Donoghue, Mary
; APPLICANT: Stagliano, Nancy
; APPLICANT: Perodin, Jacquelin
; APPLICANT: Rodrigue-Way, Amelie
; TITLE OF INVENTION: Methods and compositions for treating
; TITLE OF INVENTION: cardiovascular disease using 1682, 6169, 6193, 7771, 14395,
; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 1720,
; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
; TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,
; TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,
; TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,
; TITLE OF INVENTION: 9792, 15400, 1452 or 6585 molecules
; FILE REFERENCE: MPI02-018P1RNOMNIM
; CURRENT APPLICATION NUMBER: US/10/353,690
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 60/353,224
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/364,529
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/373,861
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/376,287
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 60/388,080
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: 60/390,971
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/394,130
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/394,797
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/404,904
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/405,450
; PRIOR FILING DATE: 2002-08-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 55
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-353-690-55

Query Match 18.4%; Score 492; DB 17; Length 2335;
Best Local Similarity 59.3%; Pred. No. 1.4e-140;
Matches 1087; Conservative 0; Mismatches 555; Indels 192; Gaps 7;

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Qy        337 ACCATCCCTGAGCACACAAAATTGGCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATG 396

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Qy        397 ATTGTCGTCTTTGGTTTGGAGTTCATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGA 456

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Qy        457 TATAGAGGATGGCAAGGAAGACTGAGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACC 516

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Qy        637 AGGGGAGGCACTTGGAAATTACTGGGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATC 696

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Qy        697 ACAGCTTGGTACATAGGATTTTTGGTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTG 756

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Db        980 GCTGCTGGCTTCGCCTTACTGGGCATCTCTTTCTTTGCCCTGCCTGCCGGCATCCTAGGC 1039

Qy        937 TCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAGAAACACTTTGAGAAAAGAAGG 996

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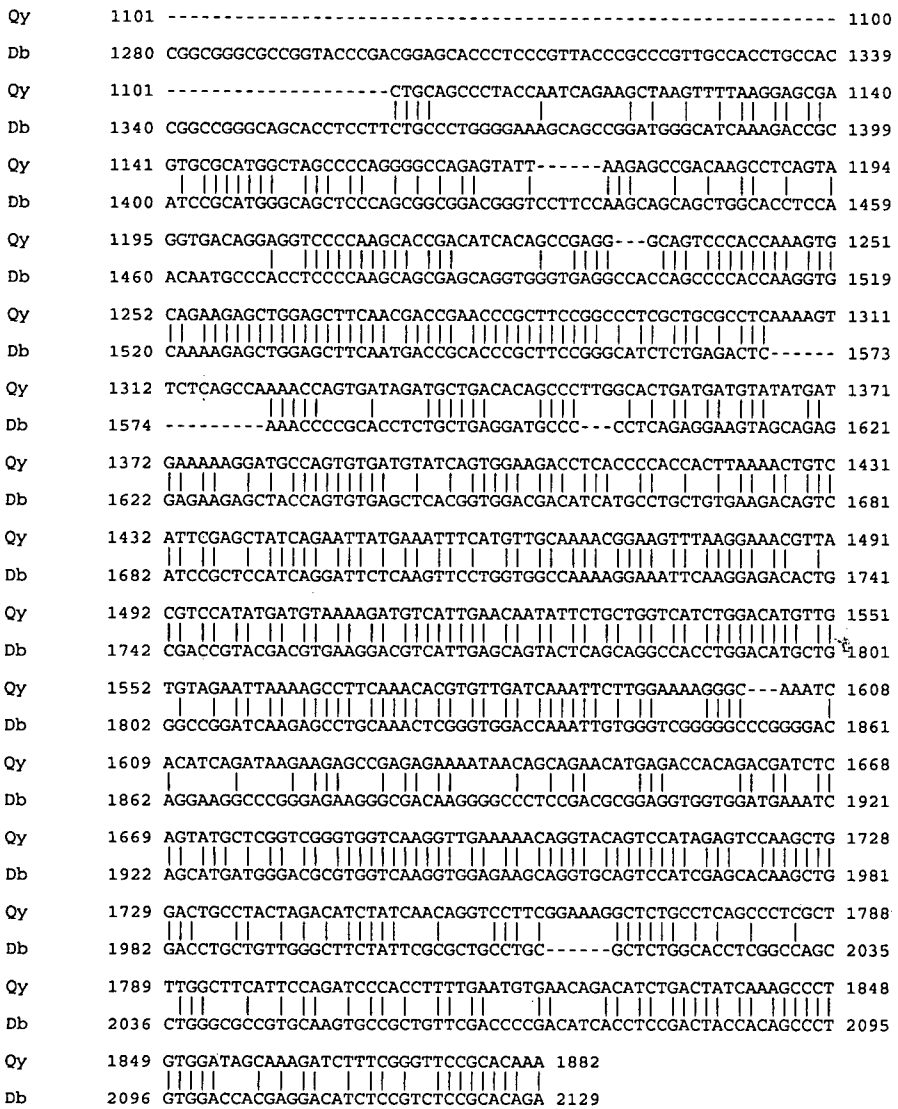
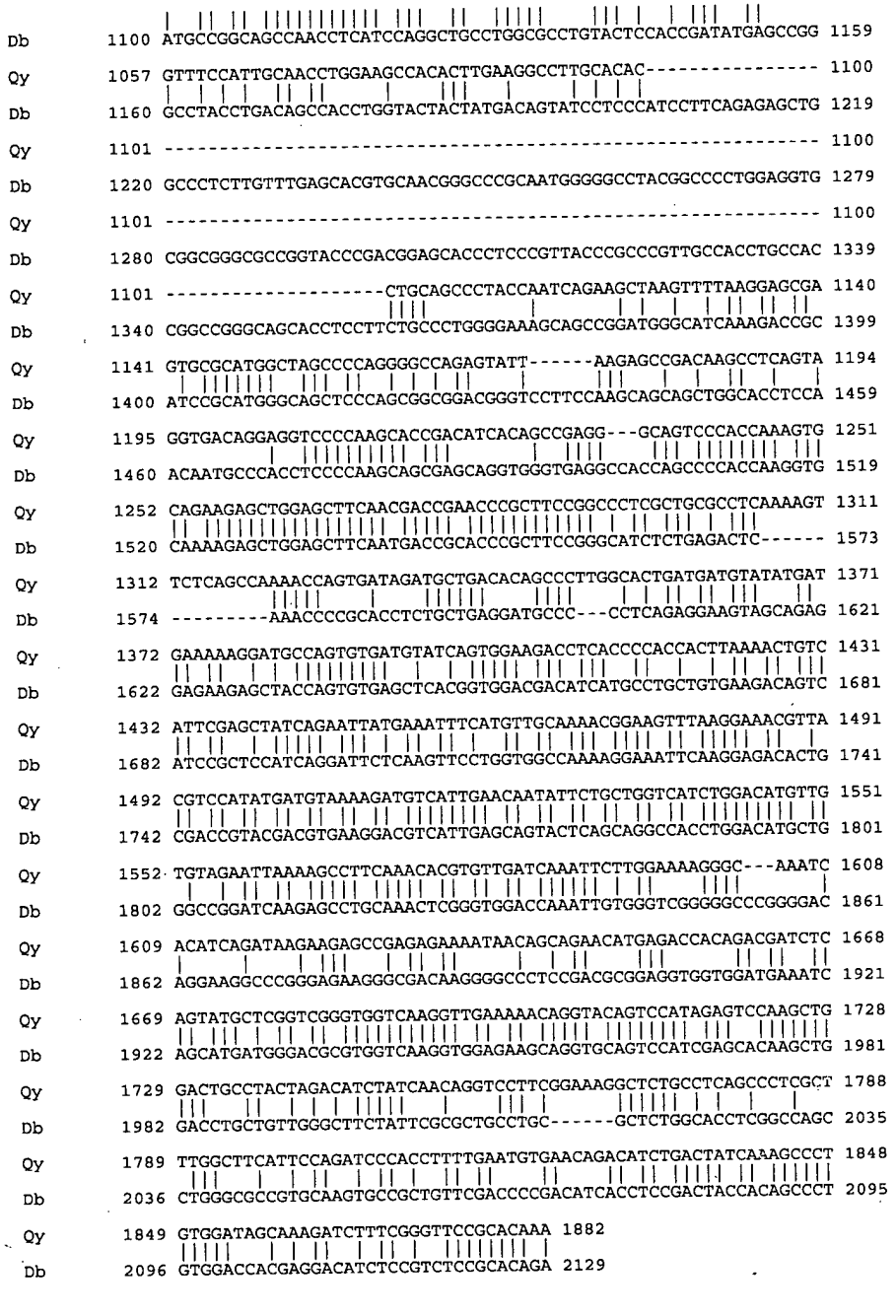


RESULT 14
US-10-850-928-1
; Sequence 1, Application US/10850928
; Publication No. US20050037460A1
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas J.
; TITLE OF INVENTION: POTASSIUM CHANNELS AND GENES ENCODING THESE
; TITLE OF INVENTION: POTASSIUM CHANNELS
; FILE REFERENCE: 2815-127PUS2
; CURRENT APPLICATION NUMBER: US/10/850,928
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: 09/492,361
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(2335)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (83)..(2170)
US-10-850-928-1

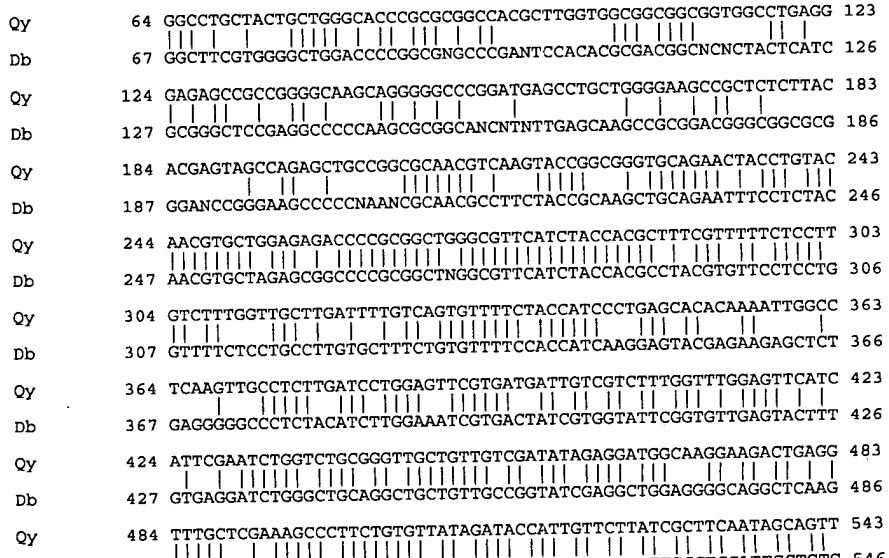
Query Match 18.4%; Score 492; DB 19; Length 2335;
Best Local Similarity 59.3%; Pred. No. 1.4e-140;
Matches 1087; Conservative 0; Mismatches 555; Indels 192; Gaps 7;



RESULT 15

US-10-096-578-88
; Sequence 88, Application US/10096578
; Publication No. US20030165874A1
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; TITLE OF INVENTION: AND OTHER EPILEPSIES
; FILE REFERENCE: 2323-160
; CURRENT APPLICATION NUMBER: US/10/096,578
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: US 09/177,650
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/063,147
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 2273
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2271)
; NAME/KEY: misc_feature
; LOCATION: (1)..(2273)
; OTHER INFORMATION: n may be any nucleotide except at position
; OTHER INFORMATION: 272 at which n may be t, c or g.
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(757)
; OTHER INFORMATION: Xaa may be: S or R at 18, 19 and 69; V, A, E or G
; OTHER INFORMATION: at 31; D or E at 33; S, P, T or A at 39; I, T, N or
; OTHER INFORMATION: S at 52; F, L, I, M or V at 53; S, P, T or A at 64;
; OTHER INFORMATION: P at 68; L, S or W at 91; R at 365; V at 509 and 516.
US-10-096-578-88

Query Match 18.3%; Score 489.2; DB 16; Length 2273;
Best Local Similarity 57.0%; Pred. No. 1e-139;
Matches 1020; Conservative 2; Mismatches 667; Indels 99; Gaps 4;



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Qy       604 CTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTGGGT 663
Db       607 TTGCAAATCTTGCGGATGATCCGTATGGACCGGAGGGGTGGCACCTGGAAGCTCTTGGGA 666

Qy       664 TCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTGGTT 723
Db       667 TCGGTAGTCTACGCTCACAGCAAGGAGCTGGTGACTGCCTGGTACATTGGCTTCCTCTGC 726

Qy       724 CTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTTTCT 783
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Qy       784 ACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGAGAC 843
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Qy       844 AAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGCATT 903
Db       847 AAGTACCCTCAGACCTGGAACGGGAGGCTGCTGGCAGCGACCTTTACCCTCATTGGTGTC 906

Qy       904 TCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAAGAA 963
Db       907 TCGTTCTTTGCTCTTCCGGCTGGCATTTTGGGATCCGGCTTTGCCCTGAAAGTCCAAGAG 966

Qy       964 CAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAGTGT 1023
Db       967 CAGCATCGGCAAAAACACTTTGAGAAACGGCGGAACCCTGCGGCAGGTCTGATCCAGTCT 1026

Qy      1024 GTTTGGCGTAGTTACGCAGCTGAT---------------------------------- 1047
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Qy      1048 ---GAGAAATCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGCACACCTGC 1104
Db      1087 TACGAGCGNACAGTCACTGTCCCCATGTACAGCTCACAAACTCAAACCTATGGGGCCTCC 1146

Qy      1105 AGCCCTACC--------------------------------AATCAGAAGCTAAGTTTTA 1132
Db      1147 AGACTCATCCCACCTCTGAACCAGCTGGAGCTGCTGAGGAATCTCAAGAGCAAATCTGGA 1206

Qy      1133 AGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAG 1192
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Qy      1193 TAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGC---------------------- 1229
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Qy      1230 --CGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTC 1287
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Qy      1288 CGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCC 1347
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Qy      1468 AAACGGAAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATAT 1527
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 09:10:16 ; Search time 8429.33 Seconds
(without alignments)
12043.352 Million cell updates/sec

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Perfect score: 2667
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
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9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	1859.2	69.7	2014	9	AY407014	AY407014 Pan trogl
	4	1351.4	50.7	2276	3	AK033079	AK033079 Mus muscu
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	6	637.2	23.9	658	2	BE158938	BE158938 MR0-HT040
c	7	636.2	23.9	732	6	CD629756	CD629756 55049343J
c	8	625.2	23.4	742	6	CD629754	CD629754 55049327J
c	9	595	22.3	678	6	CD629758	CD629758 55049351J
c	10	592.2	22.2	717	6	CD629766	CD629766 55049391J
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c	14	559.6	21.0	724	6	CD629752	CD629752 55049303J
	15	553.8	20.8	734	4	BG532543	BG532543 602562103
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	19	530.4	19.9	599	6	CD629765	CD629765 55049391H
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	23	516.8	19.4	584	2	AW049888	AW049888 UI-M-BH1-
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ALIGNMENTS

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ACCESSION AY407013
VERSION AY407013.1 GI:39762984
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2733)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2733)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
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/mol_type="genomic DNA"
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gene <1. .>2733
/gene="KCNQ5"
/locus_tag="HCM2749"
ORIGIN

Query Match 99.5%; Score 2653.6; DB 9; Length 2733;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2656; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60

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Db      67 ATGAAGGATGTGGAGTCCGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 126
Qy      61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
Db     127 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTCGGTGGCGGCGGCGGTGGCCTG 186
Qy     121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
Db     187 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 246
Qy     181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
Db     247 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 306
Qy     241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
Db     307 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 366
Qy     301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
Db     367 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 426
Qy     361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
Db     427 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 486
Qy     421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
Db     487 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 546
Qy     481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
Db     547 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 606
Qy     541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
Db     607 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 666
Qy     601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
Db     667 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 726
Qy     661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
Db     727 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 786
Qy     721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
Db     787 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 846
Qy     781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
Db     847 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 906
Qy     841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
Db     907 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 966
Qy     901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
Db     967 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 1026
Qy     961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
Db    1027 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1086
Qy    1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Db    1087 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1146
Qy    1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAATCAGAAGCTAAGTTTTAAGGAGCGA 1140
Db    1147 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAATCAGAAGCTAAGTTTTAAGGAGCGA 1206

Qy    1141 GTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGAC 1200
Db    1207 GTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGAC 1266
Qy    1201 AGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGC 1260
Db    1267 AGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGC 1326
Qy    1261 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 1320
Db    1327 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 1386
Qy    1321 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 1380
Db    1387 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 1446
Qy    1381 TGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCT 1440
Db    1447 TGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCT 1506
Qy    1441 ATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATAT 1500
Db    1507 ATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACATTACGTCCATAT 1566
Qy    1501 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 1560
Db    1567 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 1626
Qy    1561 AAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAG 1620
Db    1627 AAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAG 1686
Qy    1621 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGT 1680
Db    1687 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGT 1746
Qy    1681 CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGCTGGACTGCCTACTA 1740
Db    1747 CGGGTGGTCAAGGTTGANNNNNNNGTACAGTCCATAGAATCCAAGCTGGACTGCCTACTA 1806
Qy    1741 GACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1800
Db    1807 GACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1866
Qy    1801 CAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAA 1860
Db    1867 CAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAA 1926
Qy    1861 GATCTTTCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATC 1920
Db    1927 GATCTTTCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATC 1986
Qy    1921 TCGAGAGGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCG 1980
Db    1987 TCGAGAGGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCG 2046
Qy    1981 CTTAGCCCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCA 2040
Db    2047 CTTAGCCCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCA 2106
Qy    2041 GCAGTGGCAGCCACCAACACCATTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCC 2100
Db    2107 GCAGTGGCAGCCACCAACACCATTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCC 2166
Qy    2101 CCAACAACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAA 2160
Db    2167 CCAACAACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAA 2226
Qy    2161 ACTCTGCACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTT 2220
Db    2227 ACTCTGCACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTT 2286
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Qy       2221 GTTGCCTCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATG 2280
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Db       2287 GTTGCCTCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATG 2346

Qy       2281 AGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2347 AGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAG 2406

Qy       2341 GACTTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATA 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2407 GACTTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATA 2466

Qy       2401 CAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGG 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2467 CAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGG 2526

Qy       2461 AGGGAATCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGAC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2527 AGGGAATCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGAC 2586

Qy       2521 ACTTTTGATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGG 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2587 ACTTTTGATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGG 2646

Qy       2581 ACTGGAAGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTC 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2647 ACTGGAAGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTC 2706

Qy       2641 AGCTTGCCTCATGTCAAACTGAAATAA 2667
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Db       2707 AGCTTGCCTCATGTCAAACTGAAATAA 2733
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RESULT 2
AY407015
LOCUS       AY407015                2729 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Mus musculus KCNQ5 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY407015
VERSION     AY407015.1  GI:39762986
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2729)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2729)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .2729
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene            <1. .>2729
                     /gene="KCNQ5"
                     /locus_tag="HCM2749"
ORIGIN
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 Query Match           80.3%;  Score 2142.2;  DB 9;  Length 2729;
 Best Local Similarity  88.6%;  Pred. No. 0;
 Matches 2363;  Conservative    0;  Mismatches  258;  Indels   46;  Gaps    2;

Qy          1 ATGAAGGATGTGGAGTCGGGCCGGGGCAGGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
              |||||||||||||||| ||||| |||||||||||||||||||||| ||||||||||||
Db        109 ATGAAGGATGTGGAGTCCGGCCGCGGCAGGGTGCTGCTGAACTCGGCGGCCGCCAGGGGC 168

Qy         61 GACGGCCTGCTACTGCTGGGCACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGCCTG 120
              |||||||||||  |||| |||||||||||||  |||| || || |||||||| ||| ||
Db        169 GACGGCCTGCTGTTGCTCGGCACCCGCGCGGCGGCGCTCGGCGGAGGCGGCGGCGGCTTG 228

Qy        121 AGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
              || |||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        229 AGAGAGAGCCGCCGGGGCAAGCAGGGGGCCCGAATGAGCCTGCTGGGGAAGCCGCTCTCC 288

Qy        181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTG 240
              ||||| || |||||||||| ||||||||||||||||||||||||||||||||||| |||
Db        289 TACACCAGCAGCCAGAGCTGTCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTATCTG 348

Qy        241 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCACGCTTTCGTTTTTCTC 300
              |||||||||||||||                                        |||||||
Db        349 TACAACGTGCTGGA----------------------------------------TTTTCTC 369

Qy        301 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 360
              ||||| ||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        370 CTTGTGTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAGCATACAAAATTG 429

Qy        361 GCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTTGGAGTTC 420
              || |||||||||||||| || |||||||||||||||| || |||||||| |||||||||
Db        430 GCTTCAAGTTGCCTCTTAATTCTGGAGTTCGTGATGATCGTTGTCTTTGGCTTGGAGTTC 489

Qy        421 ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
              |||||||||||||||||||| |||||||||||||||| |||||||||||||||||||||
Db        490 ATCATTCGAATCTGGTCTGCAGGTTGCTGTTGTCGTTATAGAGGATGGCAAGGAAGACTG 549

Qy        481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGCTTCAATAGCA 540
              |||||||||||||| || |||||||| |||||||||||||||| ||||||||||||||||
Db        550 AGGTTTGCTCGAAAACCATTCTGTGTAATAGATACCATTGTTCTCATCGCTTCAATAGCA 609

Qy        541 GTTGTTTCTGCAAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 600
              ||||| |||||||||||||||||||||||||| |||||||| || ||||||||||||||
Db        610 GTTGTCTCTGCAAAAACTCAGGGTAATATTTTCGCCACGTCAGCGCTCAGAAGTCTCCGG 669

Qy        601 TTCCTACAGATCCTCCGCATGGTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTG 660
              |||||||||||||||| || |||||||||||||| |||||||||| || |||||  | ||
Db        670 TTCCTACAGATCCTGCGTATGGTGCGCATGGACAGAAGGGGAGGGACCTGGAAGCTGCTC 729

Qy        661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTTG 720
              || || |||||||||||||||||||||||||||||||| |||||||| |||||| ||
Db        730 GGCTCTGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCCTGGTACATTGGATTTCTG 789

Qy        721 GTTCTTATTTTTTCGTCTTTCCTTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTT 780
              |||||||||||||| || |||||||||||| |||||||||||||||||||||||||||||
Db        790 GTTCTTATTTTTTCATCCTTCCTTGTCTATCTTGTGGAAAAGGATGCCAATAAAGAGTTT 849

Qy        781 TCTACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGA 840
              || |||||||| |||||||||||||||||||||||||| ||| ||||||| ||||||||||
Db        850 TCGACATATGCGGATGCTCTCTGGTGGGGCACAATCACACTGACAACCATTGGCTATGGA 909

Qy        841 GACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
              |||||||| |||||||| |||||||||||| |||| |||||||||| ||||||||||||
Db        910 GACAAAACACCCCTAACGTGGCTGGGAAGACTGCTCTCTGCAGGCTTCGCACTCCTTGGC 969

Qy        901 ATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAA 960
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        970 ATTTCTTTCTTTGCACTTCCTGCTGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAG 1029

Qy        961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAG 1020
              || || |||||||||| || ||||||||||||||||||||||||||||||||||| |||
Db       1030 GAGCAGCACCGCCAGAAGCATTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATCCAG 1089
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Qy       1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Db       1090 TGTGTCTGGCGTAGTTATGCAGCTGATGAAAAATCTGTTTCCATTGCAACCTGGAAGCCA 1149

Qy       1081 CACTTGAAGGCCTTGCACACCTGCAGCCCTACCAATCAGAAGCTAAGTTTTAAGGAGCGA 1140
Db       1150 CATCTGAAGGCCTTGCACACCTGCAGCCCTACCAATCAGAAGCTGAGCTTTAAGGAGCGA 1209

Qy       1141 GTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGAC 1200
Db       1210 GTGCGCATGGCTAGCCCAAGGGGCCAGAGCATTAAGAGCAGACAAGCATCAGTAGGTGAC 1269

Qy       1201 AGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGC 1260
Db       1270 AGGAGATCCCCGAGCACTGACATCACTGCCGAGGGCAGCCCCACCAAAGTCCAGAAGAGT 1329

Qy       1261 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 1320
Db       1330 TGGAGCTTCAACGACCGAACCCGCTTCAGGCCCTCACTACGGCTCAAGAGTTCCCAGCCA 1389

Qy       1321 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 1380
Db       1390 AAGCCAGTGATAGACGCCGACACAGCCCTTGGCATTGATGATGTGTATGATGAGAAAGGA 1449

Qy       1381 TGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCT 1440
Db       1450 TGCCAGTGTGACGTCTCTGTGGAGGACCTCACCCCACCACTTAAAACCGTCATCCGAGCA 1509

Qy       1441 ATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATAT 1500
Db       1510 ATCAGAATTATGAAGTTTCATGTTGCAAAGCGGAAGTTTAAGGAAACATTACGCCCATAT 1569

Qy       1501 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 1560
Db       1570 GATGTAAAAGATGTCATTGAACAATACTCTGCTGGTCACCTGGACATGCTTTGTAGAATA 1629

Qy       1561 AAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAG 1620
Db       1630 AAAAGCCTTCAGACACG-------CAAATTCTTGGAAAAGGACAAATGACGTCAGATAAG 1682

Qy       1621 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGT 1680
Db       1683 AAGAGCCGAGAGAAAATAACAGCAGAACACGAGACAACAGATGACCCCAGCATGCTCGCC 1742

Qy       1681 CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGCTGGACTGCCTACTA 1740
Db       1743 CGGGTTGTGAAGGTTGAGAAACAGGTCCAGTCCATCGAATCCAAGCTGGACTGCCTGCTG 1802

Qy       1741 GACATCTATCAACAGGTCCTTCGGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1800
Db       1803 GATATCTATCAACAGGTCCTCCGGAAAGGCTCTGCCTCCGCCCTCACTCTGGCATCCTTT 1862

Qy       1801 CAGATCCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAGCCCTGTGGATAGCAAA 1860
Db       1863 CAGATCCCGCCTTTTGAATGTGAACAGACCTCTGACTATCAAAGTCCTGTGGATAGCAAA 1922

Qy       1861 GATCTTTCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATC 1920
Db       1923 GACCTGTCTGGCTCAGCACAAAACAGCGGCTGTTTAACGAGGTCAGCCAGTGCCAACATC 1982

Qy       1921 TCGAGAGGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCG 1980
Db       1983 TCAAGAGGCCTGCAGTTCATCCTAACACCAAATGAGTTCAGTGCTCAGACTTTCTATGCG 2042

Qy       1981 CTTAGCCCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCA 2040
Db       2043 CTTAGCCCTACTATGCACAGCCAAGCTACCCAGGTACCCATGAGTCAAAATGACGGCTCC 2102

Qy       2041 GCAGTGGCAGCCACCAACACCATTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCC 2100
Db       2103 TCCGTGGTAGCCACCAATAACATTGCAAACCAAATAAGCGCCGCACCCAAGCCAGCAGCC 2162

Qy       2101 CCAACAACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAA 2160
Db       2163 CCAACAACTTTACAGATCCCTCCTCCTCTCTCGGCCATCAAGCACTTGTCCAGGCCAGAA 2222

Qy       2161 ACTCTGCACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTT 2220
Db       2223 CCTCTGCTCTCAAACCCCACCGGCTTACAAGAGAGTATTTCTGATGTCACCACCTGCCTT 2282

Qy       2221 GTTGCCTCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATG 2280
Db       2283 GTTGCCTCCAAGGAAAGTGTTCAGTTTGCACAGTCAAACCTGACCAAGGACCGTTCCCTG 2342

Qy       2281 AGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAG 2340
Db       2343 AGGAAAAGTTTCGACATGGGAGGAGAAACTCTGTTGTCTGTCCGCCCCATGGTGCCCAAG 2402

Qy       2341 GACTTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATA 2400
Db       2403 GATTTGGGCAAATCTCTGTCTGTACAAAACCTGATCAGGTCGACAGAAGAACTGAACTTA 2462

Qy       2401 CAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGG 2460
Db       2463 CAGTTTTCAGGCAGCGAGTCAAGCGGCTCTCGAGGCAGTCAAGATTTTTATCCCAAGTGG 2522

Qy       2461 AGGGAATCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGAC 2520
Db       2523 AGAGAATCCAAATTGTTTATAACTGATGAGGAGGTCGGTGCCGAAGAGACAGAAACAGAT 2582

Qy       2521 ACTTTTGATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGG 2580
Db       2583 ACTTTTGACGGCACCCCACCGCCTGCGGGGGAGGCTGCTTTCTCATCAGACTCTCTAAGG 2642

Qy       2581 ACTGGAAGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTC 2640
Db       2643 ACTGGAAGGTCACGGTCATCTCAGAACATTTGTAAGACAGGAGACAGTACAGACGCCCTC 2702

Qy       2641 AGCTTGCCTCATGTCAAACTGAAATAA 2667
Db       2703 AGTTTGCCTCACGTCAAACTGAACTAA 2729
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RESULT 3
AY407014

LOCUS	AY407014 2014 bp DNA linear GSS 15-DEC-2003
DEFINITION	Pan troglodytes KCNQ5 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION	AY407014
VERSION	AY407014.1 GI:39762985
KEYWORDS	GSS.
SOURCE	Pan troglodytes (chimpanzee)
ORGANISM	Pan troglodytes Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE	1 (bases 1 to 2014)
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL	Science 302 (5652), 1960-1963 (2003)
PUBMED	14671302
REFERENCE	2 (bases 1 to 2014)
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Direct Submission
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES	Location/Qualifiers
source	1. .2014

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ORIGIN

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Db         61 GCCACGCTCGGTGGCGGCGGCGGTGGCCTGAGGGAGAGCCGCCGGGGCAAGCAGGGGGCC 120

Qy        151 CGGATGAGCCTGCTGGGGAAGCCGCTCTCTTACACGAGTAGCCAGAGCTGCCGGCGCAAC 210
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Qy        271 GCGTTCATCTACCACGCTTTCGTTTTTCTCCTTGTCTTTGGTTGCTTGATTTTGTCAGTG 330
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RESULT 4
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ACCESSION   AK033079
VERSION     AK033079.1  GI:26328812
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2276)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches 1503;  Conservative    0;  Mismatches  191;  Indels   27;  Gaps    1;

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Db        1081 AAAATGACGGCTCCTCCGTGGTAGCCACCAATAACATTGCAAACCAAATAAGCGCCGCAC 1140

Qy       2087 CCAAGCCAGCAGCCCCAACAACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATC 2146
              |||||||||||||||||||||||||||||||||||||| ||||||||| | ||||||||||
Db        1141 CCAAGCCAGCAGCCCCAACAACTTTACAGATCCCTCCTCCTCTCTCGGCCATCAAGCACT 1200

Qy       2147 TGCCCAGGCCAGAAACTCTGCACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACG 2206
              || |||||||||| |||||| | | |||||  | ||||||||| || || ||||||||| |
Db        1201 TGTCCAGGCCAGAACCTCTGCTCTCAAACCCCACCGGCTTACAAGAGAGTATTTCTGATG 1260

Qy       2207 TCACCACCTGCCTTGTTGCCTCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCA 2266
              |||||||||||||||||||||||||||||||| ||||||| |||||||||||||| || ||||
Db        1261 TCACCACCTGCCTTGTTGCCTCCAAGGAAAGTGTTCAGTTTGCACAGTCAAACCTGACCA 1320

Qy       2267 AGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTC 2326
              ||||||||||  |||||||||| || ||||||||||||||||||||||||||||| | |
Db        1321 AGGACCGTTCCCTGAGGAAAAGTTTCGACATGGGAGGAGAAACTCTGTTGTCTGTCCGCC 1380

Qy       2327 CCATGGTGCCGAAGGACTTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCG 2386
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Db        1381 CCATGGTGCCCAAGGATTTGGGCAAATCTCTGTCTGTACAAAACCTGATCAGGTCGACAG 1440

Qy       2387 AGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATT 2446
              | ||||||||  ||||  ||||||| || |||||||| |||||  ||||||| |||||||
Db        1441 AAGAACTGAACTTACAGTTTTCAGGCAGCGAGTCAAGCGGCTCTCGAGGCAGTCAAGATT 1500

Qy       2447 TTTACCCCAAATGGAGGGAATCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAG 2506
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Db        1501 TTTATCCCAAGTGGAGAGAATCCAAATTGTTTATAACTGATGAGGAGGTCGGTGCCGAAG 1560

Qy       2507 AGACAGAGACAGACACTTTTGATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCAT 2566
              ||||||| ||||| |||||||| | | | || | ||||||  |||| ||||| ||  |||
Db        1561 AGACAGAAACAGATACTTTTGACGGCACCCCACCGCCTGCGGGGGAGGCTGCTTTCTCAT 1620

Qy       2567 CAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAA 2626
              |||||||||||||||||||||||||||||||| |||||||||| |||||||||| ||||||| |
Db        1621 CAGACTCTCTAAGGACTGGAAGGTCACGGTCATCTCAGAACATTTGTAAGACAGGAGACA 1680

Qy       2627 GTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2667
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Db        1681 GTACAGGCGCCCTCAGTTTGCCTCACGTCAAACTGAACTAA 1721
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RESULT 5
CD629762/c

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LOCUS       CD629762                797 bp    mRNA    linear   EST 12-JAN-2004
DEFINITION  55049367J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD629762
VERSION     CD629762.1  GI:40278028
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 797)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .797
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="FLP"
                     /note="Vector: pDrive Cloning Vector"
ORIGIN
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Query Match 25.1%; Score 670.6; DB 6; Length 797;
Best Local Similarity 95.0%; Pred. No. 1.2e-180;
Matches 725; Conservative 0; Mismatches 9; Indels 29; Gaps 2;

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Qy        989 AAAGAAGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGTTACGCAGCTGATG 1048
              |||||| | |||||||||||||| |||||||||||||| |||||||||||||| |||||
Db        763 AAAGAAAGGACCCAGCTGCCAACTTCATTCAGTGTGTTT-GCGTAGTTACGCAGTTGATG 705

Qy       1049 AGAAATCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGCACACCTGCAGCC 1108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 AGAAATCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGCACACCTGCAGCC 645

Qy       1109 ----------------------------CTACCAATCAGAAGCTAAGTTTTAAGGAGCGA 1140
                                          | | || ||||||||||||||||||||||||||
Db        644 CCTACCAAGAAAGGACAAGGGGAAGCATCAAGCAGTCAGAAGCTAAGTTTTAAGGAGCGA 585

Qy       1141 GTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        584 GTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGAC 525

Qy       1201 AGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        524 AGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGC 465

Qy       1261 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 1320
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Db        464 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 405

Qy       1321 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 1380

Db        404 AAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGA 345

Qy       1381 TGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCT 1440

Db        344 TGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGTCATTCGAGCT 285

Qy       1441 ATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATAT 1500

Db        284 ATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAGGAAACATTACGTCCATAT 225

Qy       1501 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 1560

Db        224 GATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATT 165

Qy       1561 AAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAG 1620

Db        164 AAAAGCCTTCAAACACGTGTTGATCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAG 105

Qy       1621 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGT 1680

Db        104 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGT 45

Qy       1681 CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCA 1723

Db          44 CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAATCCA 2
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RESULT 6
BE158938
LOCUS       BE158938                658 bp    mRNA    linear   EST 21-JUN-2000
DEFINITION  MR0-HT0404-210200-001-c04 HT0404 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE158938
VERSION     BE158938.1  GI:8621659
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 658)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=MR0-HT0404-210
            200-001-c04&t3=2000-02-21&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 657.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="HT0404"
                     /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN
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  Query Match           23.9%;  Score 637.2;  DB 2;  Length 658;
  Best Local Similarity  99.5%;  Pred. No. 4.6e-171;
  Matches  639;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        831 TGGCTATGGAGACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGC 890

Db         17 TGGCTATGGAGACAAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGC 76

Qy        891 ACTCCTTGGCATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATT 950

Db         77 ACTCCTTGGCATTTCTTTCTTTGCACTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATT 136

Qy        951 AAAAGTACAAGAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAA 1010

Db        137 AAAAGTACAAGAACAACACCGCCAGAAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAA 196

Qy       1011 CCTCATTCAGTGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAAC 1070

Db        197 CCTCATTCAGTGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAAC 256

Qy       1071 CTGGAAGCCACACTTGAAGGCCTTGCACACCTGCAGCCCTACCAATCAGAAGCTAAGTTT 1130

Db        257 CTGGAAGCCACACTTGAAGGCCTTGCACACCTGCAGCCCTACCAATCAGAAGCTAAGTTT 316

Qy       1131 TAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTC 1190

Db        317 TAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCCTC 376

Qy       1191 AGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCACCAAAGT 1250

Db        377 AGTAGGTGACAGGAGGTCCCCAAGCACCGACGTCACAGCCGAGGGCAGTCCCACCAAAGT 436

Qy       1251 GCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAG 1310

Db        437 GCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAAAAG 496

Qy       1311 TTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGA 1370

Db        497 TTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGA 556

Qy       1371 TGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGT 1430

Db        557 TGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAACTGT 616

Qy       1431 CATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACG 1472

Db        617 CATTCGAGCTATCAGAATTATGAAATTTCTTGTTGCCAAACG 658
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RESULT 7
CD629756/c
LOCUS       CD629756                732 bp    mRNA    linear   EST 12-JAN-2004
DEFINITION  55049343J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD629756
VERSION     CD629756.1  GI:40278022
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 732)
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```
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .732
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="FLP"
                     /note="Vector: pDrive Cloning Vector"
ORIGIN

  Query Match             23.9%;  Score 636.2;  DB 6;  Length 732;
  Best Local Similarity   95.4%;  Pred. No. 9.3e-171;
  Matches  699;  Conservative    0;  Mismatches    3;  Indels   31;  Gaps    3;

Qy       1014 CATTCAGTGTGTTTGGCGTAGTT-ACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCT 1072
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Db        732 CATTCAGTGTGTTTGGCGTAGTTAACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCT 673

Qy       1073 GGAAGCCACACTTGAAGGCCTTGCACACCTGCAGCCCTAC---------- 1112
             ||||||||||||||||||||||||||||||||||||||||||
Db        672 GGAAGCCACACTTGAAGGCCTTGCACACCTGCAGCCCTACCCAAGAAAGAACAAGGGGGA 613

Qy       1113 ---------CAATCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGG 1163
                      || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        612 AGCATCAAGCAGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGG 553

Qy       1164 CCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACAT 1223
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Db        552 CCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACAT 493

Qy       1224 CACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCG 1283
             ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        492 CACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGGCCGAACCCG 433

Qy       1284 CTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACAC 1343
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 CTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACAC 373

Qy       1344 AGCCCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGA 1403
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 AGCCCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGA 313

Qy       1404 AGACCTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGT 1463
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 AGACCTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGT 253

Qy       1464 TGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACA 1523
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        252 TGCAAAACGGAAGTTTAAGGAAACATTACGTCCATATGATGTAAAAGATGTCATTGAACA 193

Qy       1524 ATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGA 1583
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 ATATTCTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGA 133

Qy       1584 TCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGC 1643
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 TCAAATTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGC 73

Qy       1644 AGAACATGAGACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACA 1703
             ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db          72 AGAACATGAGACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTC-AGGTTGAAAAACA 14

Qy       1704 GGTACAGTCCATA 1716
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Db          13 GGTACAGTCCATA 1


RESULT 8
CD629754/c
LOCUS       CD629754                742 bp    mRNA    linear   EST 12-JAN-2004
DEFINITION  55049327J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD629754
VERSION     CD629754.1  GI:40278020
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 742)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .742
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="FLP"
                     /note="Vector: pDrive Cloning Vector"
ORIGIN

  Query Match             23.4%;  Score 625.2;  DB 6;  Length 742;
  Best Local Similarity   94.7%;  Pred. No. 1.4e-167;
  Matches  701;  Conservative    0;  Mismatches    8;  Indels   31;  Gaps    4;

Qy       1016 TTCAGTGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGA 1075
             |||||||| |||| |||| ||||||||||||||||||||||||||||||||  |||
Db        742 TTCAGTGTTTTTGCCGTA-TTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACTGGGA 684

Qy       1076 AGCCACACTTGAAGGCCTTGCACACCTGCAGCCCTACCAA---------- 1115
             |||||||||||||||||||||||||||||||||||||||||
Db        683 AGCCACACTTGAAGGCCTTGCACACCTGCAGCCCTACCAAGAAAGAACCAAGGGGAAGCA 624

Qy       1116 --------TCAGAAGCTAAGTTTTAAGGAG-CGAGTGCGCATGGCTAGCCCCAGGGGCCA 1166
                     |||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        623 TCAAGCAGTCAGAAGCTAAGTTTTAAGGAGCCGAGTGCGCATGGCTAGCCCCAGGGGCCA 564

Qy       1167 GAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCAC 1226
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 GAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCAC 504

Qy       1227 AGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTT 1286
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 AGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTT 444

Qy       1287 CCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGC 1346
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 CCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGC 384

Qy       1347 CCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGA 1406
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 CCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGA 324

Qy       1407 CCTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGC 1466
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 CCTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGC 264

Qy       1467 AAAACGGAAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATA 1526
             |||||||||||||||| |||| ||||||||||||||||||||||||||||||||||||||
Db        263 AAAACGGAAGTTTAAGTAAACATTACGTCCATATGATGTAAAAGATGTCATTGAACAATA 204

Qy       1527 TTCTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCA 1586
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Db        203 TTCTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCA 144

Qy       1587 AATTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGA 1646
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 AATTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGA 84

Qy       1647 ACATGAGACCACAGACGATCTCAGTATGCTCGGTCGGG-TGGTCAAGGTTGAAAAACAGG 1705
                ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
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Qy       1706 TACAGTCCATAGAGTCCAAG 1725
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Db          23 TACAGTCCATAGAATCCTAG 4


RESULT 9
CD629758/c
LOCUS       CD629758                678 bp    mRNA    linear   EST 12-JAN-2004
DEFINITION  55049351J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD629758
VERSION     CD629758.1  GI:40278024
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 678)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .678
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="FLP"
                     /note="Vector: pDrive Cloning Vector"
ORIGIN

  Query Match             22.3%;  Score 595;  DB 6;  Length 678;
  Best Local Similarity   99.0%;  Pred. No. 6.3e-159;
  Matches  609;  Conservative    0;  Mismatches    5;  Indels    1;  Gaps    1;

Qy       1109 CTACCAATCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGA 1168
                | | || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 CAAGCAGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGA 559

Qy       1169 GTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAG 1228
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 GTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAG 499

Qy       1229 CCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCC 1288
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 CCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCC 439

Qy       1289 GGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCC 1348
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 GGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCC 379

Qy       1349 TTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACC 1408
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 TTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACC 319

Qy       1409 TCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAA 1468
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 TCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAA 259

Qy       1469 AACGGAAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATT 1528
                ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        258 AACGGAAGTTTAAGGAAACATTACGTCCATATGATGTAAAAGATGTCATTGAACAATATT 199

Qy       1529 CTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAA 1588
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 CTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAAA 139

Qy       1589 TTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAAC 1648
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 TTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAAC 79

Qy       1649 ATGAGACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTAC 1708
                ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db         78 ATGAGACCACAGACGATCTCAGTATGCTCGGTCGGGTGGT-AAGGTTGAAAAACAGGTAC 20

Qy       1709 AGTCCATAGAGTCCA 1723
                ||||||||||| ||||
Db         19 AGTCCATAGAATCCA 5


RESULT 10
CD629766/c
LOCUS       CD629766                717 bp    mRNA    linear   EST 12-JAN-2004
DEFINITION  55049391J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD629766
VERSION     CD629766.1  GI:40278032
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 717)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .717
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="FLP"
                     /note="Vector: pDrive Cloning Vector"
ORIGIN

  Query Match             22.2%;  Score 592.2;  DB 6;  Length 717;
  Best Local Similarity   94.6%;  Pred. No. 4.1e-158;
  Matches  678;  Conservative    0;  Mismatches    8;  Indels   31;  Gaps    5;

Qy       1031 GTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGG 1090
                ||||||||||||||||||||||||||||||||| ||||||||||||||| ||||||||||
Db         717 GTAGTTACGCAGCTGATGAGAAATCTGTTGCCATTGCAACCTGGAGGCCACACTTGAAGG 658

Qy       1091 CCTTGCACACCTGCAGCCCTACCAA-------------------------TCAGAAGC 1123
                | ||||||||||||||||||||||                         ||||||||
Db         657 CTTTGCACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGC 598

Qy       1124 TAAGTT-TTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCC-G 1181
                |||||| |||||||||||||||||||||||||||||||||| |||||||||||||||| |
Db         597 TAAGTTATTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCGGAGTATTAAGAGCCGG 538

Qy       1182 ACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCC 1241
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         537 ACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCC 478

Qy       1242 CACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCG 1301
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Db        477 CACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCG 418

Qy       1302 CCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGA 1361
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 CCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGA 358

Qy       1362 TGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACT 1421
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 TGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACT 298

Qy       1422 TAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAA 1481
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 TAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAA 238

Qy       1482 GGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCT 1541
                | |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 GTAAACATTACGTCCATATGATGTAAAAGATGTCATTGAACAATATTCTGCTGGTCATCT 178

Qy       1542 GGACATGTTGTGTAGAATTAAAAGCCTTCA-AACACGTGTTGATCAAATTCTTGGAAAAG 1600
                |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        177 GGACATGTTGTGTAGAATTAAAAGCCTTCATAACACGTGTTGATCAAATTCTTGGAAAAG 118

Qy       1601 GGCAAATCACATCAGATAAGAA-GAGCCGAGAGAAAATAACAGCAGAACATGAGACCACA 1659
                |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        117 GGCAAATCACATCAGATAAGAACGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACA 58

Qy       1660 GACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATA 1716
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Db          57 GACGATCTCACTATGCTCGGTCGGGTGGTCAAGGTTGTAAAACAGGTACAGTCCATA 1
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RESULT 11
CD629755
LOCUS CD629755 691 bp mRNA linear EST 12-JAN-2004
DEFINITION 55049343H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD629755
VERSION CD629755.1 GI:40278021
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 691)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES Location/Qualifiers
source 1..691
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"
ORIGIN

Query Match 21.9%; Score 583.6; DB 6; Length 691;
Best Local Similarity 95.1%; Pred. No. 1.2e-155;
Matches 656; Conservative 0; Mismatches 4; Indels 30; Gaps 4;

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Qy        796 GCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGAGACAAAACTCCCCTA 855
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGAGACAAAACTCCCCTA 60

Qy        856 ACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGCATTTCTTTCTTTGCA 915
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGCATTTCTTTCTTTGCA 120

Qy        916 CTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAG 975
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCCTGCCGGCATTCTTGGCTCAGGTTTTGCATTAAAAGTACAAGAACAACACCGCCAG 180

Qy        976 AAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGT 1035
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAACACTTTGAGAAAAGAAGGAACCCAGCTGCCAACCTCATTCAGTGTGTTTGGCGTAGT 240

Qy       1036 TACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTG 1095
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTG 300

Qy       1096 CACACCTGCAGCCCTACCAA----------------------------TCAGAAGCTAAGT 1128
                |||||||||||||||||||                            ||||||||||||
Db        301 CACACCTGCAGCCCTACCAAGAAAGAACAAGGGGAAGCATCAAGCAGTCAGAAGCTAAGT 360

Qy       1129 TTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAGCC 1188
                |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        361 TTTAAGGAGCGAGTGCGCATGGCTAGCCCCA-GGGCCAGAGTATTAAGAGCCGACAAGCC 419

Qy       1189 TCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGA-GGGCAGTCCCACCAA 1247
                |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        420 TCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGGCAGTCCCACCAA 479

Qy       1248 AGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAA 1307
                |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        480 AGTGCAGAAGAGCTGGAGCTTCAACGGCCGAACCCGCTTCCGGCCCTCGCTGCGCCTCAA 539

Qy       1308 AAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATA 1367
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 AAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGTATA 599

Qy       1368 TGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGACCTCACCCCACCACTTAAAAC 1427
                |||||||||||||||||||||||||||||||||||||||||||||| |||||||  ||||| ||||
Db        600 TGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGAACTCACCCCCACACTT-AAAC 658

Qy       1428 TGTCATTCGAGCTATCAGAATTATGAAATT 1457
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Db        659 TGTCATTCGAGCTATCAGAATTATGAAATT 688
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RESULT 12
CB244389
LOCUS CB244389 744 bp mRNA linear EST 09-JUL-2003
DEFINITION UI-M-FY0-cdq-c-03-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
IMAGE:6832924 5', mRNA sequence.
ACCESSION CB244389
VERSION CB244389.1 GI:28366033
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 744)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
FEATURES Location/Qualifiers
source 1..744
/organism="Mus musculus"

/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6832924"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FYO"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 21.4%; Score 570.2; DB 6; Length 744;
Best Local Similarity 85.6%; Pred. No. 8.7e-152;
Matches 632; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

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Qy       1864 CTTTCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATCTCG 1923
Db          7 CTGTCTGGCTCAGCACAAAACAGCGGCTGTTTAACGAGGTCAGCCAGTGCCAACATCTCA 66

Qy       1924 AGAGGCCTGCAGTTCATTCTGACGCCAAATGAGTTCAGTGCCCAGACTTTCTACGCGCTT 1983
Db         67 AGAGGCCTGCAGTTCATCCTAACACCAAATGAGTTCAGTGCTCAGACTTTCTATGCGCTT 126

Qy       1984 AGCCCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCAGCA 2043
Db        127 AGCCCTACTATGCACAGCCAAGCTACCCAGGTACCCATGAGTCAAAATGACGGCTCCTCC 186

Qy       2044 GTGGCAGCCACCAACACCATTGCAAACCAAATAAATACGGCACCCAAGCCAGCAGCCCCA 2103
Db        187 GTGGTAGCCACCAATAACATTGCAAACCAAATAAGCGCCGCACCCAAGCCAGCAGCCCCA 246

Qy       2104 ACAACTTTACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAAACT 2163
Db        247 ACAACTTTACAGATCCCTCCTCCTCTCTCGGCCATCAAGCACTTGTCCAGGCCAGAACCT 306

Qy       2164 CTGCACCCTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTTGTT 2223
Db        307 CTGCTCTCAAACCCCACCGGCTTACAAGAGAGTATTTCTGATGTCACCACCTGCCTTGTT 366

Qy       2224 GCCTCCAAGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATGAGG 2283
Db        367 GCCTCCAAGGAAAGTGTTCAGTTTGCACAGTCAAACCTGACCAAGGACCGTTCCCTGAGG 426

Qy       2284 AAAAGCTTTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAGGAC 2343
Db        427 AAAAGTTTCGACATGGGAGGAGAAACTCTGTTGTCTGTCCGCCCCATGGTGCCCAAGGAT 486

Qy       2344 TTGGGCAAATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATACAA 2403
Db        487 TTGGGCAAATCTCTGTCTGTACAAAACCTGATCAGGTCGACAGAAGAACTGAACTTACAG 546

Qy       2404 CTTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGCAGCCAAGATTTTTACCCCAAATGGAGG 2463
Db        547 TTTTCAGGCAGCGAGTCAAGCGGCTCTCGAGGCAGTCAAGATTTTTATCCCAAGTGGAGA 606

Qy       2464 GAATCCAAATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGACACT 2523
Db        607 GAATCCANATTGTTTATAACTGATGAGGAGGTCNGGTGCGAAGAGACAGAAACAGATACT 666
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Qy       2524 TTTGATGCCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGGACT 2583
Db        667 TTTGACGGCACCCCACCGCCTGCGGGGGAGGCTGCTTTCTCATCAGACTCTCNTAGGACT 726

Qy       2584 GGAAGGTCACGATCATCT 2601
Db        727 GGAAGGTCACGGTCATCT 744
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RESULT 13
CD629760/c
LOCUS CD629760 714 bp mRNA linear EST 12-JAN-2004
DEFINITION 55049359J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD629760
VERSION CD629760.1 GI:40278026
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 714)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES Location/Qualifiers
source 1. .714
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 21.3%; Score 567.6; DB 6; Length 714;
Best Local Similarity 98.3%; Pred. No. 4.8e-151;
Matches 584; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

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Qy       1109 CTACCAATCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGA 1168
Db        614 CAAGCAGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGA 555

Qy       1169 GTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAG 1228
Db        554 GTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAG 495

Qy       1229 CCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAA-CGACCGAACCCGCTTC 1287
Db        494 CCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAAGCGACCGAACCCGCTTC 435

Qy       1288 CGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCC 1347
Db        434 CGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGACACAGCC 375

Qy       1348 CTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGAC 1407
Db        374 CTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAAGAC 315

Qy       1408 CTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCA 1467
Db        314 CTCACCCCACCACTTAAAACTGTCATTCGAGCTATCAGAATTATGAAATTTCATGTTGCA 255

Qy       1468 AAACGGAAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAACAATAT 1527
Db        254 AAACGGAAGTTTAAGGAAACATTACGTCCATATGATGTAAAAGATGTCATTGAACAATAT 195

Qy       1528 TCTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAA 1587
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Db        194 TCTGCTGGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTCAAACACGTGTTGATCAA 135

Qy       1588 ATTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAA 1647
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Db        134 ATTCTTGGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAA 75

Qy       1648 CATGAGACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAA 1701
             |||||||||||||||||||||||||||||||||||||||||| | |  ||| |
Db         74 CATGAGACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAGGTTGAAAACA 21


RESULT 14
CD629752/c
LOCUS       CD629752                724 bp    mRNA    linear   EST 12-JAN-2004
DEFINITION  55049303J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD629752
VERSION     CD629752.1  GI:40278018
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 724)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .724
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="FLP"
                     /note="Vector: pDrive Cloning Vector"
ORIGIN

  Query Match             21.0%;  Score 559.6;  DB 6;  Length 724;
  Best Local Similarity   97.1%;  Pred. No. 9.6e-149;
  Matches  602;  Conservative    0;  Mismatches   14;  Indels    4;  Gaps    3;

Qy       1109 CTACCAATCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGA 1168
             | | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        622 CAAGCAGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGA 563

Qy       1169 GTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAG 1228
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Db        562 GTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAG 503

Qy       1229 CCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCC 1288
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Qy       1469 AACGGAAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGA-TGTCATTGAACAATAT 1527
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RESULT 15
BG532543
LOCUS       BG532543                734 bp    mRNA    linear   EST 03-APR-2001
DEFINITION  602562103F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4699776 5',
            mRNA sequence.
ACCESSION   BG532543
VERSION     BG532543.1  GI:13524082
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 734)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1532  row: f  column: 01
            High quality sequence stop: 699.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:4699776"
                     /tissue_type="embryonal carcinoma"
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                     /clone_lib="NIH_MGC_61"
                     /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc);
                     Double-stranded cDNA was prepared from cell line RNA.  5'
                     and 3' adaptors were used in cloning as follows: 5'
                     adaptor sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor
                     sequence:  5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
                     (where B = A, C, or G and N = A, C,  G, or T).  Average
                     insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
                     contained  inserts by PCR. This library was enriched for
                     full-length clones and was constructed by Clontech
                     Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                     Library."
ORIGIN

  Query Match             20.8%;  Score 553.8;  DB 4;  Length 734;
  Best Local Similarity   99.6%;  Pred. No. 4.5e-147;
  Matches  555;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db          1 TACAGATCCCACCTCCTCTCCCAGCCATCAAGCATCTGCCCAGGCCAGAAACTCTGCACC 60

Qy       2171 CTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCA 2230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAACCCTGCAGGCTTACAGGAAAGCATTTCTGACGTCACCACCTGCCTTGTTGCCTCCA 120

Qy       2231 AGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCT 2290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGAAAATGTTCAGGTTGCACAGTCAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCT 180

Qy       2291 TTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCA 2350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTGACATGGGAGGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGCCGAAGGACTTGGGCA 240

Qy       2351 AATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATACAACTTTCAG 2410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AATCTTTGTCTGTGCAAAACCTGATCAGGTCGACCGAGGAACTGAATATACAACTTTCAG 300

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Qy       2471 AATTGTTTATAACTGATGAAGAGGTGGGTCCCGAAGAGACAGAGACAGACACTTTTGATG 2530
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Qy       2531 CCGCACCGCAGCCTGCCAGGGAAGCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGT 2590
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
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Qy       2591 CACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTC 2650
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Db        481 CACGATCATCTCAGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCCCAGCTTGCCTC 540

Qy       2651 ATGTCAAACTGAAATAA 2667
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Db        541 ATGTCAAACTGAAATAA 557
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Search completed: April 11, 2005, 21:32:05
Job time : 8438.33 secs

STIC-Biotech/ChemLib 150062

From: Bunner, Bridget
Sent: Wednesday, April 06, 2005 2:08 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like to request a sequence search for case 09/810,796:

1. the amino acid sequence of SEQ ID NO: 5 - 888AA

CRF

Thanks!

Bridget Bunner

Art Unit 1647
Rem 4C65
(571) 272-0881
mailbox 4C70

****
STAFF USE ONLY

Searcher:_____
Searcher Phone: 2-
Date Searcher Picked up:____
Date Completed:_____
Searcher Prep/Rev. Time:___
Online Time:_____

****
Type of Search

NA#:_____ AA#:_____
Interference:____ SPDI:___
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure#:_____ Text:___
Inventor:____ Litigation:___

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Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other(Specify):_____

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 8, 2005, 16:33:11 ; Search time 44 Seconds
(without alignments)
1506.554 Million cell updates/sec

Title: US-09-810-796-5
Perfect score: 4547
Sequence: 1 MKDVESGRGRVLLNSAAARG.....SICKAGESTDALSLPHVKLK 888

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4547	100.0	923	4	US-09-825-147-2	Sequence 2, Appli
2	4527.5	99.6	897	4	US-09-590-304-2	Sequence 2, Appli
3	4527.5	99.6	932	4	US-09-813-148-2	Sequence 2, Appli
4	4300.5	94.6	854	4	US-09-590-304-7	Sequence 7, Appli
5	1985	43.7	695	4	US-09-590-304-6	Sequence 6, Appli
6	1985	43.7	695	4	US-09-492-361-2	Sequence 2, Appli
7	1985	43.7	696	4	US-09-813-148-6	Sequence 6, Appli
8	1980	43.5	676	4	US-09-949-016-7694	Sequence 7694, Ap
9	1792	39.4	844	4	US-09-813-148-4	Sequence 4, Appli
10	1792	39.4	844	4	US-09-590-304-4	Sequence 4, Appli
11	1792	39.4	844	4	US-09-492-361-34	Sequence 34, Appl
12	1790.5	39.4	722	4	US-09-105-058C-23	Sequence 23, Appl
13	1788.5	39.3	930	4	US-09-177-650-96	Sequence 96, Appl
14	1787.5	39.3	871	4	US-09-105-058C-20	Sequence 20, Appl
15	1783	39.2	872	4	US-09-177-650-2	Sequence 2, Appli
16	1759	38.7	757	4	US-09-177-650-89	Sequence 89, Appl
17	1587.5	34.9	854	4	US-09-105-058C-27	Sequence 27, Appl
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19	1587.5	34.9	872	4	US-09-813-148-5	Sequence 5, Appli
20	1587.5	34.9	872	4	US-09-590-304-5	Sequence 5, Appli
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37	1102	24.2	676	4	US-09-840-125-2	Sequence 2, Appli
38	1102	24.2	676	4	US-09-492-361-33	Sequence 33, Appl
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42	1091.5	24.0	581	3	US-09-135-010A-116	Sequence 116, App
43	1091.5	24.0	581	4	US-09-597-735-116	Sequence 116, App
44	1091.5	24.0	581	4	US-09-597-732-116	Sequence 116, App
45	1091.5	24.0	581	4	US-09-597-731-116	Sequence 116, App

ALIGNMENTS

RESULT 1
US-09-825-147-2
; Sequence 2, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 923
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-825-147-2

Query Match 100.0%; Score 4547; DB 4; Length 923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 888; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        541 KSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASF 600
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Qy        781 DLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEEVGPEETETD 840
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RESULT 2
US-09-590-304-2
; Sequence 2, Application US/09590304
; Patent No. 6649371
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANN
; FILE REFERENCE: 2815-0136P
; CURRENT APPLICATION NUMBER: US/09/590,304
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 897
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-590-304-2

Query Match 99.6%; Score 4527.5; DB 4; Length 897;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

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Qy         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
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Qy        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
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Qy        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
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Qy        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
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Qy        361 HLKALHTCSPT---------NQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 411
              |||||||||||         :||||||||||||||||||||||||||||||||||||||
Db        361 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420

Qy        412 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480

Qy        472 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy        532 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600

Qy        592 ASALALASFQIPPPECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 651
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ASALALASFQIPPPECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660

Qy        652 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 711
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 720

Qy        712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780

Qy        772 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840

Qy        832 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897
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RESULT 3
US-09-813-148-2
; Sequence 2, Application US/09813148
; Patent No. 6617131
; GENERAL INFORMATION:
; APPLICANT: STEINMEYER, Klaus
; APPLICANT: LERCHE, Christian
; APPLICANT: SCHERER, Constanze
; APPLICANT: SEEBOHM, Guiscard
; APPLICANT: BUSCH, Andreas E.
; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN
; TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
; FILE REFERENCE: 38005-119
; CURRENT APPLICATION NUMBER: US/09/813,148
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: DE 100 13 732.6
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/194,041
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 2
;   LENGTH: 932
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-813-148-2

  Query Match             99.6%;  Score 4527.5;  DB 4;  Length 932;
  Best Local Similarity   98.9%;  Pred. No. 0;
  Matches  887;  Conservative    1;  Mismatches    0;  Indels    9;  Gaps    1;

Qy          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         36 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 95

Qy         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 155

Qy        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 215

Qy        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 275

Qy        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 335

Qy        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 395

Qy        361 HLKALHTCSPT---------NQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 411
              |||||||||||         :||||||||||||||||||||||||||||||||||||||
Db        396 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 455

Qy        412 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 515

Qy        472 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 575

Qy        532 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 635

Qy        592 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 651
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 695

Qy        652 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 711
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        696 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 755

Qy        712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        756 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 815

Qy        772 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        816 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 875

Qy        832 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        876 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 932


RESULT 4
US-09-590-304-7
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```
; Sequence 7, Application US/09590304
; Patent No. 6649371
; GENERAL INFORMATION:
;  APPLICANT: JENTSCH, Thomas
;  TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNE
;  FILE REFERENCE: 2815-0136P
;  CURRENT APPLICATION NUMBER: US/09/590,304
;  CURRENT FILING DATE:  2000-06-09
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 854
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-590-304-7

  Query Match             94.6%;  Score 4300.5;  DB 4;  Length 854;
  Best Local Similarity   98.8%;  Pred. No. 0;
  Matches  841;  Conservative    1;  Mismatches    0;  Indels    9;  Gaps    1;

Qy          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60

Qy         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120

Qy        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180

Qy        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300

Qy        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360

Qy        361 HLKALHTCSPT---------NQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 411
              |||||||||||         :||||||||||||||||||||||||||||||||||||||
Db        361 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420

Qy        412 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480

Qy        472 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy        532 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600

Qy        592 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 651
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660

Qy        652 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 711
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Db        661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 720

Qy        712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780

Qy        772 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 831
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Db        781 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840

Qy        832 VGPEETETDTF 842
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Db        841 VGPEETETDTF 851


RESULT 5
US-09-590-304-6
; Sequence 6, Application US/09590304
; Patent No. 6649371
; GENERAL INFORMATION:
;  APPLICANT: JENTSCH, Thomas
;  TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANN
;  FILE REFERENCE: 2815-0136P
;  CURRENT APPLICATION NUMBER: US/09/590,304
;  CURRENT FILING DATE:  2000-06-09
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-590-304-6

  Query Match             43.7%;  Score 1985;  DB 4;  Length 695;
  Best Local Similarity   60.3%;  Pred. No. 4.8e-171;
  Matches  409;  Conservative   76;  Mismatches  101;  Indels   92;  Gaps   13;

Qy         35 GGGGGLRESRRGKQGARMSLLGKPL--------------SYTSSQSCRRNVKYRRVQNYL 80
              ||||  |          |: ||| ||              |    :|   : :|||:||::
Db         37 GGGGSPR---------RLGLLGSPLPPGAPLPGPGSGSGSACGQRSSAAHKRYRRLQNWV 87

Qy         81 YNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEF 140
              |||||||||||||:|| |:||||| ||:||| ||| || :||: |||||||||||||||:
Db         88 YNVLERPRGWAFVYHVFIFLLVFSCLVLSVLSTIQEHQELANECLLILEFVMIVVFGLEY 147

Qy        141 IIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLR 200
              |:|:|||||||||||||| |||||||||| || :||:||::| |||||||||||||:|
Db        148 IVRVWSAGCCCRYRGWQGRFRFARKPFCVIDFIVFVASVAVIAAGTQGNIFATSALRSMR 207

Qy        201 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKEF 260
              ||||||||||||||||||||||||||||||||||||||||:|||||| ||||| :|
Db        208 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFASFLVYLAEKDANSDF 267

Qy        261 STYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQ 320
              |:|||:|||||||||||||||| ||||||:|:|||||||||||||||||||||||||||||
Db        268 SSYADSLWWGTITLTTIGYGDKTPHTWLGRVLAAGFALLGISFFALPAGILGSGFALKVQ 327

Qy        321 EQHRQKHFEKRRNPAANLIQCVWRSYAAD-EKSVSIATW---------------------- 358
              |||||||||||| ||||||| || |: |  ::   |||
Db        328 EQHRQKHFEKRRMPAANLIQAAWRLYSTDMSRAYLTATWYYYDSILPSFRELALLFEHVQ 387

Qy        359 -----------------------KPHLKALHT------CSPTNQKLSFKERVRMASPRG 388
                                    | :  |       |   : ::  |:|:|| | :
Db        388 RARNGGLRPLEVRRAPVPDGAPSRYPPVATCHRPGSTSFCPGESSRMGIKDRIRMGSSQR 447

Qy        389 QSIKSRQ--ASVGDRRSPSTDITAEG-SPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVID 445
              ::  |:|  |      |||::   |  ||||||||||||||||| ||||     ||
Db        448 RTGPSKQQLAPPTMPTSPSSEQVGEATSPTKVQKSWSFNDRTRFRASLRL-----KPRTS 502

Qy        446 ADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDV 505
              |: |  :::| :||  ||:::|:|: | :|||||:|||:|| ||||||||||||||||||
Db        503 AEDA-PSEEVAEEKSYQCELTVDDIMPAVKTVIRSIRILKFLVAKRKFKETLRPYDVKDV 561

Qy        506 IEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSRE---KITAEHETTDDLSMLGRV 562
              |||||||||||| ||||||||||:|:|    |:|:||   |  :: |  |::||:|||
Db        562 IEQYSAGHLDMLGRIKSLQTRVDQIVGRG--PGDRKAREKGDKGPSDAEVVDEISMMGRV 619

Qy        563 VKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFECEQTSDYQSPVDSKDL 622
              |||||||||||| ||| ||  | : || |:::  :| : |:| |: : |||| |||| :|:
Db        620 VKVEKQVQSIEHKLDLLLGFYSRCLRSGTSA--SLGAVQVPLFDPDITSDYHSPVDHEDI 677
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Qy        623 SGSAQNSGCLSRSTSANI 640
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Db        678 SVSAQTLS-ISRSVSTNM 694


RESULT 6
US-09-492-361-2
; Sequence 2, Application US/09492361
; Patent No. 6794161
; GENERAL INFORMATION:
;  APPLICANT: JENTSCH, Thomas J.
;  TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
;  TITLE OF INVENTION:  POTASSIUM CHANNELS
;  FILE REFERENCE: 2815-127P
;  CURRENT APPLICATION NUMBER: US/09/492,361
;  CURRENT FILING DATE:  2000-01-27
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-492-361-2

  Query Match             43.7%;  Score 1985;  DB 4;  Length 695;
  Best Local Similarity   60.3%;  Pred. No. 4.8e-171;
  Matches  409;  Conservative   76;  Mismatches  101;  Indels   92;  Gaps   13;

Qy         35 GGGGGLRESRRGKQGARMSLLGKPL--------------SYTSSQSCRRNVKYRRVQNYL 80
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Db         37 GGGGSPR---------RLGLLGSPLPPGAPLPGPGSGSGSACGQRSSAAHKRYRRLQNWV 87

Qy         81 YNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEF 140
              |||||||||||||:|| |:||||| ||:||| ||| || :||: |||||||||||||||:
Db         88 YNVLERPRGWAFVYHVFIFLLVFSCLVLSVLSTIQEHQELANECLLILEFVMIVVFGLEY 147

Qy        141 IIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLR 200
              |:|:|||||||||||||| |||||||||| || :||:||::| |||||||||||||:|
Db        148 IVRVWSAGCCCRYRGWQGRFRFARKPFCVIDFIVFVASVAVIAAGTQGNIFATSALRSMR 207

Qy        201 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKEF 260
              ||||||||||||||||||||||||||||||||||||||||:|||||| ||||| :|
Db        208 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFASFLVYLAEKDANSDF 267

Qy        261 STYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQ 320
              |:|||:|||||||||||||||| ||||||:|:|||||||||||||||||||||||||||||
Db        268 SSYADSLWWGTITLTTIGYGDKTPHTWLGRVLAAGFALLGISFFALPAGILGSGFALKVQ 327

Qy        321 EQHRQKHFEKRRNPAANLIQCVWRSYAAD-EKSVSIATW---------------------- 358
              |||||||||||| ||||||| || |: |  ::   |||
Db        328 EQHRQKHFEKRRMPAANLIQAAWRLYSTDMSRAYLTATWYYYDSILPSFRELALLFEHVQ 387

Qy        359 -----------------------KPHLKALHT------CSPTNQKLSFKERVRMASPRG 388
                                    | :  |       |   : ::  |:|:|| | :
Db        388 RARNGGLRPLEVRRAPVPDGAPSRYPPVATCHRPGSTSFCPGESSRMGIKDRIRMGSSQR 447

Qy        389 QSIKSRQ--ASVGDRRSPSTDITAEG-SPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVID 445
              ::  |:|  |      |||::   |  ||||||||||||||||| ||||     ||
Db        448 RTGPSKQQLAPPTMPTSPSSEQVGEATSPTKVQKSWSFNDRTRFRASLRL-----KPRTS 502

Qy        446 ADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDV 505
              |: |  :::| :||  ||:::|:|: | :|||||:|||:|| ||||||||||||||||||
Db        503 AEDA-PSEEVAEEKSYQCELTVDDIMPAVKTVIRSIRILKFLVAKRKFKETLRPYDVKDV 561

Qy        506 IEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSRE---KITAEHETTDDLSMLGRV 562
              |||||||||||| ||||||||||:|:|    |:|:||   |  :: |  |::||:|||
Db        562 IEQYSAGHLDMLGRIKSLQTRVDQIVGRG--PGDRKAREKGDKGPSDAEVVDEISMMGRV 619

Qy        563 VKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFECEQTSDYQSPVDSKDL 622
              |||||||||||| ||| ||  | : || |:::  :| : |:| |: : |||| |||| :|:
Db        620 VKVEKQVQSIEHKLDLLLGFYSRCLRSGTSA--SLGAVQVPLFDPDITSDYHSPVDHEDI 677
```

```
Qy        623 SGSAQNSGCLSRSTSANI 640
              | |||    :||| | |:
Db        678 SVSAQTLS-ISRSVSTNM 694


RESULT 7
US-09-813-148-6
; Sequence 6, Application US/09813148
; Patent No. 6617131
; GENERAL INFORMATION:
;  APPLICANT: STEINMEYER, Klaus
;  APPLICANT:  LERCHE, Christian
;  APPLICANT:  SCHERER, Constanze
;  APPLICANT:  SEEBOHM, Guiscard
;  APPLICANT:  BUSCH, Andreas E.
;  TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN
;  TITLE OF INVENTION:  NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
;  FILE REFERENCE: 38005-119
;  CURRENT APPLICATION NUMBER: US/09/813,148
;  CURRENT FILING DATE:  2001-03-21
;  PRIOR APPLICATION NUMBER: DE 100 13 732.6
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: US 60/194,041
;  PRIOR FILING DATE: 2000-04-03
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 696
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-813-148-6

  Query Match             43.7%;  Score 1985;  DB 4;  Length 696;
  Best Local Similarity   60.3%;  Pred. No. 4.8e-171;
  Matches  409;  Conservative   76;  Mismatches  101;  Indels   92;  Gaps   13;

Qy         35 GGGGGLRESRRGKQGARMSLLGKPL--------------SYTSSQSCRRNVKYRRVQNYL 80
              ||||  |          |: ||| ||              |    :|   : :|||:||::
Db         37 GGGGSPR---------RLGLLGSPLPPGAPLPGPGSGSGSACGQRSSAAHKRYRRLQNWV 87

Qy         81 YNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEF 140
              |||||||||||:|| |:||||| ||:||| ||| || :||: |||||||||||||||:
Db         88 YNVLERPRGWAFVYHVFIFLLVFSCLVLSVLSTIQEHQELANECLLILEFVMIVVFGLEY 147

Qy        141 IIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLR 200
              |:|:|||||||||||||| |||||||||| || :||:||::| |||||||||||||:|
Db        148 IVRVWSAGCCCRYRGWQGRFRFARKPFCVIDFIVFVASVAVIAAGTQGNIFATSALRSMR 207

Qy        201 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKEF 260
              |||||||||||||||||||||||||||||||||||||||||:|||||| ||||| :|
Db        208 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFASFLVYLAEKDANSDF 267

Qy        261 STYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQ 320
              |:|||:|||||||||||||||||| |||||:|:|||||||||||||||||||||||||||
Db        268 SSYADSLWWGTITLTTIGYGDKTPHTWLGRVLAAGFALLGISFFALPAGILGSGFALKVQ 327

Qy        321 EQHRQKHFEKRRNPAANLIQCVWRSYAAD-EKSVSIATW---------------------- 358
              |||||||||||| |||||||  || |: |  ::   |||
Db        328 EQHRQKHFEKRRMPAANLIQAAWRLYSTDMSRAYLTATWYYYDSILPSFRELALLFEHVQ 387

Qy        359 ------------------------KPHLKALHT------CSPTNQKLSFKERVRMASPRG 388
                                     | :   |       |   : ::  |:|:|| | :
Db        388 RARNGGLRPLEVRRAPVPDGAPSRYPPVATCHRPGSTSFCPGESSRMGIKDRIRMGSSQR 447

Qy        389 QSIKSRQ--ASVGDRRSPSTDITAEG-SPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVID 445
              ::  |:|  |      |||::   |  ||||||||||||||||| ||||     ||
Db        448 RTGPSKQQLAPPTMPTSPSSEQVGEATSPTKVQKSWSFNDRTRFRASLRL-----KPRTS 502

Qy        446 ADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDV 505
              |: |  :::| :||  ||:::|:|: | :||||:|||:|| ||||||||||||||||||
Db        503 AEDA-PSEEVAEEKSYQCELTVDDIMPAVKTVIRSIRILKFLVAKRKFKETLRPYDVKDV 561

Qy        506 IEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSRE---KITAEHETTDDLSMLGRV 562
              |||||||||||| ||||||||||||:|:|    |:|:||   |  :: |  |::||:|||
Db        562 IEQYSAGHLDMLGRIKSLQTRVDQIVGRG--PGDRKAREKGDKGPSDAEVVDEISMMGRV 619

Qy        563 VKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFECEQTSDYQSPVDSKDL 622
              |||||||||| ||| ||  | : || |:::  :| : |:| |: : |||| |||| :|:
Db        620 VKVEKQVQSIEHKLDLLLGFYSRCLRSGTSA--SLGAVQVPLFDPDITSDYHSPVDHEDI 677

Qy        623 SGSAQNSGCLSRSTSANI 640
              | |||    :||| | |:
Db        678 SVSAQTLS-ISRSVSTNM 694


RESULT 8
US-09-949-016-7694
; Sequence 7694, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7694
;   LENGTH: 676
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-7694

  Query Match             43.5%;  Score 1980;  DB 4;  Length 676;
  Best Local Similarity   60.3%;  Pred. No. 1.3e-170;
  Matches  409;  Conservative   75;  Mismatches  102;  Indels   92;  Gaps   13;

Qy         35 GGGGGLRESRRGKQGARMSLLGKPL--------------SYTSSQSCRRNVKYRRVQNYL 80
              ||||  |          |: ||| ||              |    :|   : :|||:||::
Db         18 GGGGSPR---------RLGLLGSPLPPGAPLPGPGSGSGSACGQRSSAAHKRYRRLQNWG 68

Qy         81 YNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEF 140
              |||||||||||:|| |:||||| ||:||| ||| || :||: |||||||||||||||:
Db         69 YNVLERPRGWAFVYHVFIFLLVFSCLVLSVLSTIQEHQELANECLLILEFVMIVVFGLEY 128

Qy        141 IIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLR 200
              |:|:|||||||||||||| |||||||||| || :||:||::| |||||||||||||:|
Db        129 IVRVWSAGCCCRYRGWQGRFRFARKPFCVIDFIVFVASVAVIAAGTQGNIFATSALRSMR 188

Qy        201 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKEF 260
              |||||||||||||||||||||||||||||||||||||||||:|||||| ||||| :|
Db        189 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFASFLVYLAEKDANSDF 248

Qy        261 STYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQ 320
              |:|||:|||||||||||||||||| |||||:|:|||||||||||||||||||||||||||
Db        249 SSYADSLWWGTITLTTIGYGDKTPHTWLGRVLAAGFALLGISFFALPAGILGSGFALKVQ 308

Qy        321 EQHRQKHFEKRRNPAANLIQCVWRSYAAD-EKSVSIATW---------------------- 358
              |||||||||||| |||||||  || |: |  ::   |||
Db        309 EQHRQKHFEKRRMPAANLIQAAWRLYSTDMSRAYLTATWYYYDSILPSFRELALLFEHVQ 368

Qy        359 ------------------------KPHLKALHT------CSPTNQKLSFKERVRMASPRG 388
                                     | :   |       |   : ::  |:|:|| | :
Db        369 RARNGGLRPLEVRRAPVPDGAPSRYPPVATCHRPGSTSFCPGESSRMGIKDRIRMGSSQR 428

Qy        389 QSIKSRQ--ASVGDRRSPSTDITAEG-SPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVID 445
              ::  |:|  |      |||::   |  ||||||||||||||||| ||||     ||
Db        429 RTGPSKQHLAPPTMPTSPSSEQVGEATSPTKVQKSWSFNDRTRFRASLRL-----KPRTS 483
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Qy        446 ADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDV 505
              |:  |   :::| :||   ||:::|:|:  | :|||||:|||:|| ||||||||||||||||||
Db        484 AEDA-PSEEVAEEKSYQCELTVDDIMPAVKTVIRSIRILKFLVAKRKFKETLRPYDVKDV 542

Qy        506 IEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSRE---KITAEHETTDDLSMLGRV 562
              |||||||||||| ||||||||||||:|:|    |:|:||   |  :: |  |::||:|||
Db        543 IEQYSAGHLDMLGRIKSLQTRVDQIVGRG--PGDRKAREKGDKGPSDAEVVDEISMMGRV 600

Qy        563 VKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFECEQTSDYQSPVDSKDL 622
              |||||||||| ||| ||  | : || |:::  :| : |:| |: : |||| |||| :|:
Db        601 VKVEKQVQSIEHKLDLLLGFYSRCLRSGTSA--SLGAVQVPLFDPDITSDYHSPVDHEDI 658

Qy        623 SGSAQNSGCLSRSTSANI 640
              | |||    :||| | |:
Db        659 SVSAQTLS-ISRSVSTNM 675


RESULT 9
US-09-813-148-4
; Sequence 4, Application US/09813148
; Patent No. 6617131
; GENERAL INFORMATION:
;  APPLICANT: STEINMEYER, Klaus
;  APPLICANT:  LERCHE, Christian
;  APPLICANT:  SCHERER, Constanze
;  APPLICANT:  SEEBOHM, Guiscard
;  APPLICANT:  BUSCH, Andreas E.
;  TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN
;  TITLE OF INVENTION:  NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
;  FILE REFERENCE: 38005-119
;  CURRENT APPLICATION NUMBER: US/09/813,148
;  CURRENT FILING DATE:  2001-03-21
;  PRIOR APPLICATION NUMBER: DE 100 13 732.6
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: US 60/194,041
;  PRIOR FILING DATE: 2000-04-03
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 844
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-813-148-4

  Query Match             39.4%;  Score 1792;  DB 4;  Length 844;
  Best Local Similarity   49.5%;  Pred. No. 2.3e-153;
  Matches  406;  Conservative   88;  Mismatches  179;  Indels  148;  Gaps   24;

Qy         17 AARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLSYTSSQSCRRNVKYRRV 76
              : |   ||: |: |       |  | : | |  ||     |||          :|| ||::
Db         34 STRDGALLIAGSEAPK---RGSILSKPRAGGAGA-----GKP--------PKRNAFYRKL 77

Qy         77 QNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVF 136
              ||:|||||||||||||||:|||||| ||:|||||| |: | :   | ||| | ||||
Db         78 QNFLYNVLERPRGWAFIYHAYVFLLVFSCLVLSVFSTIKEYEKSSEGALYILEIVTIVVF 137

Qy        137 GLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSAL 196
              |:|: :|||:|||||||||:|||:|||||||||| :||||||::| :|||:||||||
Db        138 GVEYFVRIWAAGCCCRYRGWRGRLKFARKPFCVIDIMVLIASIAVLAAGSQGNVFATSAL 197

Qy        197 RSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDA 256
              ||||||||||:|||||||||||||||||||||:|||||| || :|||||| ||
Db        198 RSLRFLQILRMIRMDRRGGTWKLLGSVVYAHSKELVTAWYIGFLCLILASFLVYLAEKGE 257

Qy        257 NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFA 316
              |  | ||||||||| |||||||||| | || ||||:| | |:|:|||||||||||||||
Db        258 NDHFDTYADALWWGLITLTTIGYGDKYPQTWNGRLLAATFTLIGVSFFALPAGILGSGFA 317

Qy        317 LKVQEQHRQKHFEKRRNPAANLIQCVWRSYAAD------------EKSVSIATWK--PH 361
              |||||||||||||||||| |||  || || :             |::|::  ::  |
Db        318 LKVQEQHRQKHFEKRRNPAAGLIQSAWRFYATNLSRTDLHSTWQYYERTVTVPMYRLIPP 377

Qy        362 LKALHTC------------------SPTNQKLSFKERVRMASPRGQSIKSRQASVGD-- 400
```

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              | |                    || :||:| |:||  :|||| : | : :
Db        378 LNQLELLRNLKSKSGLAFRKDPPPEPSP-SQKVSLKDRV-FSSPRGVAAKGKGSPQAQTV 435

Qy        401 RRSPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKG 460
              ||||| | : | ||:|| ||||| ||:| | : |:| : :   : : :|  :|: |:|
Db        436 RRSPSADQSLEDSPSKVPKSWSFGDRSRARQAFRIKGAASRQNSE-EASLPGEDIVDDKS 494

Qy        461 CQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRI 520
              | |:   ||||| ||  |||: :|:| |:||||||:|||||| |||||||||||||| ||
Db        495 CPCEFVTEDLTPGLKVSIRAVCVMRFLVSKRKFKESLRPYDVMDVIEQYSAGHLDMLSRI 554

Qy        521 KSLQTRVDQILGKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLL 580
              ||||:|||||:|:|   :| | | |  || |  :| ||:||: |||||| |:| ||| |:
Db        555 KSLQSRVDQIVGRGPAITD-KDRTKGPAEAELPEDPSMMGRLGKVEKQVLSMEKKLDFLV 613

Qy        581 DIYQQVLRKGSASALALASFQIPPFEC---------EQTSDYQSPVDSKDLSGSAQNSGC 631
              :|| |  | |            ||| |         |     | || ||::         ||
Db        614 NIYMQ--RMG-----------IPPTETEAYFGAKEPEPAPPYHSPEDSRE---HVDRHGC 657

Qy        632 LSRSTSANISRGLQFILTPNEFSAQTFYALSPTMHSQATQVPISQS--------DGSAVA 683
              : :   :: | |          |||    | |       | | | |        |   :
Db        658 IVKIVRSSSSTG------QKNFSAPP--AAPP------VQCPPSTSWQPQSHPRQGHGTS 703

Qy        684 ATNTIANQINTAPKPAAPTTLQI---------------------PP-----------PLP 711
                  : :   | ||   :|                        ||           :|
Db        704 PVGDHGSLVRIPPPPAHERSLSAYGGGNRASMEFLRQEDTPGCRPPEGTLRDSDTSISIP 763

Qy        712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQS 752
              :: |    | |  : :|   |||       ||||:    |
Db        764 SVDH----EELERSFSGF--SISQ-------SKENLDALNS 791


RESULT 10
US-09-590-304-4
; Sequence 4, Application US/09590304
; Patent No. 6649371
; GENERAL INFORMATION:
;  APPLICANT: JENTSCH, Thomas
;  TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNE
;  FILE REFERENCE: 2815-0136P
;  CURRENT APPLICATION NUMBER: US/09/590,304
;  CURRENT FILING DATE:  2000-06-09
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 844
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-590-304-4

  Query Match             39.4%;  Score 1792;  DB 4;  Length 844;
  Best Local Similarity   49.5%;  Pred. No. 2.3e-153;
  Matches  406;  Conservative   88;  Mismatches  179;  Indels  148;  Gaps   24;

Qy         17 AARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLSYTSSQSCRRNVKYRRV 76
              : |   ||: |: |       |  | : | |  ||      |||          :|| ||::
Db         34 STRDGALLIAGSEAPK---RGSILSKPRAGGAGA-----GKP--------PKRNAFYRKL 77

Qy         77 QNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVF 136
              ||:|||||||||||||||:|||||| ||:|||||| |: | :   | ||| | ||||
Db         78 QNFLYNVLERPRGWAFIYHAYVFLLVFSCLVLSVFSTIKEYEKSSEGALYILEIVTIVVF 137

Qy        137 GLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSAL 196
              |:|: :|||:|||||||||:|||:|||||||||| :||||||::| :|||:||||||
Db        138 GVEYFVRIWAAGCCCRYRGWRGRLKFARKPFCVIDIMVLIASIAVLAAGSQGNVFATSAL 197

Qy        197 RSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDA 256
              ||||||||||:|||||||||||||||||||||:|||||| || :|||||| ||
Db        198 RSLRFLQILRMIRMDRRGGTWKLLGSVVYAHSKELVTAWYIGFLCLILASFLVYLAEKGE 257

Qy        257 NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFA 316
              |  | ||||||||| |||||||||| | || ||||:| | |:|:|||||||||||||||
Db        258 NDHFDTYADALWWGLITLTTIGYGDKYPQTWNGRLLAATFTLIGVSFFALPAGILGSGFA 317
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```
Qy        317 LKVQEQHRQKHFEKRRNPAANLIQCVWRSYAAD------------EKSVSIATWK--PH 361
              ||||||||||||||||||| ||| || || :             |::|::  ::  |
Db        318 LKVQEQHRQKHFEKRRNPAAGLIQSAWRFYATNLSRTDLHSTWQYYERTVTVPMYRLIPP 377

Qy        362 LKALHTC------------------SPTNQKLSFKERVRMASPRGQSIKSRQASVGD-- 400
              | |                      || :||:| |:||  :|||| : | : :
Db        378 LNQLELLRNLKSKSGLAFRKDPPPEPSP-SQKVSLKDRV-FSSPRGVAAKGKGSPQAQTV 435

Qy        401 RRSPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKG 460
              ||||| | : | ||:|| ||||| ||:| | : |:| :  :   : : :|  :|: |:|
Db        436 RRSPSADQSLEDSPSKVPKSWSFGDRSRARQAFRIKGAASRQNSE-EASLPGEDIVDDKS 494

Qy        461 CQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRI 520
              | |:   ||||| ||  |||: :|:| |:||||||:|||||| |||||||||||||| ||
Db        495 CPCEFVTEDLTPGLKVSIRAVCVMRFLVSKRKFKESLRPYDVMDVIEQYSAGHLDMLSRI 554

Qy        521 KSLQTRVDQILGKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLL 580
              ||||:|||||:|:|   :| | | |  || |  :| ||:||: ||||||  |:|  ||| |:
Db        555 KSLQSRVDQIVGRGPAITD-KDRTKGPAEAELPEDPSMMGRLGKVEKQVLSMEKKLDFLV 613

Qy        581 DIYQQVLRKGSASALALASFQIPPPEC---------EQTSDYQSPVDSKDLSGSAQNSGC 631
              :|| |  | |           ||| |           |    | || ||::        ||
Db        614 NIYMQ--RMG-----------IPPTETEAYFGAKEPEPAPPYHSPEDSRE---HVDRHGC 657

Qy        632 LSRSTSANISRGLQFILTPNEFSAQTFYALSPTMHSQATQVPISQS--------DGSAVA 683
              : :   :: | |           |||    | |       | | | |          |   :
Db        658 IVKIVRSSSSTG------QKNFSAPP--AAPP------VQCPPSTSWQPQSHPRQGHGTS 703

Qy        684 ATNTIANQINTAPKPAAPTTLQI----------------------PP-----------PLP 711
                  : :   | ||   :|                        ||           :|
Db        704 PVGDHGSLVRIPPPPAHERSLSAYGGGNRASMEFLRQEDTPGCRPPEGTLRDSDTSISIP 763

Qy        712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQS 752
              :: |    | |  : :|  |||        ||||:   |
Db        764 SVDH----EELERSFSGF--SISQ-------SKENLDALNS 791
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RESULT 11
US-09-492-361-34
; Sequence 34, Application US/09492361
; Patent No. 6794161
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
; TITLE OF INVENTION: POTASSIUM CHANNELS
; FILE REFERENCE: 2815-127P
; CURRENT APPLICATION NUMBER: US/09/492,361
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-492-361-34

Query Match 39.4%; Score 1792; DB 4; Length 844;
Best Local Similarity 49.5%; Pred. No. 2.3e-153;
Matches 406; Conservative 88; Mismatches 179; Indels 148; Gaps 24;

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Qy         17 AARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLSYTSSQSCRRNVKYRRV 76
              : |   ||: |: |       |  | : | |  ||     |||          :||  ||::
Db         34 STRDGALLIAGSEAPK---RGSILSKPRAGGAGA-----GKP--------PKRNAFYRKL 77

Qy         77 QNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVF 136
              ||:||||||||||||||:|||||  ||:|||||| |: | :   | ||| | ||||
Db         78 QNFLYNVLERPRGWAFIYHAYVFLLVFSCLVLSVFSTIKEYEKSSEGALYILEIVTIVVF 137

Qy        137 GLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSAL 196
              |:|: :|||:||||||||||:|||:|||||||||| :|||||||::| :|||:||||||
Db        138 GVEYFVRIWAAGCCCRYRGWRGRLKFARKPFCVIDIMVLIASIAVLAAGSQGNVFATSAL 197
```

```
Qy        197 RSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDA 256
              ||||||||||:|||||||||||||||||||||||:|||||||| || :|||||| ||
Db        198 RSLRFLQILRMIRMDRRGGTWKLLGSVVYAHSKELVTAWYIGFLCLILASFLVYLAEKGE 257

Qy        257 NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFA 316
              |  | ||||||||| |||||||||| | || ||||:| | |:|:|||||||||||||||
Db        258 NDHFDTYADALWWGLITLTTIGYGDKYPQTWNGRLLAATFTLIGVSFFALPAGILGSGFA 317

Qy        317 LKVQEQHRQKHFEKRRNPAANLIQCVWRSYAAD------------EKSVSIATWK--PH 361
              ||||||||||||||||||| ||| || || :             |::|::  ::  |
Db        318 LKVQEQHRQKHFEKRRNPAAGLIQSAWRFYATNLSRTDLHSTWQYYERTVTVPMYRLIPP 377

Qy        362 LKALHTC------------------SPTNQKLSFKERVRMASPRGQSIKSRQASVGD-- 400
              | |                      || :||:| |:||  :|||| : | : :
Db        378 LNQLELLRNLKSKSGLAFRKDPPPEPSP-SQKVSLKDRV-FSSPRGVAAKGKGSPQAQTV 435

Qy        401 RRSPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKG 460
              |||||  | : | ||:|| |||||  ||:|  | : |:|  :  :   : : :|  :|: |:|
Db        436 RRSPSADQSLEDSPSKVPKSWSFGDRSRARQAFRIKGAASRQNSE-EASLPGEDIVDDKS 494

Qy        461 CQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRI 520
              | |:   ||||| ||  |||: :|:| |:||||||:|||||| |||||||||||||| ||
Db        495 CPCEFVTEDLTPGLKVSIRAVCVMRFLVSKRKFKESLRPYDVMDVIEQYSAGHLDMLSRI 554

Qy        521 KSLQTRVDQILGKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLL 580
              ||||:|||||:|:|   :| | | |  || |  :| ||:||: ||||||  |:|  ||| |:
Db        555 KSLQSRVDQIVGRGPAITD-KDRTKGPAEAELPEDPSMMGRLGKVEKQVLSMEKKLDFLV 613

Qy        581 DIYQQVLRKGSASALALASFQIPPPEC---------EQTSDYQSPVDSKDLSGSAQNSGC 631
              :|| |  | |           ||| |           |    | || ||::        ||
Db        614 NIYMQ--RMG-----------IPPTETEAYFGAKEPEPAPPYHSPEDSRE---HVDRHGC 657

Qy        632 LSRSTSANISRGLQFILTPNEFSAQTFYALSPTMHSQATQVPISQS--------DGSAVA 683
              : :   :: | |           |||    | |       | | | |          |   :
Db        658 IVKIVRSSSSTG------QKNFSAPP--AAPP------VQCPPSTSWQPQSHPRQGHGTS 703

Qy        684 ATNTIANQINTAPKPAAPTTLQI----------------------PP-----------PLP 711
                  : :   | ||   :|                        ||           :|
Db        704 PVGDHGSLVRIPPPPAHERSLSAYGGGNRASMEFLRQEDTPGCRPPEGTLRDSDTSISIP 763

Qy        712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQS 752
              :: |    | |  : :|  |||        ||||:   |
Db        764 SVDH----EELERSFSGF--SISQ-------SKENLDALNS 791
```

RESULT 12
US-09-105-058C-23
; Sequence 23, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blanar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 722
; TYPE: PRT
; ORGANISM: mouse
US-09-105-058C-23

Query Match 39.4%; Score 1790.5; DB 4; Length 722;
Best Local Similarity 55.0%; Pred. No. 2.4e-153;

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  Matches  390;  Conservative   72;  Mismatches  146;  Indels  101;  Gaps   18;

Qy         17 AARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLSYTSSQSCRRNVKYRRV 76
              :|   ||: |: |       |  | : | |  ||      |||          :||  ||::
Db         34 STRDGALLIAGSEAPK---RGSVLSKPRTGGAGA-----GKP--------PKRNAFYRKL 77

Qy         77 QNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVF 136
              ||:|||||||||||||||:|||||| ||:|||||| |: | :   | ||| | ||||
Db         78 QNFLYNVLERPRGWAFIYHAYVFLLVFSCLVLSVFSTIKEYEKSSEGALYILEIVTIVVF 137

Qy        137 GLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSAL 196
              |:|: :|||:||||||||||:|||:|||||||||| :||||||||::| :|||:||||||
Db        138 GVEYFVRIWAAGCCCRYRGWRGRLKFARKPFCVIDIMVLIASIAVLAAGSQGNVFATSAL 197

Qy        197 RSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDA 256
              ||||||||||:|||||||||||||||||||||||:|||||||| || :|||||| ||
Db        198 RSLRFLQILRMIRMDRRGGTWKLLGSVVYAHSKELVTAWYIGFLCLILASFLVYLAEKGE 257

Qy        257 NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFA 316
              |  | ||||||||| |||||||||| | || ||||:| | |:|:|||||||||||||||
Db        258 NDHFDTYADALWWGLITLTTIGYGDKYPQTWNGRLLAATFTLIGVSFFALPAGILGSGFA 317

Qy        317 LKVQEQHRQKHFEKRRNPAANLIQCVWRSYAAD------------EKSVSIATWK--PH 361
              |||||||||||||||||| |||  || || :            |::|::  ::  |
Db        318 LKVQEQHRQKHFEKRRNPAAGLIQSAWRFYATNLSRTDLHSTWQYYERTVTVPMYRLIPP 377

Qy        362 LKALHTC------------------SPTNQKLSFKERVRMASPRGQSIKSRQASVGD-- 400
              | |                    || :||:| |:||  :|||| : | : :
Db        378 LNQLELLRNLKSKSGLTFRKEPQPEPSP-SQKVSLKDRV-FSSPRGMAAKGKGSPQAQTV 435

Qy        401 RRSPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKG 460
              ||||| | : : ||:|| ||||| ||:| | : |:| :  :   :|    | | | | |
Db        436 RRSPSADQSLDDSPSKVPKSWSFGDRSRTRQAFRIKGAASRQNSEASLP-GEDIVEDNKS 494

Qy        461 CQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRI 520
              | |:   ||||| ||  |||: :|:| |:|||||:|||||| |||||||||||||| ||
Db        495 CNCEPVTEDLTPGLKVSIRAVCVMRFLVSKRKFKESLRPYDVMDVIEQYSAGHLDMLSRI 554

Qy        521 KSLQTRVDQILGKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLL 580
              ||||:|||||:|:|   :| | | |  || |  :| ||:||: |||||| |:| ||| |:
Db        555 KSLQSRVDQIVGRGPTITD-KDRTKGPAETELPEDPSMMGRLGKVEKQVLSMEKKLDFLV 613

Qy        581 DIYQQVLRKGSASALALASFQIPPPFEC---------EQTSDYQSPVDSKDLSGSAQNSGC 631
               || |  | |          ||| |          |  | || ||:|    |  ||
Db        614 SIYTQ--RMG-----------IPPAETEAYFGAKEPEPAPPYHSPEDSRD---HADKHGC 657

Qy        632 ---LSRSTSANISRGLQFILTPNEFSAQTFYALSPTMHSQATQVPISQS 677
                 : ||||:               : |  ||  | :     | | | |
Db        658 IIKIVRSTSS---------------TGQRNYAAPPAI--PPAQCPPSTS 689


RESULT 13
US-09-177-650-96
; Sequence 96, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
;  APPLICANT: Leppert, Mark F.
;  APPLICANT: Singh, Nanda
;  APPLICANT: Charlier, Carole
;  TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
;  TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
;  TITLE OF INVENTION: AND OTHER EPILEPSIES
;  FILE REFERENCE: 2323-134
;  CURRENT APPLICATION NUMBER: US/09/177,650
;  CURRENT FILING DATE: 1998-10-23
;  EARLIER APPLICATION NUMBER: 60/063,147
;  EARLIER FILING DATE: 1997-10-24
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 96
;   LENGTH: 930
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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US-09-177-650-96

  Query Match           39.3%;  Score 1788.5;  DB 4;  Length 930;
  Best Local Similarity   44.8%;  Pred. No. 5.6e-153;
  Matches  428;  Conservative  105;  Mismatches  230;  Indels  193;  Gaps   25;

Qy         17 AARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLSYTSSQSCRRNVKYRRV 76
              : |   ||: |: |       |  | : | |  ||      |||          :||  ||::
Db         34 STRDGALLIAGSEAPK---RGSILSKPRAGGAGA-----GKP--------PKRNAFYRKL 77

Qy         77 QNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVF 136
              ||:|||||||||||||||:|||||| ||:|||||| |: | :   | ||| | ||||
Db         78 QNFLYNVLERPRGWAFIYHAYVFLLVFSCLVLSVFSTIKEYEKSSEGALYILEIVTIVVF 137

Qy        137 GLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSAL 196
              |:|: :|||:||||||||||:|||:|||||||||| :||||||||::| :|||:||||||
Db        138 GVEYFVRIWAAGCCCRYRGWRGRLKFARKPFCVIDIMVLIASIAVLAAGSQGNVFATSAL 197

Qy        197 RSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDA 256
              ||||||||||:|||||||||||||||||||||||:|||||||| || :|||||| ||
Db        198 RSLRFLQILRMIRMDRRGGTWKLLGSVVYAHSKELVTAWYIGFLCLILASFLVYLAEKGE 257

Qy        257 NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFA 316
              |  | ||||||||| |||||||||| | || ||||:| | |:|:|||||||||||||||
Db        258 NDHFDTYADALWWGLITLTTIGYGDKYPQTWNGRLLAATFTLIGVSFFALPAGILGSGFA 317

Qy        317 LKVQEQHRQKHFEKRRNPAANLIQCVWRSYAAD------------EKSVSIATWK---- 359
              |||||||||||||||||| |||  || || :            |::|::  :
Db        318 LKVQEQHRQKHFEKRRNPAAGLIQSAWRFYATNLSRTDLHSTWQYYERTVTVPMYSSQTQ 377

Qy        360 --------PHLKALHT-----------------------------------CSP--TNQKL 375
                     | | |                                     | |  ::||:
Db        378 TYGASRLIPPLNQLELLRNLKSKSGLAFRKDPPPEPSPSKGSPCRGPLCGCCPGRSSQKV 437

Qy        376 SFKERVRMASPRGQSIKSRQASVGD--RRSPSTDITAEGSPTKVQKSWSFNDRTRFRPSL 433
              | |:||  :|||| : | : :      |||| | : | ||:|| ||||| ||:| | :
Db        438 SLKDRV-FSSPRGVAAKGKGSPQAQTVRRSPSADQSLEDSPSKVPKSWSFGDRSRARQAF 496

Qy        434 RLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKF 493
              |:| :  :   : : :|  :|: |:| | |:   ||||| ||  |||: :|:| |:||||
Db        497 RIKGAASRQNSE-EASLPGEDIVDDKSCPCEFVTEDLTPGLKVSIRAVCVMRFLVSKRKF 555

Qy        494 KETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSREKITAEHETT 553
              ||:|||||| |||||||||||||| ||||||:|||||:|:|   :| | | |  || |
Db        556 KESLRPYDVMDVIEQYSAGHLDMLSRIKSLQSRVDQIVGRGPAITD-KDRTKGPAEAELP 614

Qy        554 DDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPPFEC------ 607
              :| ||:||: |||||| |:| ||| |::|| |  | |           ||| |
Db        615 EDPSMMGRLGKVEKQVLSMEKKLDFLVNIYMQ--RMG-----------IPPTETEAYFGA 661

Qy        608 ---EQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPNEFSAQTFYALSPT 664
                 |    | || ||::        ||: :   :: | |
Db        662 KEPEPAPPYHSPEDSRE---HVDRHGCIVKIVRSSSSTG---------------------- 697

Qy        665 MHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPL-------PAIKHLP 717
                                    | | :  ||||  :| ||          |   |
Db        698 ------------------------QKNFSAPPAAP-PVQCPPSTSWQPQSHPRQGHGT 730

Qy        718 RPETLH------PNPAGLQESISDVTTCLVASKENVQVAQSNLTK--DRSMRKSFDMGGE 769
               |   |      | |   : |:|        || | ::   :   :  : ::| |   :
Db        731 SPVGDHGSLVRIPPPPAHERSLSAYGGGNRASMEFLRQEDTPGCRPPEGNLRDS-----D 785

Qy        770 TLLSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITD 829
              | :|:  :  ::| :| |  :: :| | |:    |  :           |    ||    ||
Db        786 TSISIPSVDHEELERSFSGFSISQSKENLDALNSCYAAVAPCAKVRPYIAEGESD---TD 842

Qy        830 EEV----GP-------EETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAG 874
               ::    ||       |   |   | | |  |||      :  | | | : |  |
Db        843 SDLCTPCGPPPRSATGEGPFGDVGWAGPGPGSEAALG----QWTRPRPSSARCLRG 894


RESULT 14
US-09-105-058C-20
```

```
; Sequence 20, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
;  APPLICANT:  Blanar, Michael A.
;  APPLICANT:  Dworetzky, Steven
;  APPLICANT:  Gribkoff, Valentin K.
;  APPLICANT:  Levesque, Paul C.
;  APPLICANT:  Little, Wayne A.
;  APPLICANT:  Neubauer, Michael G.
;  APPLICANT:  Yang, Wen-Pin
;  TITLE OF INVENTION:  KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
;  FILE REFERENCE:  3053-4052
;  CURRENT APPLICATION NUMBER: US/09/105,058C
;  CURRENT FILING DATE:  1998-06-26
;  PRIOR APPLICATION NUMBER:  US 60/055,599
;  PRIOR FILING DATE:  1997-08-12
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 20
;   LENGTH: 871
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-105-058C-20

  Query Match             39.3%;  Score 1787.5;  DB 4;  Length 871;
  Best Local Similarity   47.9%;  Pred. No. 6.2e-153;
  Matches  406;  Conservative   89;  Mismatches  178;  Indels  175;  Gaps   24;

Qy         17 AARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLSYTSSQSCRRNVKYRRV 76
Db         34 STRDGALLIAGSEAPK---RGSILSKPRAGGAGA-----GKP--------PKRNAFYRKL 77

Qy         77 QNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVF 136
Db         78 QNFLYNVLERPRGWAFIYHAYVFLLVFSCLVLSVFSTIKEYEKSSEGALYILEIVTIVVF 137

Qy        137 GLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSAL 196
Db        138 GVEYFVRIWAAGCCCRYRGWRGRLKFARKPFCVIDIMVLIASIAVLAAGSQGNVFATSAL 197

Qy        197 RSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDA 256
Db        198 RSLRFLQILRMIRMDRRGGTWKLLGSVVYAHSKELVTAWYIGFLCLILASFLVYLAEKGE 257

Qy        257 NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFA 316
Db        258 NDHFDTYADALWWGLITLTTIGYGDKYPQTWNGRLLAATFTLIGVSFFALPAGILGSGFA 317

Qy        317 LKVQEQHRQKHFEKRRNPAANLIQCVWRSYAAD------------EKSVSIATWK---- 359
Db        318 LKVQEQHRQKHFEKRRNPAAGLIQSAWRFYATNLSRTDLHSTWQYYERTVTVPMYSSQTQ 377

Qy        360 --------PHLKALHT---------------------------------CSP--TNQKL 375
Db        378 TYGASRLIPPLNQLELLRNLKSKSGLAFRKDPPPEPSPSKGSPCRGPLCGCCPGRSSQKV 437

Qy        376 SFKERVRMASPRGQSIKSRQASVGD--RRSPSTDITAEGSPTKVQKSWSFNDRTRFRPSL 433
Db        438 SLKDRV-FSSPRGVAAKGKGSPQAQTVRRSPSADQSLEDSPSKVPKSWSFGDRSRARQAF 496

Qy        434 RLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKF 493
Db        497 RIKGAASRQ--NSEASLPGEDIVDDKSCPCEFVTEDLTPGLKVSIRAVCVMRFLVSKRKF 554

Qy        494 KETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSREKITAEHETT 553
Db        555 KESLRPYDVMDVIEQYSAGHLDMLSRIKSLQSRVDQIVGRGPAITD-KDRTKGPAEAELP 613

Qy        554 DDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFEC------ 607
Db        614 EDPSMMGRLGKVEKQVLSMEKKLDFLVNIYMQ--RMG-----------IPPTETEAYFGA 660

Qy        608 ---EQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPNEFSAQTFYALSPT 664
Db        661 KEPEPAPPYHSPEDSRE---HVDRHGCIVKIVRSSSSTG------QKNFSAPP--AAPP- 708

Qy        665 MHSQATQVPISQS--------DGSAVAATNTIANQINTAPKPAAPTTLQI---------- 706
Db        709 -----VQCPPSTSWQPQSHPRQGHGTSPVGDHGSLVRIPPPPAHERSLSAYGGGNRASME 763

Qy        707 -----------PP-----------PLPAIKHLPRPETLHPNPAGLQESISDVTTCLVASK 744
Db        764 FLRQEDTPGCRPPEGTLRDSDTSISIPSVDH----EELERSFSGF--SISQ-------SK 810

Qy        745 ENVQVAQS 752
Db        811 ENLDALNS 818


RESULT 15
US-09-177-650-2
; Sequence 2, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
;  APPLICANT: Leppert, Mark F.
;  APPLICANT: Singh, Nanda
;  APPLICANT: Charlier, Carole
;  TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
;  TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
;  TITLE OF INVENTION: AND OTHER EPILEPSIES
;  FILE REFERENCE: 2323-134
;  CURRENT APPLICATION NUMBER: US/09/177,650
;  CURRENT FILING DATE: 1998-10-23
;  EARLIER APPLICATION NUMBER: 60/063,147
;  EARLIER FILING DATE: 1997-10-24
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 872
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-177-650-2

  Query Match             39.2%;  Score 1783;  DB 4;  Length 872;
  Best Local Similarity   47.9%;  Pred. No. 1.6e-152;
  Matches  406;  Conservative   88;  Mismatches  180;  Indels  174;  Gaps   24;

Qy         17 AARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLSYTSSQSCRRNVKYRRV 76
Db         34 STRDGALLIAGSEAPK---RGSILSKPRAGGAGA-----GKP--------PKRNAFYRKL 77

Qy         77 QNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVF 136
Db         78 QNFLYNVLERPRGWAFIYHAYVFLLVFSCLVLSVFSTIKEYEKSSEGALYILEIVTIVVF 137

Qy        137 GLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSAL 196
Db        138 GVEYFVRIWAAGCCCRYRGWRGRLKFARKPFCVIDIMVLIASIAVLAAGSQGNVFATSAL 197

Qy        197 RSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDA 256
Db        198 RSLRFLQILRMIRMDRRGGTWKLLGSVVYAHSKELVTAWYIGFLCLILASFLVYLAEKGE 257

Qy        257 NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFA 316
Db        258 NDHFDTYADALWWGLITLTTIGYGDKYPQTWNGRLLAATFTLIGVSFFALPAGILGSGFA 317

Qy        317 LKVQEQHRQKHFEKRRNPAANLIQCVWRSYAAD------------EKSVSIATWK---- 359
Db        318 LKVQEQHRQKHFEKRRNPAAGLIQSAWRFYATNLSRTDLHSTWQYYERTVTVPMYSSQTQ 377

Qy        360 --------PHLKALHT---------------------------------CSP--TNQKL 375
Db        378 TYGASRLIPPLNQLELLRNLKSKSGLAFRKDPPPEPSPSKGSPCRGPLCGCCPGRSSQKV 437

Qy        376 SFKERVRMASPRGQSIKSRQASVGD--RRSPSTDITAEGSPTKVQKSWSFNDRTRFRPSL 433
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                | |:||  :|||| : | : :      |||||  | : | ||:|| |||||  ||:| | :
Db        438 SLKDRV-FSSPRGVAAKGKGSPQAQTVRRSPSADQSLEDSPSKVPKSWSFGDRSRARQAF 496

Qy        434 RLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKF 493
                |:| :  :   : : :|  :|: |:| | |:   ||||| ||  |||: :|:| |:||||
Db        497 RIKGAASRQNSE-EASLPGEDIVDDKSCPCEFVTEDLTPGLKVSIRAVCVMRFLVSKRKF 555

Qy        494 KETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSREKITAEHETT 553
                ||:|||||| |||||||||||||| ||||||:|||||:|:|   :| | | |  || |
Db        556 KESLRPYDVMDVIEQYSAGHLDMLSRIKSLQSRVDQIVGRGPAITD-KDRTKGPAEAELP 614

Qy        554 DDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFEC------ 607
                :| ||:||: |||||| |:| ||| |::|| |  | |           ||| |
Db        615 EDPSMMGRLGKVEKQVLSMEKKLDFLVNIYMQ--RMG-----------IPPTETEAYFGA 661

Qy        608 ---EQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPNEFSAQTFYALSPT 664
                   |    | || ||::        ||: :   :: | |         |||    |  |
Db        662 KEPEPAPPYHSPEDSRE---HVDRHGCIVKIVRSSSSTG------QKNFSAPP--AAPP- 709

Qy        665 MHSQATQVPISQS--------DGSAVAATNTIANQINTAPKPAAPTTLQI---------- 706
                  | | | |         |   :      : :   | ||   :|
Db        710 -----VQCPPSTSWQPQSHPRQGHGTSPVGDHGSLVRIPPPPAHERSLSAYGGGNRASME 764

Qy        707 -----------PP-----------PLPAIKHLPRPETLHPNPAGLQESISDVTTCLVASK 744
                        ||           :|:: |    | |  : :|   |||         ||
Db        765 FLRQEDTPGCRPPEGNLRDSDTSISIPSVDH----EELERSFSGF--SISQ-------SK 811

Qy        745 ENVQVAQS 752
                ||:   |
Db        812 ENLDALNS 819
```

Search completed: April 8, 2005, 16:43:40
Job time : 48 secs

Bunner, B.
09/810796
Seq. ID 5

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 16:23:30 ; Search time 180 Seconds
(without alignments)
1908.018 Million cell updates/sec

Title: US-09-810-796-5
Perfect score: 4547
Sequence: 1 MKDVESGRGRVLLNSAAARG.....SICKAGESTDALSLPHVKLK 888

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4547	100.0	888	4	AAU09021	Aau09021 Human vol
2	4547	100.0	923	4	AAB47678	Aab47678 Human ion
3	4527.5	99.6	897	4	AAU09020	Aau09020 Human vol
4	4527.5	99.6	897	4	AAB47046	Aab47046 Human KCN
5	4527.5	99.6	897	5	AAE16599	Aae16599 Human pot
6	4524.5	99.5	897	4	AAU09025	Aau09025 Human vol
7	4524.5	99.5	897	4	AAU09023	Aau09023 Human vol
8	4523.5	99.5	897	4	AAU09024	Aau09024 Human vol
9	4521.5	99.4	897	4	AAU09022	Aau09022 Human vol
10	4513.5	99.3	932	4	AAB86979	Aab86979 Human KCN
11	4269.5	93.9	846	3	AAB24241	Aab24241 Human KCN
12	1985	43.7	695	3	AAB01476	Aab01476 KCNQ4 Pot
13	1985	43.7	695	5	AAE16621	Aae16621 Human pot
14	1985	43.7	695	7	ADE31699	Ade31699 Human 323
15	1803.5	39.7	852	8	ADS17852	Ads17852 Rattus no
16	1792	39.4	844	5	AAE16619	Aae16619 Human pot
17	1792	39.4	844	7	ADB78617	Adb78617 Human pot
18	1792	39.4	844	7	ADN38964	Adn38964 Cancer/an
19	1792	39.4	844	8	ADL06572	Adl06572 Human tum
20	1790.5	39.4	722	2	AAY01530	Aay01530 Amino aci
21	1788.5	39.3	930	2	AAY08347	Aay08347 Human mut
22	1787.5	39.3	871	2	AAY01529	Aay01529 Amino aci
23	1785	39.3	854	2	AAY23215	Aay23215 Human bra
24	1785	39.3	912	4	ABG10644	Abg10644 Novel hum
25	1783	39.2	872	2	AAY08341	Aay08341 Human KCN
26	1783	39.2	872	7	AAE38588	Aae38588 Human pot
27	1783	39.2	872	8	ADH51121	Adh51121 Potassium
28	1783	39.2	872	8	ADM77997	Adm77997 KCNQ2-fl
29	1783	39.2	914	4	ABG10643	Abg10643 Novel hum
30	1775	39.0	872	8	ADS17845	Ads17845 Human KCN
31	1762	38.8	842	8	ADS17846	Ads17846 Human KCN
32	1759	38.7	757	2	AAY08345	Aay08345 Mouse par
33	1710.5	37.6	942	4	ABG10645	Abg10645 Novel hum
34	1611	35.4	615	8	ADH51120	Adh51120 Potassium
35	1611	35.4	615	8	ADM77996	Adm77996 KCNQ2-15b
36	1604	35.3	625	8	ADH51118	Adh51118 Potassium
37	1604	35.3	625	8	ADM77994	Adm77994 KCNQ2-15b
38	1602	35.2	643	8	ADH51116	Adh51116 Potassium
39	1602	35.2	643	8	ADM77992	Adm77992 KCNQ2-15b
40	1587.5	34.9	825	8	ADS17848	Ads17848 Human KCN
41	1587.5	34.9	854	2	AAY01534	Aay01534 Amino aci
42	1587.5	34.9	872	2	AAY08344	Aay08344 Human KCN
43	1587.5	34.9	872	5	AAE16620	Aae16620 Human pot
44	1587.5	34.9	872	7	ADB78616	Adb78616 Human pot
45	1587.5	34.9	872	7	ADE55396	Ade55396 Human Pro

ALIGNMENTS

RESULT 1
AAU09021
ID AAU09021 standard; protein; 888 AA.
XX
AC AAU09021;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human voltage gated potassium channel hKVNQ5-2.
XX
KW Human; voltage-gated potassium channel; hKCNQ5-2; nootropic;
KW cerebroprotective; neurotropic; analgesic; vision disorder;
KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder; stroke;
KW pain; gene therapy; splice variant.
XX
OS Homo sapiens.
XX
PN WO200170759-A1.
XX
PD 27-SEP-2001.
XX
PF 20-MAR-2001; 2001WO-US009328.
XX
PR 21-MAR-2000; 2000US-0190954P.
XX
PA (ICAG-) ICAGEN INC.
XX
PI Jegla TJ;
XX
DR WPI; 2001-611467/70.
DR N-PSDB; AAS14653.
XX
PT Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT identifying a compound modulating ion flux in eukaryotic cell or cell
PT membrane expressing the protein, comprises KCNQ approximatelya- subunits.
XX
PS Claim 17; Page 64; 78pp; English.
XX
CC The invention relates to an isolated polypeptide comprising an alpha-
CC subunit of a KCNQ potassium channel, with a subsequence having 65%
CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
CC and forms a KCNQ potassium channel having the characteristic of voltage-
CC gating with at least an additional KCNQ alpha-subunit. Also included in
CC the scope of the invention are the nucleic acids encoding hKCNQ5
CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
CC vectors encoding them, antibodies against them, the use of 3-dimensional
CC computer modelling to identify molecules that bind to a KCNQ containing

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CC   potassium channel and modulate ion flux through the channel. The KCNQ
CC   polypeptide is useful for identifying a compound that increases or
CC   decreases ion flux through a potassium channel expressed in an eukaryotic
CC   host cell or cell membrane. The compound (and the KCNQ nucleic acid when
CC   used in gene therapy)is useful as a pharmaceutical agent for treating
CC   diseases involving abnormal ion flux, such as disorders of the central
CC   nervous system, such as epilepsy, migraines, hearing and vision problems,
CC   psychotic disorders, seizures, learning and memory disorders, stroke and
CC   pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
CC   human tissue and the use of a nucleotide sequence of KCNQ5 to search
CC   computer databases to find variants of the sequence which are associated
CC   with disease states, is useful for screening mutations of KCNQ5. The
CC   present sequence is encoded by a splice variant of hKCNQ5 and is hKCNQ5-2
XX
SQ   Sequence 888 AA;

  Query Match             100.0%;  Score 4547;  DB 4;  Length 888;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  888;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60

Qy         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120

Qy        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180

Qy        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300

Qy        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360

Qy        361 HLKALHTCSPTNQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAEGSPTKVQKS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 HLKALHTCSPTNQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAEGSPTKVQKS 420

Qy        421 WSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 WSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRA 480

Qy        481 IRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 IRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDK 540

Qy        541 KSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASF 600

Qy        601 QIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPNEFSAQTFYA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 QIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPNEFSAQTFYA 660

Qy        661 LSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLPAIKHLPRPE 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLPAIKHLPRPE 720

Qy        721 TLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETLLSVCPMVPK 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETLLSVCPMVPK 780

Qy        781 DLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEEVGPEETETD 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 DLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEEVGPEETETD 840

Qy        841 TFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888


RESULT 2
AAB47678
ID   AAB47678 standard; protein; 923 AA.
XX
AC   AAB47678;
XX
DT   21-JAN-2002  (first entry)
XX
DE   Human ion-channel forming protein.
XX
KW   Ion-channel forming protein; voltage-gated potassium channel; fetal;
KW   brain; thymus; prostate; heart; skeletal muscle; probe.
XX
OS   Homo sapiens.
XX
PN   WO200175108-A1.
XX
PD   11-OCT-2001.
XX
PF   03-APR-2001; 2001WO-US010875.
XX
PR   03-APR-2000; 2000US-0194255P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Hu Y,  Kieke JA,  Turner AC,  Nehls MC,  Friedrich G,  Zambrowicz B;
PI   Sands AT;
XX
DR   WPI; 2001-656987/75.
DR   N-PSDB; AAH43633, AAH43634.
XX
PT   New human ion channel protein and polynucleotides encoding the protein,
PT   useful in diagnosing or treating diseases, in drug screening, and in
PT   clinical trial monitoring.
XX
PS   Claim 2; Page 35-37; 41pp; English.
XX
CC   This sequence represent a novel ion-channel forming protein. This protein
CC   shares structural similarity with mammalian ion channel proteins,
CC   particularly voltage-gated potassium channel proteins. The protein is
CC   expressed in many human cell lines including fetal brain, brain,
CC   thymus,prostate, heart and skeletal muscle. The novel protein can be used
CC   in the diagnosis or treatment of diseases, in drug screening, and in
CC   clinical trial monitoring. The oligonucleotides may be used as
CC   hybridization probes for screening libraries, and assessing gene
CC   expression patterns (particularly using a micro array or high throughput
CC   chip format). The nucleic acids and novel protein can also be used in the
CC   identification, selection and validation of novel molecular targets for
CC   drug discovery, to screen collections of genetic material from patients
CC   who have a particular medical condition, to identify mutations associated
CC   with a particular disease, as a diagnostic or prognostic assay, and to
CC   screen for drugs which can be used to treat symptomatic or phenotypic
CC   manifestations of perturbing the normal function of novel human protein.
CC   The polypeptides are further used in generating antibodies
XX
SQ   Sequence 923 AA;

  Query Match             100.0%;  Score 4547;  DB 4;  Length 923;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  888;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         36 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 95
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```
Qy          61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          96 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 155

Qy         121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         156 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 215

Qy         181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         216 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 275

Qy         241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         276 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 335

Qy         301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         336 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 395

Qy         361 HLKALHTCSPTNQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAEGSPTKVQKS 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         396 HLKALHTCSPTNQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAEGSPTKVQKS 455

Qy         421 WSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         456 WSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRA 515

Qy         481 IRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDK 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         516 IRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDK 575

Qy         541 KSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASF 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         576 KSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASF 635

Qy         601 QIPPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPNEFSAQTFYA 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         636 QIPPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPNEFSAQTFYA 695

Qy         661 LSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLPAIKHLPRPE 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         696 LSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLPAIKHLPRPE 755

Qy         721 TLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETLLSVCPMVPK 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         756 TLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETLLSVCPMVPK 815

Qy         781 DLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEEVGPEETETD 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         816 DLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEEVGPEETETD 875

Qy         841 TFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888
               ||||||||||||||||||||||||||||||||||||||||||||||||
Db         876 TFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 923
```

RESULT 3
AAU09020
ID AAU09020 standard; protein; 897 AA.
XX
AC AAU09020;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human voltage gated potassium channel hKVNQ5-1.
XX
KW Human; voltage-gated potassium channel; hKCNQ5-1; nootropic;
KW cerebroprotective; neurotropic; analgesic; vision disorder;
KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder; stroke;
KW pain; gene therapy; splice variant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 343. .640
FT /label= Conserved_region
FT /note= "This sequence is specifically claimed in claim
FT 13"
XX
PN WO200170759-A1.
XX
PD 27-SEP-2001.
XX
PF 20-MAR-2001; 2001WO-US009328.
XX
PR 21-MAR-2000; 2000US-0190954P.
XX
PA (ICAG-) ICAGEN INC.
XX
PI Jegla TJ;
XX
DR WPI; 2001-611467/70.
DR N-PSDB; AAS14652.
XX
PT Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT identifying a compound modulating ion flux in eukaryotic cell or cell
PT membrane expressing the protein, comprises KCNQ approximatelya- subunits.
XX
PS Claim 17; Page 64; 78pp; English.
XX
CC The invention relates to an isolated polypeptide comprising an alpha-
CC subunit of a KCNQ potassium channel, with a subsequence having 65%
CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
CC and forms a KCNQ potassium channel having the characteristic of voltage-
CC gating with at least an additional KCNQ alpha-subunit. Also included in
CC the scope of the invention are the nucleic acids encoding hKCNQ5
CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
CC vectors encoding them, antibodies against them, the use of 3-dimensional
CC computer modelling to identify molecules that bind to a KCNQ containing
CC potassium channel and modulate ion flux through the channel. The KCNQ
CC polypeptide is useful for identifying a compound that increases or
CC decreases ion flux through a potassium channel expressed in an eukaryotic
CC host cell or cell membrane. The compound (and the KCNQ nucleic acid when
CC used in gene therapy)is useful as a pharmaceutical agent for treating
CC diseases involving abnormal ion flux, such as disorders of the central
CC nervous system, such as epilepsy, migraines, hearing and vision problems,
CC psychotic disorders, seizures, learning and memory disorders, stroke and
CC pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
CC human tissue and the use of a nucleotide sequence of KCNQ5 to search
CC computer databases to find variants of the sequence which are associated
CC with disease states, is useful for screening mutations of KCNQ5. The
CC present sequence is encoded by a splice variant of hKCNQ5 and is hKCNQ5-1
XX
SQ Sequence 897 AA;

Query Match 99.6%; Score 4527.5; DB 4; Length 897;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

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Qy           1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60

Qy          61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120

Qy         121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180

Qy         181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
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Qy        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300

Qy        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360

Qy        361 HLKALHTCSPT---------NQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 411
              ||||||||||          :|||||||||||||||||||||||||||||||||||||||
Db        361 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420

Qy        412 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480

Qy        472 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 531
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Db        481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy        532 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600

Qy        592 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 651
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660

Qy        652 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 711
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 720

Qy        712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780

Qy        772 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840

Qy        832 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897
```

```
RESULT 4
AAB47046
ID   AAB47046 standard; protein; 897 AA.
XX
AC   AAB47046;
XX
DT   20-APR-2001  (first entry)
XX
DE   Human KCNQ5 potassium channel subunit.
XX
KW   Human; KCNQ5; heteromeric channel; chromosome 6; Parkinson's disease;
KW   central nervous system; CNS; Alzheimer's disease; anxiety; ataxia;
KW   CNS damage; trauma; stroke; neurodegenerative illness; schizophrenia;
KW   compulsive behaviour; dementia; depression; Huntington's disease; mania;
KW   memory impairment; memory dysfunction; spinal cord damage; phobia;
KW   pick's disease; psychosis; stroke; tremor; seizure; convulsion; epilepsy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Binding-site    93
FT                   /label= Site 1
FT   Binding-site    120. .138
FT                   /label= Site 2
FT   Binding-site    166. .185
FT                   /label= Site 3
FT   Binding-site    188. .213
FT                   /label= Site 4
FT   Binding-site    230. .252
FT                   /label= Site 5
FT   Region          265. .284
FT                   /label= P-loop
FT   Binding-site    291. .314
FT                   /label= Site 6
FT   Domain          495. .544
FT                   /label= A-domain
XX
PN   WO200077035-A2.
XX
PD   21-DEC-2000.
XX
PF   29-MAY-2000; 2000WO-DK000289.
XX
PR   11-JUN-1999;   99DK-00000828.
XX
PA   (NEUR-) NEUROSEARCH AS.
XX
PI   Jentsch TJ;
XX
DR   WPI; 2001-080678/09.
DR   N-PSDB; AAC85414.
XX
PT   Novel genes encoding KCNQ5 potassium channel subunits, useful for
PT   treating Alzheimer's disease, anxiety, ataxia, stroke, dementia,
PT   depression, Huntington's disease, schizophrenia and Parkinson's disease.
XX
PS   Claim 8; Page 48-50; 50pp; English.
XX
CC   This sequence shows the human KCNQ5 protein. The KCNQ5 protein forms
CC   heteromeric channels with other KCNQ channel subunits, in particular
CC   KCNQ3 and KCNQ4. The KCNQ5 gene has been localised to the long arm of
CC   chromosome 6 (6q14). Chemicals which have the ability to bind to KCNQ5
CC   are useful for diagnosis, treatment, prevention or alleviation of
CC   diseases related to diseases or adverse conditions of the central nervous
CC   system (CNS), including affective disorders, Alzheimer's disease,
CC   anxiety, ataxia, CNS damage caused by trauma, stroke or neurodegenerative
CC   illness, cognitive deficits, compulsive behavior, dementia, depression,
CC   Huntington's disease, mania, memory impairment, memory disorders, memory
CC   dysfunction, motion disorders, motor disorders, neurodegenerative
CC   diseases, Parkinson's disease and Parkinson-like motor disorders,
CC   phobias, pick's disease, psychosis, schizophrenia, spinal cord damage,
CC   stroke, tremor, seizures, convulsions and epilepsy
XX
SQ   Sequence 897 AA;
```

Query Match 99.6%; Score 4527.5; DB 4; Length 897;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

```
Qy          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60

Qy         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120

Qy        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180

Qy        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300

Qy        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360

Qy        361 HLKALHTCSPT---------NQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 411
                  ||||||||||         :|||||||||||||||||||||||||||||||||||||||
Db        361 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420

Qy        412 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 471
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480

Qy        472 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 531
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy        532 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 591
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600

Qy        592 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 651
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660

Qy        652 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 711
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 720

Qy        712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 771
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780

Qy        772 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 831
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840

Qy        832 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897
```

RESULT 5
AAE16599
ID AAE16599 standard; protein; 897 AA.
XX
AC AAE16599;
XX
DT 09-APR-2002 (first entry)
XX
DE Human potassium channel polypeptide, KCNQ5.
XX
KW Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;
KW dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis; ALS;
KW multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
KW anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
KW addiction; myokymia; Alzheimer's disease; age-associated memory loss;
KW learning deficiency; cognitive disorder; motor disease; neuron disease;
KW neurophysiological disorder; neuropsychological disorder; asthma;
KW neuron cell death; brain tumour; gene therapy; antisense therapy;
KW synaptic transmission; electrical excitability.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 191. .209
FT /note= "Pore region"
FT Region 265. .285
FT /note= "S4 voltage sensor region"
XX
PN WO200192526-A1.
XX
PD 06-DEC-2001.
XX
PF 24-MAY-2001; 2001WO-US017314.
XX
PR 26-MAY-2000; 2000US-0207389P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Dworetzky SI, Ramanathan CS, Trojnacki JT, Boissard CG;
PI Gribkoff VK;
XX
DR WPI; 2002-122069/16.
DR N-PSDB; AAD27192.
XX
PT Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding
PT it, for diagnosing, treating and identifying modulators useful in
PT treating neurological, neurophysiological and neuropsychological
PT diseases.
XX
PS Claim 25; Fig 2; 128pp; English.
XX
CC The invention relates to potassium channel polypeptides referred to as
CC KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5
CC polypeptides are useful for identifying compounds that modulate their
CC biological activity. The compounds identified and KCNQ5 polynucleotides
CC are useful for treating acute and chronic pain, migraine, acute stroke,
CC dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis (ALS),
CC multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety disorders,
CC depression, bipolar disorders, sleep disorders, eating disorders,
CC addiction, myokymia, Alzheimer's disease, age-associated memory loss,
CC learning deficiencies, cognitive disorders and motor neuron diseases. The
CC nucleic acid molecules of the invention are further useful for treating
CC neurophysiological, neuropsychological disorders, asthma, neuron cell
CC death and brain tumours. They are also used in gene therapy and antisense
CC therapy. KCNQ5 polypeptides modulate synaptic transmission and electrical
CC excitability in the brain and are useful for generating antibodies. They
CC are also useful to affinity purify biological effectors from biological
CC materials e.g. disease tissues or cells. The present sequence is human
CC KCNQ5 protein
XX
SQ Sequence 897 AA;

Query Match 99.6%; Score 4527.5; DB 5; Length 897;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

```
Qy          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60

Qy         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120

Qy        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180

Qy        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300

Qy        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360

Qy        361 HLKALHTCSPT---------NQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 411
              ||||||||||         :|||||||||||||||||||||||||||||||||||||||
Db        361 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420

Qy        412 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        421 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480

Qy        472 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy        532 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600

Qy        592 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 651
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660

Qy        652 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 711
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 720

Qy        712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780

Qy        772 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840

Qy        832 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897


RESULT 6
AAU09025
ID   AAU09025 standard; protein; 897 AA.
XX
AC   AAU09025;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human voltage gated potassium channel hKVNQ5-1 variant #4.
XX
KW   Human; voltage-gated potassium channel; hKCNQ5-1; nootropic;
KW   cerebroprotective; neurotropic; analgesic; vision disorder;
KW   central nervous system disorder; epilepsy; migraine; hearing disorder;
KW   psychotic disorder; seizure; learning disorder; memory disorder; stroke;
KW   pain; gene therapy; mutant; mutein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          343. .640
FT                   /label= Conserved_region
FT                   /note= "This sequence is specifically claimed in claim
FT                   13"
FT   Misc-difference 542
FT                   /note= "Wild-type Lys substituted by Arg"
XX
PN   WO200170759-A1.
XX
PD   27-SEP-2001.
XX
PF   20-MAR-2001; 2001WO-US009328.
XX
PR   21-MAR-2000; 2000US-0190954P.
XX
PA   (ICAG-) ICAGEN INC.
XX
PI   Jegla TJ;
XX
DR   WPI; 2001-611467/70.
XX
PT   Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT   identifying a compound modulating ion flux in eukaryotic cell or cell
PT   membrane expressing the protein, comprises KCNQ approximatelya- subunits.
XX
PS   Disclosure; Page; 78pp; English.
XX
CC   The invention relates to an isolated polypeptide comprising an alpha-
CC   subunit of a KCNQ potassium channel, with a subsequence having 65%
CC   sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
CC   and forms a KCNQ potassium channel having the characteristic of voltage-
CC   gating with at least an additional KCNQ alpha-subunit. Also included in
CC   the scope of the invention are the nucleic acids encoding hKCNQ5
CC   (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
CC   vectors encoding them, antibodies against them, the use of 3-dimensional
CC   computer modelling to identify molecules that bind to a KCNQ containing
CC   potassium channel and modulate ion flux through the channel. The KCNQ
CC   polypeptide is useful for identifying a compound that increases or
CC   decreases ion flux through a potassium channel expressed in an eukaryotic
CC   host cell or cell membrane. The compound (and the KCNQ nucleic acid when
CC   used in gene therapy)is useful as a pharmaceutical agent for treating
CC   diseases involving abnormal ion flux, such as disorders of the central
CC   nervous system, such as epilepsy, migraines, hearing and vision problems,
CC   psychotic disorders, seizures, learning and memory disorders, stroke and
CC   pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
CC   human tissue and the use of a nucleotide sequence of KCNQ5 to search
CC   computer databases to find variants of the sequence which are associated
CC   with disease states, is useful for screening mutations of KCNQ5. The
CC   present sequence is a polymorphic variant of hKCNQ5-1. Note: The present
CC   sequence does not appear in the specification but is based on hKCNQ5-1
CC   sequence appearing as AAU09020
XX
SQ   Sequence 897 AA;

  Query Match             99.5%;  Score 4524.5;  DB 4;  Length 897;
  Best Local Similarity   98.8%;  Pred. No. 0;
  Matches  886;  Conservative    2;  Mismatches    0;  Indels    9;  Gaps    1;

Qy          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60

Qy         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120

Qy        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180

Qy        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300

Qy        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
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Qy        412 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 471
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Db        421 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480

Qy        472 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 531
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Db        481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy        532 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 591
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Qy        652 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 711
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Qy        712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780

Qy        772 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 831
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Qy        832 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888
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Db        841 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897
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RESULT 7
AAU09023
ID AAU09023 standard; protein; 897 AA.
XX
AC AAU09023;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human voltage gated potassium channel hKVNQ5-1 variant #2.
XX
KW Human; voltage-gated potassium channel; hKCNQ5-1; nootropic;
KW cerebroprotective; neurotropic; analgesic; vision disorder;
KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder; stroke;
KW pain; gene therapy; mutant; mutein.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Misc-difference 50
FT   /note= "Wild-type Ala substituted by Ser"
FT Region   343. .640
FT   /label= Conserved_region
FT   /note= "This sequence is specifically claimed in claim
FT   13"
XX
PN WO200170759-A1.
XX
PD 27-SEP-2001.
XX
PF 20-MAR-2001; 2001WO-US009328.
XX
PR 21-MAR-2000; 2000US-0190954P.
XX
PA (ICAG-) ICAGEN INC.
XX
PI Jegla TJ;
XX
DR WPI; 2001-611467/70.
XX
PT Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT identifying a compound modulating ion flux in eukaryotic cell or cell
PT membrane expressing the protein, comprises KCNQ approximatelya- subunits.
XX
PS Disclosure; Page; 78pp; English.
XX
CC The invention relates to an isolated polypeptide comprising an alpha-
CC subunit of a KCNQ potassium channel, with a subsequence having 65%
CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
CC and forms a KCNQ potassium channel having the characteristic of voltage-
CC gating with at least an additional KCNQ alpha-subunit. Also included in
CC the scope of the invention are the nucleic acids encoding hKCNQ5
CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
CC vectors encoding them, antibodies against them, the use of 3-dimensional
CC computer modelling to identify molecules that bind to a KCNQ containing
CC potassium channel and modulate ion flux through the channel. The KCNQ
CC polypeptide is useful for identifying a compound that increases or
CC decreases ion flux through a potassium channel expressed in an eukaryotic
CC host cell or cell membrane. The compound (and the KCNQ nucleic acid when
CC used in gene therapy)is useful as a pharmaceutical agent for treating
CC diseases involving abnormal ion flux, such as disorders of the central
CC nervous system, such as epilepsy, migraines, hearing and vision problems,
CC psychotic disorders, seizures, learning and memory disorders, stroke and
CC pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
CC human tissue and the use of a nucleotide sequence of KCNQ5 to search
CC computer databases to find variants of the sequence which are associated
CC with disease states, is useful for screening mutations of KCNQ5. The
CC present sequence is a polymorphic variant of hKCNQ5-1. Note: The present
CC sequence does not appear in the specification but is based on hKCNQ5-1
CC sequence appearing as AAU09020
XX
SQ Sequence 897 AA;

Query Match 99.5%; Score 4524.5; DB 4; Length 897;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 886; Conservative 2; Mismatches 0; Indels 9; Gaps 1;

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Db          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGSRMSLLGKPLS 60

Qy         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
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Qy        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
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Db        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180

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Qy        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
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Db        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300

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Qy        361 HLKALHTCSPT---------NQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 411
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Db        361 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420

Qy        412 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480

Qy        472 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy        532 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600

Qy        592 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 651
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Db        601 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660

Qy        652 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 711
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Db        661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 720

Qy        712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 771
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Db        721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780

Qy        772 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 831
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Qy        832 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888
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Db        841 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897


RESULT 8
AAU09024
ID   AAU09024 standard; protein; 897 AA.
XX
AC   AAU09024;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human voltage gated potassium channel hKVNQ5-1 variant #3.
XX
KW   Human; voltage-gated potassium channel; hKCNQ5-1; nootropic;
KW   cerebroprotective; neurotropic; analgesic; vision disorder;
KW   central nervous system disorder; epilepsy; migraine; hearing disorder;
KW   psychotic disorder; seizure; learning disorder; memory disorder; stroke;
KW   pain; gene therapy; mutant; mutein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          343. .640
FT                   /label= Conserved_region
FT                   /note= "This sequence is specifically claimed in claim
FT                   13"
FT   Misc-difference 446
FT                   /note= "Wild-type Ser substituted by Gly"
XX
PN   WO200170759-A1.
XX
PD   27-SEP-2001.
XX
PF   20-MAR-2001; 2001WO-US009328.
XX
PR   21-MAR-2000; 2000US-0190954P.
XX
PA   (ICAG-) ICAGEN INC.
XX
PI   Jegla TJ;
XX
DR   WPI; 2001-611467/70.
XX
PT   Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT   identifying a compound modulating ion flux in eukaryotic cell or cell
PT   membrane expressing the protein, comprises KCNQ approximatelya- subunits.
XX
PS   Disclosure; Page; 78pp; English.
XX
CC   The invention relates to an isolated polypeptide comprising an alpha-
CC   subunit of a KCNQ potassium channel, with a subsequence having 65%
CC   sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
CC   and forms a KCNQ potassium channel having the characteristic of voltage-
CC   gating with at least an additional KCNQ alpha-subunit. Also included in
CC   the scope of the invention are the nucleic acids encoding hKCNQ5
CC   (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
CC   vectors encoding them, antibodies against them, the use of 3-dimensional
CC   computer modelling to identify molecules that bind to a KCNQ containing
CC   potassium channel and modulate ion flux through the channel. The KCNQ
CC   polypeptide is useful for identifying a compound that increases or
CC   decreases ion flux through a potassium channel expressed in an eukaryotic
CC   host cell or cell membrane. The compound (and the KCNQ nucleic acid when
CC   used in gene therapy)is useful as a pharmaceutical agent for treating
CC   diseases involving abnormal ion flux, such as disorders of the central
CC   nervous system, such as epilepsy, migraines, hearing and vision problems,
CC   psychotic disorders, seizures, learning and memory disorders, stroke and
CC   pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
CC   human tissue and the use of a nucleotide sequence of KCNQ5 to search
CC   computer databases to find variants of the sequence which are associated
CC   with disease states, is useful for screening mutations of KCNQ5. The
CC   present sequence is a polymorphic variant of hKCNQ5-1. Note: The present
CC   sequence does not appear in the specification but is based on hKCNQ5-1
CC   sequence appearing as AAU09020
XX
SQ   Sequence 897 AA;

  Query Match            99.5%;  Score 4523.5;  DB 4;  Length 897;
  Best Local Similarity  98.8%;  Pred. No. 0;
  Matches  886;  Conservative    1;  Mismatches    1;  Indels    9;  Gaps    1;

Qy          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
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Qy         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
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Db        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300

Qy        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
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Db        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360

Qy        361 HLKALHTCSPT---------NQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 411
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Qy        532 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 591
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Qy        592 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 651
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Qy        652 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 711
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Db        661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 720

Qy        712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 771
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Db        721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780

Qy        772 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 831
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Db        781 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840

Qy        832 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897


RESULT 9
AAU09022
ID   AAU09022 standard; protein; 897 AA.
XX
AC   AAU09022;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human voltage gated potassium channel hKVNQ5-1 variant #1.
XX
KW   Human; voltage-gated potassium channel; hKCNQ5-1; nootropic;
KW   cerebroprotective; neurotropic; analgesic; vision disorder;
KW   central nervous system disorder; epilepsy; migraine; hearing disorder;
KW   psychotic disorder; seizure; learning disorder; memory disorder; stroke;
KW   pain; gene therapy; mutant; mutein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 36
FT                   /note= "Wild-type Gly substituted by Ala"
FT   Region          343. .640
FT                   /label= Conserved_region
FT                   /note= "This sequence is specifically claimed in claim
FT                   13"
XX
PN   WO200170759-A1.
XX
PD   27-SEP-2001.
XX
PF   20-MAR-2001; 2001WO-US009328.
XX
PR   21-MAR-2000; 2000US-0190954P.
XX
PA   (ICAG-) ICAGEN INC.
XX
PI   Jegla TJ;
XX
DR   WPI; 2001-611467/70.
XX
PT   Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT   identifying a compound modulating ion flux in eukaryotic cell or cell
PT   membrane expressing the protein, comprises KCNQ approximatelya- subunits.
XX
PS   Disclosure; Page; 78pp; English.
XX
CC   The invention relates to an isolated polypeptide comprising an alpha-
CC   subunit of a KCNQ potassium channel, with a subsequence having 65%
CC   sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
CC   and forms a KCNQ potassium channel having the characteristic of voltage-
CC   gating with at least an additional KCNQ alpha-subunit. Also included in
CC   the scope of the invention are the nucleic acids encoding hKCNQ5
CC   (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
CC   vectors encoding them, antibodies against them, the use of 3-dimensional
CC   computer modelling to identify molecules that bind to a KCNQ containing
CC   potassium channel and modulate ion flux through the channel. The KCNQ
CC   polypeptide is useful for identifying a compound that increases or
CC   decreases ion flux through a potassium channel expressed in an eukaryotic
CC   host cell or cell membrane. The compound (and the KCNQ nucleic acid when
CC   used in gene therapy)is useful as a pharmaceutical agent for treating
CC   diseases involving abnormal ion flux, such as disorders of the central
CC   nervous system, such as epilepsy, migraines, hearing and vision problems,
CC   psychotic disorders, seizures, learning and memory disorders, stroke and
CC   pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
CC   human tissue and the use of a nucleotide sequence of KCNQ5 to search
CC   computer databases to find variants of the sequence which are associated
CC   with disease states, is useful for screening mutations of KCNQ5. The
CC   present sequence is a polymorphic variant of hKCNQ5-1. Note: The present
CC   sequence does not appear in the specification but is based on hKCNQ5-1
CC   sequence appearing as AAU09020
XX
SQ   Sequence 897 AA;

  Query Match             99.4%;  Score 4521.5;  DB 4;  Length 897;
  Best Local Similarity   98.8%;  Pred. No. 0;
  Matches  886;  Conservative    1;  Mismatches    1;  Indels    9;  Gaps    1;

Qy          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGAGGGLRESRRGKQGARMSLLGKPLS 60

Qy         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120

Qy        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300

Qy        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360

Qy        361 HLKALHTCSPT---------NQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 411
              |||||||||||         :||||||||||||||||||||||||||||||||||||||
Db        361 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420

Qy        412 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480

Qy        472 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy        532 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600

Qy        592 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 651
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660

Qy        652 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 711
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 720

Qy        712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780

Qy        772 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840

Qy        832 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897


RESULT 10
```

```
AAB86979
ID   AAB86979 standard; protein; 932 AA.
XX
AC   AAB86979;
XX
DT   11-DEC-2001  (first entry)
XX
DE   Human KCNQ5 protein.
XX
KW   KCNQ5; potassium channel protein; human; neurological; cardiovascular;
KW   anticonvulsant; excitablilty modulator; membrane potential; neuron;
KW   voltage-dependent KCNQ5 potassium channel; cardiomyocyte; epilepsy;
KW   screening; central nervous system disease; cardiovascular disease.
XX
OS   Homo sapiens.
XX
PN   DE10013732-A1.
XX
PD   27-SEP-2001.
XX
PF   21-MAR-2000; 2000DE-01013732.
XX
PR   21-MAR-2000; 2000DE-01013732.
XX
PA   (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI   Steinmeyer K,  Lerche C,  Scherer C,  Seebohm G,  Busch AE;
XX
DR   WPI; 2001-571700/65.
DR   N-PSDB; AAH49499.
XX
PT   New DNA sequence encoding potassium channel KCNQ5, useful in screening
PT   for specific modulators, potential agents for treating central nervous
PT   system and cardiovascular diseases.
XX
PS   Claim 1b; Page 10-14; 20pp; German.
XX
CC   This invention describes a novel DNA sequence (I) encoding: (i) a
CC   polypeptide (II) with potassium channel KCNQ5 activity; (ii) a
CC   polypeptide with the amino acid (aa) sequence of KCNQ5. The products of
CC   the invention have neurological, cardiovascular and anticonvulsant
CC   activity and act as modulators of the voltage-dependent KCNQ5 potassium
CC   channel, a key regulator of membrane potential and modulator of
CC   excitability of electrically activated cells such as neurons and
CC   cardiomyocytes. KCNQ5 may be implicated in some forms of epilepsy. (II)
CC   are used to screen for compounds that modulate the activity of KCNQ5,
CC   potentially useful for treating central nervous system (e.g. epilepsy)
CC   and cardiovascular diseases. This sequence represents the human potassium
CC   channel KCNQ5 protein described in the invention
XX
SQ   Sequence 932 AA;

  Query Match             99.3%;  Score 4513.5;  DB 4;  Length 932;
  Best Local Similarity   98.7%;  Pred. No. 0;
  Matches  885;  Conservative    1;  Mismatches    2;  Indels    9;  Gaps    1;

Qy          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db         36 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGSRLS 95

Qy         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 155

Qy        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 215

Qy        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 275

Qy        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 335

Qy        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 395

Qy        361 HLKALHTCSPT---------NQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 411
              |||||||||||         :||||||||||||||||||||||||||||||||||||||
Db        396 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 455

Qy        412 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 515

Qy        472 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 575

Qy        532 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 635

Qy        592 ASALALASFQIPPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 651
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 ASALALASFQIPPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 695

Qy        652 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 711
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        696 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 755

Qy        712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        756 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 815

Qy        772 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        816 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 875

Qy        832 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        876 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 932
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RESULT 11
AAB24241
ID   AAB24241 standard; protein; 846 AA.
XX
AC   AAB24241;
XX
DT   07-FEB-2001  (first entry)
XX
DE   Human KCNQ5 (KCN6q) protein sequence SEQ ID NO:3.
XX
KW   Human; KCNQ5; KCN6q; chromosome 6; voltage-gated potassium channel;
KW   Stargardt-like macular dystrophy; cone-rod macular dystrophy;
KW   Salla disease; ophthalmological; auditory; central nervous system;
KW   cardioactive; anticonvulsant; gastrointestinal; muscular active;
KW   age-related macular degeneration; macular degeneration; deafness;
KW   epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
KW   gastrointestinal disorder.
XX
OS   Homo sapiens.
XX
PN   WO200061606-A1.
XX
PD   19-OCT-2000.
XX
PF   10-APR-2000; 2000WO-US009587.
XX
PR   14-APR-1999;   99US-0129274P.
XX
PA   (MERI ) MERCK & CO INC.
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XX
PI   Petrukhin K,  Caskey CT,  Li W,  Metzker ML;
XX
DR   WPI; 2000-647417/62.
DR   N-PSDB; AAC64370, AAC64371.
XX
PT   Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
PT   inhibitors and activators which can treat e.g. Stargardt-like macular
PT   dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy.
XX
PS   Claim 8; Fig 2; 99pp; English.
XX
CC   The present sequence represents the human KCNQ5 (also called KCN6q)
CC   protein, which is a voltage-gated potassium channel protein. Human KCNQ5
CC   has ophthalmological, auditory, central nervous system (CNS),
CC   cardioactive, anticonvulsant, gastrointestinal and muscular active
CC   activities. Sequences and methods from the present invention are useful
CC   for identifying activators or inhibitors of KCNQ5 protein. These
CC   activators and inhibitors are useful for treating Stargardt-like macular
CC   dystrophy, cone-rod dystrophy, Salla disease, age-related macular
CC   degeneration, other forms of macular degeneration, deafness, epilepsy,
CC   and different forms of neuropsychiatric, heart, gastrointestinal, and
CC   muscle disorders. Stargardt-like macular dystrophy and cone-rod
CC   dystrophies are located at chromosome 6q
XX
SQ   Sequence 846 AA;

  Query Match             93.9%;  Score 4269.5;  DB 3;  Length 846;
  Best Local Similarity   98.7%;  Pred. No. 0;
  Matches  835;  Conservative    1;  Mismatches    1;  Indels    9;  Gaps    1;

Qy         52 MSLLGKPLSYTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVF 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSLLGKPLSYTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVF 60

Qy        112 STIPEHTKLASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVID 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STIPEHTKLASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVID 120

Qy        172 TIVLIASIAVVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKEL 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TIVLIASIAVVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKEL 180

Qy        232 ITAWYIGFLVLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRL 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ITAWYIGFLVLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRL 240

Qy        292 LSAGFALLGISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEK 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LSAGFALLGISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEK 300

Qy        352 SVSIATWKPHLKALHTCSPT---------NQKLSFKERVRMASPRGQSIKSRQASVGDRR 402
              ||||||||||||||||||||         :||||||||||||||||||||||||||||||
Db        301 SVSIATWKPHLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRR 360

Qy        403 SPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQ 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 SPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQ 420

Qy        463 CDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKS 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKS 480

Qy        523 LQTRVDQILGKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDI 582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LQTRVDQILGKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDI 540

Qy        583 YQQVLRKGSASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISR 642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 YQQVLRKGSASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISR 600

Qy        643 GLQFILTPNEFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPT 702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GLQFILTPNEFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPT 660

Qy        703 TLQIPPPLPAIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRK 762
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TLQIPPPLPAIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRK 720

Qy        763 SFDMGGETLLSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRE 822
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        721 SFDMGGETLLSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSASRGSQDFYPKWRE 780

Qy        823 SKLFITDEEVGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSL 882
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 SKLFITDEEVGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSL 840

Qy        883 PHVKLK 888
              ||||||
Db        841 PHVKLK 846


RESULT 12
AAB01476
ID   AAB01476 standard; protein; 695 AA.
XX
AC   AAB01476;
XX
DT   08-NOV-2000  (first entry)
XX
DE   KCNQ4 Potassium channel protein.
XX
KW   KCNQ4; potassium channel; cardiac arrhythmia; neonatal epilepsy;
KW   deafness; probes; treatment; therapy; transgenic animal; antibody;
KW   agonist; antagonist; tinnitus; hearing loss; neonatal deafness;
KW   presbyacusis; affective disorder, Alzheimer's disease; anxiety; ataxia;
KW   cognitive deficits; compulsive behavior; dementia; depression;
KW   Huntington's disease; mania; memory impairment; motor disorders;
KW   neurodegenerative disease; Parkinson's disease; Pick's disease;
KW   psychosis; schizophrenia; spinal cord damage; stroke; tremor.
XX
OS   Homo sapiens.
XX
PN   WO200044786-A1.
XX
PD   03-AUG-2000.
XX
PF   19-JAN-2000; 2000WO-DK000024.
XX
PR   26-JAN-1999;   99DK-00000076.
PR   19-MAY-1999;   99DK-00000693.
XX
PA   (NEUR-) NEUROSEARCH AS.
XX
PI   Jentsch TJ;
XX
DR   WPI; 2000-548813/50.
DR   N-PSDB; AAA47618.
XX
PT   Nucleic acids encoding the novel KCNQ4 potassium channel subunit, useful
PT   e.g. for treating tinnitus, deafness, Alzheimer's and Parkinson's
PT   diseases.
XX
PS   Claim 8; Page 48-51; 65pp; English.
XX
CC   Mutations in 3 known genes of the KCNQ branch of the potassium channel
CC   gene family underlie inherited cardiac arrhythmia's, neonatal epilepsy
CC   and in some cases associated with deafness. KCNQ4 has been mapped to the
CC   DFNA2 locus for autosomal dominant hearing loss, and a dominant negative
CC   KCNQ4 mutation that causes deafness in a DFNA2 pedigree has been
CC   identified. KCNQ4 is the first potassium channel gene underlying non-
CC   syndromic deafness. KCNQ4 forms heteromeric channels with other KCNQ
CC   channel subunits, especially KCNQ3. Nucleotides encoding the KCNQ4
CC   protein and the protein itself may be used in the prevention, treatment
CC   and diagnosis of diseases associated with inappropriate KCNQ4 expression.
CC   The nucleotides may also be used as DNA probes in diagnostic assays (e.g.
```

CC polymerase chain reactions (PCR)) to detect and quantitate the presence
CC of similar nucleic acid sequences in samples and to identify mutations
CC within them, and hence which patients may be in need of restorative
CC therapy. They may also be used to study the expression and function of
CC KCNQ4 polypeptides and their role in metabolism, for example through the
CC production of transgenic animals. The KCNQ4 polypeptides may be used as
CC antigens in the production of antibodies and to identify modulators
CC (agonists and antagonists) of KCNQ4 expression and activity. The anti-
CC KCNQ4 antibodies and KCNQ4 antagonists may also be used to down regulate
CC KCNQ4 expression and activity. They may be used in this way to treat
CC tinnitus, loss of hearing (especially progressive hearing loss, neonatal
CC deafness and presbyacusis (deafness of the elderly)) and disease or
CC adverse conditions of the central nervous system (CNS) such as affective
CC disorder, Alzheimer's disease, anxiety, ataxia, CNS damage caused by
CC trauma, stroke or neurodegenerative illness, cognitive deficits,
CC compulsive behavior, dementia, depression, Huntington's disease, mania,
CC memory impairment, memory disorders and dysfunctions, motion disorders,
CC motor disorders, neurodegenerative diseases, Parkinson's disease,
CC Parkinson-like motor disorders, phobias, Pick's disease, psychosis,
CC schizophrenia, spinal cord damage, stroke and/or tremor. Conversely,
CC antisense nucleic acid molecules may be administered to down regulate
CC KCNQ4 expression by binding with the cells own KCNQ4 genes and preventing
CC their expression
XX
SQ Sequence 695 AA;

Query Match 43.7%; Score 1985; DB 3; Length 695;
Best Local Similarity 60.3%; Pred. No. 1.1e-167;
Matches 409; Conservative 76; Mismatches 101; Indels 92; Gaps 13;

```
Qy         35 GGGGGLRESRRGKQGARMSLLGKPL----------SYTSSQSCRRNVKYRRVQNYL 80
              ||||  |        |: ||| ||             |    :|   : :|||:||:: 
Db         37 GGGGSPR---------RLGLLGSPLPPGAPLPGPGSGSGSACGQRSSAAHKRYRRLQNWV 87

Qy         81 YNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEF 140
              ||||||||||||:|| |:|||| ||:||| ||| || :||: ||||||||||||||||: 
Db         88 YNVLERPRGWAFVYHVFIFLLVFSCLVLSVLSTIQEHQELANECLLILEFVMIVVFGLEY 147

Qy        141 IIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLR 200
              |:|:|||||||||||||| |||||||||| || :||:||::| |||||||||||||:| 
Db        148 IVRVWSAGCCCRYRGWQGRFRFARKPFCVIDPIVFVASVAVIAAGTQGNIFATSALRSMR 207

Qy        201 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKEF 260
              |||||||||||||||||||||||||||||||||||||||||||:|||||| ||||| :| 
Db        208 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFASFLVYLAEKDANSDF 267

Qy        261 STYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQ 320
              |:|||:|||||||||||||||| |||||:|:|||||||||||||||||||||||||||| 
Db        268 SSYADSLWWGTITLTTIGYGDKTPHTWLGRVLAAGFALLGISFFALPAGILGSGFALKVQ 327

Qy        321 EQHRQKHFEKRRNPAANLIQCVWRSYAAD-EKSVSIATW---------------------- 358
              |||||||||||| |||||||  || |: |  ::   |||
Db        328 EQHRQKHFEKRRMPAANLIQAAWRLYSTDMSRAYLTATWYYYDSILPSFRELALLFEHVQ 387

Qy        359 ------------------------KPHLKALHT------CSPTNQKLSFKERVRMASPRG 388
                                     | :  |        |   : ::  |:|:|| | : 
Db        388 RARNGGLRPLEVRRAPVPDGAPSRYPPVATCHRPGSTSFCPGESSRMGIKDRIRMGSSQR 447

Qy        389 QSIKSRQ--ASVGDRRSPSTDITAEG-SPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVID 445
              ::  |:|  |      |||::   |  ||||||||||||||||||| ||||     ||
Db        448 RTGPSKQQLAPPTMPTSPSSEQVGEATSPTKVQKSWSFNDRTRFRASLRL-----KPRTS 502

Qy        446 ADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDV 505
              |: |  :::| :||  ||:::|:|: | :|||||:|||:|| ||||||||||||||||| 
Db        503 AEDA-PSEEVAEEKSYQCELTVDDIMPAVKTVIRSIRILKFLVAKRKFKETLRPYDVKDV 561

Qy        506 IEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSRE---KITAEHETTDDLSMLGRV 562
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Db        562 IEQYSAGHLDMLGRIKSLQTRVDQIVGRG--PGDRKAREKGDKGPSDAEVVDEISMMGRV 619

Qy        563 VKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFECEQTSDYQSPVDSKDL 622
              |||||||||||  ||| ||  | : || |:::  :| : |:| |: : |||| |||| :|: 
Db        620 VKVEKQVQSIEHKLDLLLGFYSRCLRSGTSA--SLGAVQVPLFDPDITSDYHSPVDHEDI 677
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Qy 623 SGSAQNSGCLSRSTSANI 640
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Db 678 SVSAQTLS-ISRSVSTNM 694

RESULT 13
AAE16621
ID AAE16621 standard; protein; 695 AA.
XX
AC AAE16621;
XX
DT 09-APR-2002 (first entry)
XX
DE Human potassium channel polypeptide, KCNQ4.
XX
KW Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;
KW dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis; ALS;
KW multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
KW anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
KW addiction; myokymia; Alzheimer's disease; age-associated memory loss;
KW learning deficiency; cognitive disorder; motor disease; neuron disease;
KW neurophysiological disorder; neuropsychological disorder; asthma;
KW neuron cell death; brain tumour; gene therapy; antisense therapy;
KW synaptic transmission; electrical excitability; KCNQ4 protein;
KW hearing loss.
XX
OS Homo sapiens.
XX
PN WO200192526-A1.
XX
PD 06-DEC-2001.
XX
PF 24-MAY-2001; 2001WO-US017314.
XX
PR 26-MAY-2000; 2000US-0207389P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Dworetzky SI, Ramanathan CS, Trojnacki JT, Boissard CG;
PI Gribkoff VK;
XX
DR WPI; 2002-122069/16.
XX
PT Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding
PT it, for diagnosing, treating and identifying modulators useful in
PT treating neurological, neurophysiological and neuropsychological
PT diseases.
XX
PS Disclosure; Fig 5; 128pp; English.
XX
CC The invention relates to potassium channel polypeptides referred to as
CC KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5
CC polypeptides are useful for identifying compounds that modulate their
CC biological activity. The compounds identified and KCNQ5 polynucleotides
CC are useful for treating acute and chronic pain, migraine, acute stroke,
CC dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis (ALS),
CC multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety disorders,
CC depression, bipolar disorders, sleep disorders, eating disorders,
CC addiction, myokymia, Alzheimer's disease, age-associated memory loss,
CC learning deficiencies, cognitive disorders and motor neuron diseases. The
CC nucleic acid molecules of the invention are further useful for treating
CC neurophysiological, neuropsychological disorders, asthma, neuron cell
CC death and brain tumours. They are also used in gene therapy and antisense
CC therapy. KCNQ5 polypeptides modulate synaptic transmission and electrical
CC excitability in the brain and are useful for generating antibodies. They
CC are also useful to affinity purify biological effectors from biological
CC materials e.g. disease tissues or cells. The present sequence is human
CC KCNQ4 protein. Mutations in this protein is associated with particular
CC disease e.g. hearing loss
XX
SQ Sequence 695 AA;

```
  Query Match             43.7%;  Score 1985;  DB 5;  Length 695;
  Best Local Similarity   60.3%;  Pred. No. 1.1e-167;
  Matches  409;  Conservative   76;  Mismatches  101;  Indels   92;  Gaps   13;

Qy         35 GGGGGGLRESRRGKQGARMSLLGKPL--------------SYTSSQSCRRNVKYRRVQNYL 80
              ||||  |          |: ||| ||                |    :|   : :|||:||::
Db         37 GGGGSPR---------RLGLLGSPLPPGAPLPGPGSGSGSACGQRSSAAHKRYRRLQNWV 87

Qy         81 YNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEF 140
              ||||||||||||:|| |:||||| ||:||| ||| || :||: ||||||||||||||:
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Qy        141 IIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLR 200
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Db        208 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFASFLVYLAEKDANSDF 267

Qy        261 STYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQ 320
              |:|||:|||||||||||||||| |||||:|:|||||||||||||||||||||||||||||
Db        268 SSYADSLWWGTITLTTIGYGDKTPHTWLGRVLAAGFALLGISFFALPAGILGSGFALKVQ 327

Qy        321 EQHRQKHFEKRRNPAANLIQCVWRSYAAD-EKSVSIATW---------------------- 358
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Db        328 EQHRQKHFEKRRMPAANLIQAAWRLYSTDMSRAYLTATWYYYDSILPSFRELALLFEHVQ 387

Qy        359 ------------------------KPHLKALHT------CSPTNQKLSFKERVRMASPRG 388
                                     | :   |       |   : ::  |:|:|| | :
Db        388 RARNGGLRPLEVRRAPVPDGAPSRYPPVATCHRPGSTSFCPGESSRMGIKDRIRMGSSQR 447

Qy        389 QSIKSRQ--ASVGDRRSPSTDITAEG-SPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVID 445
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Qy        446 ADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDV 505
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Db        503 AEDA-PSEEVAEEKSYQCELTVDDIMPAVKTVIRSIRILKFLVAKRKFKETLRPYDVKDV 561

Qy        506 IEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSRE---KITAEHETTDDLSMLGRV 562
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Db        562 IEQYSAGHLDMLGRIKSLQTRVDQIVGRG--PGDRKAREKGDKGPSDAEVVDEISMMGRV 619

Qy        563 VKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFECEQTSDYQSPVDSKDL 622
              |||||||||||| ||| ||  | : || |::  :| : |:| |: : |||| |||| :|:
Db        620 VKVEKQVQSIEHKLDLLLGFYSRCLRSGTSA--SLGAVQVPLFDPDITSDYHSPVDHEDI 677

Qy        623 SGSAQNSGCLSRSTSANI 640
              | |||    :||| | |:
Db        678 SVSAQTLS-ISRSVSTNM 694


RESULT 14
ADE31699
ID   ADE31699 standard; protein; 695 AA.
XX
AC   ADE31699;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human 32394 protein #SEQ ID 56.
XX
KW   Antiarteriosclerotic; cardiant; vasotropic; antiinflammatory;
KW   thrombolytic; antiarrhythmic; antianginal; hypotensive; gene therapy;
KW   cardiovascular; disorder; ischaemia; aortic bending;
KW   vascular heart disease; endocarditis; atrial fibrillation; heart failure;
KW   angina; cardiomyopathy; cardiac death.
XX
OS   Homo sapiens.
XX
PN   WO2003065984-A2.
XX
PD   14-AUG-2003.
XX
PF   29-JAN-2003; 2003WO-US002571.
XX
PR   01-FEB-2002; 2002US-0353224P.
PR   15-MAR-2002; 2002US-0364529P.
PR   19-APR-2002; 2002US-0373861P.
PR   29-APR-2002; 2002US-0376287P.
PR   12-JUN-2002; 2002US-0388080P.
PR   24-JUN-2002; 2002US-0390971P.
PR   03-JUL-2002; 2002US-0394130P.
PR   10-JUL-2002; 2002US-0394797P.
PR   21-AUG-2002; 2002US-0404904P.
PR   23-AUG-2002; 2002US-0405450P.
PR   04-SEP-2002; 2002US-0408070P.
PR   06-NOV-2002; 2002US-0424300P.
PR   05-DEC-2002; 2002US-0431042P.
PR   05-DEC-2002; 2002US-0431079P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Logan TJ,  Chun M,  Galvin KM,  Healy A,  Acton SL,  Donaghue M;
PI   Stagliano N,  Perodin J,  Rodrigue-Way A;
XX
DR   WPI; 2003-731468/69.
DR   N-PSDB; ADE31698.
XX
PT   Identifying a compound capable of treating a cardiovascular disorder
PT   (e.g. atherosclerosis) comprises assaying the ability of the compound to
PT   modulate the expression or activity of e.g. 1682, 6169 or 6193
PT   polypeptide or nucleic acid.
XX
PS   Disclosure; SEQ ID NO 56; 328pp; English.
XX
CC   The invention relates to a method for identifying a compound capable of
CC   treating a cardiovascular disorder. The present invention identifies the
CC   differential expression of 1682, 6169, 6193, 7771, 14395, 29002, 33216,
CC   43726, 69292, 21656, 32427, 2402, 7747, 1720, 9151, 60491, 1371, 7077,
CC   33207, 1419, 18036, 16105, 38650, 14245, 58848, 1870, 25856, 32394, 3484,
CC   345, 9252, 9135, 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912,
CC   2868, 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914, 51130,
CC   19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474, 9792, 15400, 1452 or
CC   6585 genes in cardiovascular disease states. The methods are useful in
CC   diagnosing, preventing and treating cardiovascular disorders, such as
CC   atherosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury,
CC   restenosis, arterial inflammation, vascular wall remodeling, coronary
CC   microembolism, tachycardia, bradycardia, pressure overload, aortic
CC   bending, coronary artery ligation, vascular heart disease, valvular
CC   disease, including but not limited to, valvular degeneration caused by
CC   calcification, rheumatic heart disease, endocarditis, or complications of
CC   artificial valves; atrial fibrillation, long-QT syndrome, congestive
CC   heart failure, sinus node dysfunction, angina, heart failure,
CC   hypertension, atrial fibrillation, atrial flutter, pericardial disease,
CC   including but not limited to, pericardial effusion and pericarditis;
CC   cardiomyopathies, e.g. dilated cardiomyopathy or idiopathic
CC   cardiomyopathy, myocardial infarction, coronary artery disease, coronary
CC   artery spasm, ischaemic disease, arrhythmia, sudden cardiac death and
CC   cardiovascular developmental disorders. The methods may also be used for
CC   identifying compounds that modulate cardiovascular disorders. Sequences
CC   given in ADE31644-ADE31769 represent the genes and proteins that may be
CC   regulated by a compound of the invention.
XX
SQ   Sequence 695 AA;

  Query Match             43.7%;  Score 1985;  DB 7;  Length 695;
  Best Local Similarity   60.3%;  Pred. No. 1.1e-167;
  Matches  409;  Conservative   76;  Mismatches  101;  Indels   92;  Gaps   13;

Qy         35 GGGGGGLRESRRGKQGARMSLLGKPL--------------SYTSSQSCRRNVKYRRVQNYL 80
              ||||  |          |: ||| ||                |    :|   : :|||:||::
Db         37 GGGGSPR---------RLGLLGSPLPPGAPLPGPGSGSGSACGQRSSAAHKRYRRLQNWV 87

Qy         81 YNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEF 140
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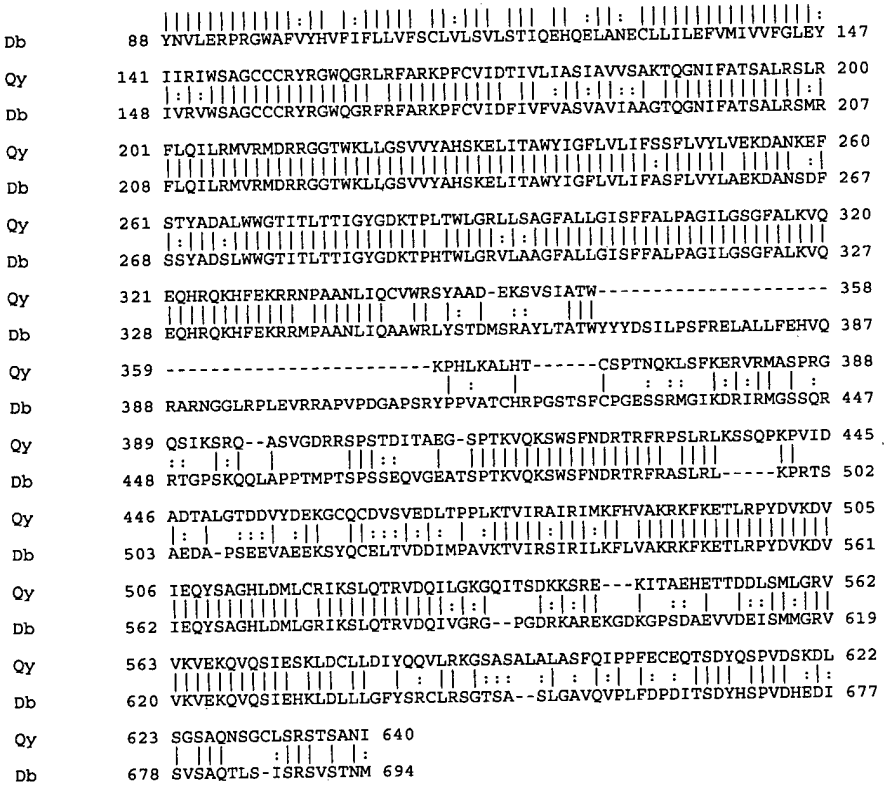
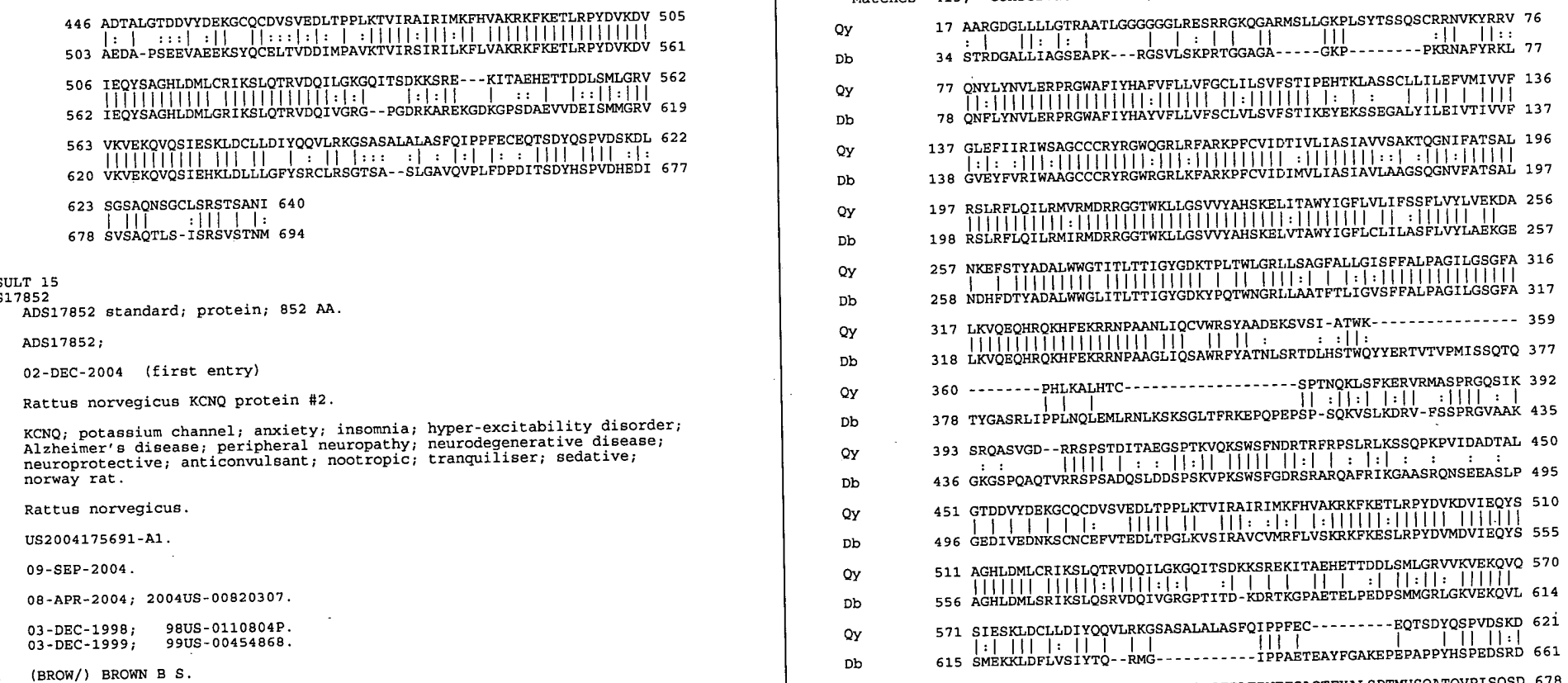


RESULT 15
ADS17852
ID ADS17852 standard; protein; 852 AA.
XX
AC ADS17852;
XX
DT 02-DEC-2004 (first entry)
XX
DE Rattus norvegicus KCNQ protein #2.
XX
KW KCNQ; potassium channel; anxiety; insomnia; hyper-excitability disorder;
KW Alzheimer's disease; peripheral neuropathy; neurodegenerative disease;
KW neuroprotective; anticonvulsant; nootropic; tranquiliser; sedative;
KW norway rat.
XX
OS Rattus norvegicus.
XX
PN US2004175691-A1.
XX
PD 09-SEP-2004.
XX
PF 08-APR-2004; 2004US-00820307.
XX
PR 03-DEC-1998; 98US-0110804P.
PR 03-DEC-1999; 99US-00454868.
XX
PA (BROW/) BROWN B S.
PA (MCKI/) MCKINNON D.
XX
PI Brown BS, Mckinnon D;
XX
DR WPI; 2004-642119/62.
DR N-PSDB; ADS17851.
XX
PT Evaluating compound for utility in treating neurological disease such as
PT epilepsy and anxiety, involves contacting compound with cell co-
PT expressing KCNQ2 and KCNQ3 that form potassium channel, and measuring
PT activity of potassium channel.
XX
PS Disclosure; SEQ ID NO 9; 38pp; English.
XX
CC The present invention relates to a method of evaluating a compound for
CC utility in treating neurological disease. The method involves contacting
CC a compound with a cell that co-expresses KCNQ2 and KCNQ3, where the KCNQ2
CC and KCNQ3 form a potassium channel and measuring the activity of the
CC potassium channel. The invention is useful for treating anxiety, insomnia
CC or other hyper-excitability disorders and Alzheimer's disease, peripheral
CC neuropathy or other neurodegenerative diseases. The present sequence is
CC the Rattus norvegicus KCNQ protein. This sequence is used to illustrate
CC the method of invention.
XX
SQ Sequence 852 AA;

Query Match 39.7%; Score 1803.5; DB 8; Length 852;
Best Local Similarity 49.0%; Pred. No. 2.6e-151;
Matches 413; Conservative 96; Mismatches 193; Indels 141; Gaps 22;



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Qy        679 GSAVAATNTIANQINTAPKPAAPTTLQIPPPLPAIKHLPRPETLHPNPAGLQESISDVTT 738
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Db        701 ------WQQSHQRHGTSPVGDHGSLVRIPPP---------------PAH-ERSLSAYSG 737

Qy        739 CLVASKENVQVAQSNLTK--DRSMRKSFDMGGETLLSVCPMVPKDLGKSLSVQNLIRSTE 796
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Db        738 GNRASTEFLRLEGTPACRPSEAALRDS-----DTSISIPSVDHEELERSFSGFSISQSKE 792

Qy        797 ELN 799
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Db        793 NLN 795
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Job time : 185 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 8, 2005, 16:35:41 ; Search time 151 Seconds
(without alignments)
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Title: US-09-810-796-5
Perfect score: 4547
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Scoring table: BLOSUM62
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Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	4547	100.0	923	16	US-10-803-268-2	Sequence 2, Appli
4	4527.5	99.6	897	9	US-09-866-020-2	Sequence 2, Appli
5	4527.5	99.6	897	9	US-09-810-796-4	Sequence 4, Appli
6	4527.5	99.6	897	16	US-10-661-629-2	Sequence 2, Appli
7	4527.5	99.6	897	17	US-10-948-493-2	Sequence 2, Appli
8	4527.5	99.6	932	9	US-09-813-148-2	Sequence 2, Appli
9	4300.5	94.6	854	16	US-10-661-629-7	Sequence 7, Appli
10	1985	43.7	695	9	US-09-866-020-31	Sequence 31, Appl
11	1985	43.7	695	9	US-09-810-796-15	Sequence 15, Appl
12	1985	43.7	695	15	US-10-353-690-56	Sequence 56, Appl
13	1985	43.7	695	16	US-10-661-629-6	Sequence 6, Appli
14	1985	43.7	695	17	US-10-850-928-2	Sequence 2, Appli
15	1985	43.7	695	17	US-10-948-493-31	Sequence 31, Appl
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17	1803.5	39.7	852	16	US-10-820-307-9	Sequence 9, Appli
18	1792	39.4	844	9	US-09-866-020-30	Sequence 30, Appl
19	1792	39.4	844	9	US-09-813-148-4	Sequence 4, Appli
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24	1792	39.4	844	17	US-10-948-493-29	Sequence 29, Appl
25	1792	39.4	844	17	US-10-948-518-152	Sequence 152, App
26	1790.5	39.4	722	13	US-10-128-870-23	Sequence 23, Appl
27	1790.5	39.4	722	14	US-10-131-685-23	Sequence 23, Appl
28	1788.5	39.3	930	14	US-10-096-578-96	Sequence 96, Appl
29	1787.5	39.3	871	13	US-10-128-870-20	Sequence 20, Appl
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36	1587.5	34.9	825	16	US-10-820-307-5	Sequence 5, Appli
37	1587.5	34.9	854	13	US-10-128-870-27	Sequence 27, Appl
38	1587.5	34.9	854	14	US-10-131-685-27	Sequence 27, Appl
39	1587.5	34.9	872	9	US-09-813-148-5	Sequence 5, Appli
40	1587.5	34.9	872	14	US-10-096-578-7	Sequence 7, Appli
41	1587.5	34.9	872	16	US-10-661-629-5	Sequence 5, Appli
42	1587.5	34.9	872	17	US-10-850-928-35	Sequence 35, Appl
43	1587.5	34.9	872	17	US-10-948-493-30	Sequence 30, Appl
44	1546	34.0	835	16	US-10-820-307-7	Sequence 7, Appli
45	1535.5	33.8	870	14	US-10-096-578-91	Sequence 91, Appl

ALIGNMENTS

RESULT 1
US-09-810-796-5
; Sequence 5, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAgen, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 888
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-2
US-09-810-796-5

Query Match 100.0%; Score 4547; DB 9; Length 888;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 888; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
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Qy        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180

Qy        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300

Qy        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360

Qy        361 HLKALHTCSPTNQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAEGSPTKVQKS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 HLKALHTCSPTNQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAEGSPTKVQKS 420

Qy        421 WSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 WSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRA 480

Qy        481 IRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 IRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDK 540

Qy        541 KSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASF 600

Qy        601 QIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPNEFSAQTFYA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 QIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPNEFSAQTFYA 660

Qy        661 LSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLPAIKHLPRPE 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLPAIKHLPRPE 720

Qy        721 TLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETLLSVCPMVPK 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETLLSVCPMVPK 780

Qy        781 DLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEEVGPEETETD 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 DLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEEVGPEETETD 840

Qy        841 TFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888


RESULT 2
US-09-825-147-2
; Sequence 2, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
;  APPLICANT: Hu, Yi
;  APPLICANT:  Kieke, James Alvin
;  APPLICANT:  Turner, C. Alexander Jr.
;  APPLICANT:  Nehls, Michael C.
;  APPLICANT:  Friedrich, Glenn
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
;  TITLE OF INVENTION:  Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0160-USA
;  CURRENT APPLICATION NUMBER: US/09/825,147
;  CURRENT FILING DATE:  2001-04-03
;  PRIOR APPLICATION NUMBER: US 60/194,255
;  PRIOR FILING DATE: 2000-04-03
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 923
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-09-825-147-2

  Query Match             100.0%;  Score 4547;  DB 9;  Length 923;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  888;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         36 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 95

Qy         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 155

Qy        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 215

Qy        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 275

Qy        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 335

Qy        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 395

Qy        361 HLKALHTCSPTNQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAEGSPTKVQKS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 HLKALHTCSPTNQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAEGSPTKVQKS 455

Qy        421 WSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 WSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRA 515

Qy        481 IRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 IRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDK 575

Qy        541 KSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 KSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASF 635

Qy        601 QIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPNEFSAQTFYA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 QIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPNEFSAQTFYA 695

Qy        661 LSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLPAIKHLPRPE 720
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Db        696 LSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLPAIKHLPRPE 755

Qy        721 TLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETLLSVCPMVPK 780
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Db        756 TLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETLLSVCPMVPK 815

Qy        781 DLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEEVGPEETETD 840
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Db        816 DLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEEVGPEETETD 875

Qy        841 TFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888
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Db        876 TFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 923


RESULT 3
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US-10-803-268-2
; Sequence 2, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
;  APPLICANT: Hu, Yi
;  APPLICANT:  Kieke, James Alvin
;  APPLICANT:  Turner, C. Alexander Jr.
;  APPLICANT:  Nehls, Michael C.
;  APPLICANT:  Friedrich, Glenn
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: Novel Human Ion Channel Protein and
;  TITLE OF INVENTION:  Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0160-USA
;  CURRENT APPLICATION NUMBER: US/10/803,268
;  CURRENT FILING DATE:  2004-03-18
;  PRIOR APPLICATION NUMBER: US/09/825,147
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: US 60/194,255
;  PRIOR FILING DATE: 2000-04-03
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 923
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-803-268-2

  Query Match            100.0%;  Score 4547;  DB 16;  Length 923;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  888;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
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Db         36 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 95

Qy         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 155

Qy        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
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Db        156 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 215

Qy        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 275

Qy        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 335

Qy        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 395

Qy        361 HLKALHTCSPTNQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAEGSPTKVQKS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 HLKALHTCSPTNQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAEGSPTKVQKS 455

Qy        421 WSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 WSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRA 515

Qy        481 IRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 IRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDK 575

Qy        541 KSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 KSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASF 635

Qy        601 QIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPNEFSAQTFYA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 QIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPNEFSAQTFYA 695

Qy        661 LSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLPAIKHLPRPE 720
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Db        696 LSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLPAIKHLPRPE 755

Qy        721 TLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETLLSVCPMVPK 780
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Db        756 TLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETLLSVCPMVPK 815

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Db        816 DLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEEVGPEETETD 875

Qy        841 TFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888
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Db        876 TFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 923


RESULT 4
US-09-866-020-2
; Sequence 2, Application US/09866020
; Publication No. US20020040000A1
; GENERAL INFORMATION:
;  APPLICANT: DWORETZKY, STEVEN I
;  APPLICANT:  RAMANATHAN, CHANDRA S
;  APPLICANT:  TROJNACKI, JOANNE T
;  APPLICANT:  BOISSARD, CHRISTOPHER G
;  APPLICANT:  GRIBKOFF, VALENTIN K
;  TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 3053-4091US1
;  CURRENT APPLICATION NUMBER: US/09/866,020
;  CURRENT FILING DATE:  2001-05-24
;  PRIOR APPLICATION NUMBER: 60/207,389
;  PRIOR FILING DATE: 2000-05-26
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 897
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-866-020-2

  Query Match            99.6%;  Score 4527.5;  DB 9;  Length 897;
  Best Local Similarity   98.9%;  Pred. No. 0;
  Matches  887;  Conservative    1;  Mismatches    0;  Indels    9;  Gaps    1;

Qy          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60

Qy         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120

Qy        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
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Db        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180

Qy        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
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Db        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300

Qy        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
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Qy        361 HLKALHTCSPT---------NQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 411
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Db        361 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420

Qy        412 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480

Qy        472 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy        532 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600

Qy        592 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 651
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660

Qy        652 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 711
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 720

Qy        712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780

Qy        772 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840

Qy        832 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897
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RESULT 5
US-09-810-796-4
; Sequence 4, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAgen, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 897
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-1
; NAME/KEY: PEPTIDE
; LOCATION: (343)..(640)
; OTHER INFORMATION: conserved region of KCNQ5-1
US-09-810-796-4

Query Match 99.6%; Score 4527.5; DB 9; Length 897;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

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Qy          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
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Db          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60

Qy         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120

Qy        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
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Db        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180

Qy        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
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Db        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300

Qy        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
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Db        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360

Qy        361 HLKALHTCSPT---------NQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 411
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Db        361 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420

Qy        412 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 471
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Db        421 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480

Qy        472 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 531
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Db        481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy        532 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 591
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Db        541 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600

Qy        592 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 651
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Db        601 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660

Qy        652 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 711
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Db        661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 720

Qy        712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 771
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Db        721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780

Qy        772 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 831
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Db        781 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840

Qy        832 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888
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Db        841 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897
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RESULT 6
US-10-661-629-2
; Sequence 2, Application US/10661629
; Publication No. US20040180405A1
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNE
; FILE REFERENCE: 2815-0236P
; CURRENT APPLICATION NUMBER: US/10/661,629
; CURRENT FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 897
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-661-629-2

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  Query Match           99.6%;  Score 4527.5;  DB 16;  Length 897;
  Best Local Similarity  98.9%;  Pred. No. 0;
  Matches  887;  Conservative    1;  Mismatches    0;  Indels    9;  Gaps    1;

Qy          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60

Qy         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120

Qy        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
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Db        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180

Qy        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
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Db        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300

Qy        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
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Db        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360

Qy        361 HLKALHTCSPT---------NQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 411
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Db        361 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420

Qy        412 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480

Qy        472 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy        532 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600

Qy        592 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 651
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Db        601 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660

Qy        652 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 711
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Db        721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780

Qy        772 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 831
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Db        781 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840

Qy        832 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888
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Db        841 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897


RESULT 7
US-10-948-493-2
; Sequence 2, Application US/10948493
; Publication No. US20050064491A1
; GENERAL INFORMATION:
;  APPLICANT: DWORETZKY, STEVEN I
;  APPLICANT:  RAMANATHAN, CHANDRA S
;  APPLICANT:  TROJNACKI, JOANNE T
;  APPLICANT:  BOISSARD, CHRISTOPHER G
;  APPLICANT:  GRIBKOFF, VALENTIN K
;  TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: D0023 DIV
;  CURRENT APPLICATION NUMBER: US/10/948,493
;  CURRENT FILING DATE:  2004-09-23
;  PRIOR APPLICATION NUMBER: 60/207,389
;  PRIOR FILING DATE: 2000-05-26
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 897
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-948-493-2

  Query Match           99.6%;  Score 4527.5;  DB 17;  Length 897;
  Best Local Similarity  98.9%;  Pred. No. 0;
  Matches  887;  Conservative    1;  Mismatches    0;  Indels    9;  Gaps    1;

Qy          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
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Db          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60

Qy         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
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Db         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120

Qy        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
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Db        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180

Qy        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
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Db        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
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Db        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300

Qy        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
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Db        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360

Qy        361 HLKALHTCSPT---------NQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 411
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Db        361 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420

Qy        412 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480

Qy        472 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 531
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Db        481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy        532 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 591
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Db        541 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600

Qy        592 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 651
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Db        601 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660

Qy        652 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 711
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Db        661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 720

Qy        712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        772 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 831
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Qy        832 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888
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Db        841 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897


RESULT 8
US-09-813-148-2
; Sequence 2, Application US/09813148
; Patent No. US20020076809A1
; GENERAL INFORMATION:
;  APPLICANT: STEINMEYER, Klaus
;  APPLICANT:  LERCHE, Christian
;  APPLICANT:  SCHERER, Constanze
;  APPLICANT:  SEEBOHM, Guiscard
;  APPLICANT:  BUSCH, Andreas E.
;  TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN
;  TITLE OF INVENTION:  NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
;  FILE REFERENCE: 38005-119
;  CURRENT APPLICATION NUMBER: US/09/813,148
;  CURRENT FILING DATE:  2001-03-21
;  PRIOR APPLICATION NUMBER: DE 100 13 732.6
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: US 60/194,041
;  PRIOR FILING DATE: 2000-04-03
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 932
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-813-148-2

  Query Match             99.6%;  Score 4527.5;  DB 9;  Length 932;
  Best Local Similarity   98.9%;  Pred. No. 0;
  Matches  887;  Conservative    1;  Mismatches    0;  Indels    9;  Gaps    1;

Qy          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
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Qy         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 155

Qy        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
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Db        156 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 215

Qy        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
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Db        216 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 275

Qy        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
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Db        276 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 335

Qy        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
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Qy        361 HLKALHTCSPT---------NQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 411
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Qy        532 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 591
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Qy        592 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 651
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Db        636 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 695

Qy        652 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 711
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Db        696 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 755

Qy        712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 771
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Db        756 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 815

Qy        772 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        816 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 875

Qy        832 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        876 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 932


RESULT 9
US-10-661-629-7
; Sequence 7, Application US/10661629
; Publication No. US20040180405A1
; GENERAL INFORMATION:
;  APPLICANT: JENTSCH, Thomas
;  TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNE
;  FILE REFERENCE: 2815-0236P
;  CURRENT APPLICATION NUMBER: US/10/661,629
;  CURRENT FILING DATE:  2003-09-15
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 854
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-661-629-7

  Query Match             94.6%;  Score 4300.5;  DB 16;  Length 854;
  Best Local Similarity   98.8%;  Pred. No. 1.1e-307;
  Matches  841;  Conservative    1;  Mismatches    0;  Indels    9;  Gaps    1;

Qy          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60

Qy         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120

Qy        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180

Qy        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300

Qy        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360

Qy        361 HLKALHTCSPT---------NQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 411
              |||||||||||         :|||||||||||||||||||||||||||||||||||||||
Db        361 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420

Qy        412 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480

Qy        472 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy        532 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600

Qy        592 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 651
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660

Qy        652 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 711
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 720

Qy        712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780

Qy        772 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840

Qy        832 VGPEETETDTF 842
              ||||||||||| 
Db        841 VGPEETETDTF 851


RESULT 10
US-09-866-020-31
; Sequence 31, Application US/09866020
; Publication No. US20020040000A1
; GENERAL INFORMATION:
;  APPLICANT: DWORETZKY, STEVEN I
;  APPLICANT:  RAMANATHAN, CHANDRA S
;  APPLICANT:  TROJNACKI, JOANNE T
;  APPLICANT:  BOISSARD, CHRISTOPHER G
;  APPLICANT:  GRIBKOFF, VALENTIN K
;  TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 3053-4091US1
;  CURRENT APPLICATION NUMBER: US/09/866,020
;  CURRENT FILING DATE:  2001-05-24
;  PRIOR APPLICATION NUMBER: 60/207,389
;  PRIOR FILING DATE: 2000-05-26
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-866-020-31

  Query Match             43.7%;  Score 1985;  DB 9;  Length 695;
  Best Local Similarity   60.3%;  Pred. No. 3.2e-137;
  Matches  409;  Conservative   76;  Mismatches  101;  Indels   92;  Gaps   13;

Qy         35 GGGGGLRESRRGKQGARMSLLGKPL----------SYTSSQSCRRNVKYRRVQNYL 80
              ||||  |         |: ||| ||              |    :|   : :|||:||::
Db         37 GGGGSPR---------RLGLLGSPLPPGAPLPGPGSGSGSACGQRSSAAHKRYRRLQNWV 87

Qy         81 YNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEF 140
              ||||||||||||:|| |:||||| ||:||| ||| || :||: ||||||||||||||||:
Db         88 YNVLERPRGWAFVYHVFIFLLVFSCLVLSVLSTIQEHQELANECLLILEFVMIVVFGLEY 147

Qy        141 IIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLR 200
              |:|:|||||||||||||| |||||||||| || :||:||::| |||||||||||||:|
Db        148 IVRVWSAGCCCRYRGWQGRFRFARKPFCVIDFIVFVASVAVIAAGTQGNIFATSALRSMR 207

Qy        201 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKEF 260
              ||||||||||||||||||||||||||||||||||||||||:|||||| ||||| :|
Db        208 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFASFLVYLAEKDANSDF 267

Qy        261 STYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQ 320
              |:|||:|||||||||||||||||| |||||:|:||||||||||||||||||||||||||
Db        268 SSYADSLWWGTITLTTIGYGDKTPHTWLGRVLAAGFALLGISFFALPAGILGSGFALKVQ 327

Qy        321 EQHRQKHFEKRRNPAANLIQCVWRSYAAD-EKSVSIATW---------------------- 358
              |||||||||||| |||||||  || |: |  ::   |||
Db        328 EQHRQKHFEKRRMPAANLIQAAWRLYSTDMSRAYLTATWYYYDSILPSFRELALLFEHVQ 387

Qy        359 ------------------------KPHLKALHT------CSPTNQKLSFKERVRMASPRG 388
                                     | :  |       |   : ::  |:|:|| | :
Db        388 RARNGGLRPLEVRRAPVPDGAPSRYPPVATCHRPGSTSFCPGESSRMGIKDRIRMGSSQR 447

Qy        389 QSIKSRQ--ASVGDRRSPSTDITAEG-SPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVID 445
              ::  |:|  |       |||::   |  ||||||||||||||||| ||||     ||
Db        448 RTGPSKQQLAPPTMPTSPSSEQVGEATSPTKVQKSWSFNDRTRFRASLRL-----KPRTS 502

Qy        446 ADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDV 505
              |: |  :::| :||  ||:::|:|: | :|||||:|||:|| ||||||||||||||||||
Db        503 AEDA-PSEEVAEEKSYQCELTVDDIMPAVKTVIRSIRILKFLVAKRKFKETLRPYDVKDV 561

Qy        506 IEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSRE---KITAEHETTDDLSMLGRV 562
              |||||||||||| ||||||||||:|:|    |:|:||   |  :: |  |::||:|||
Db        562 IEQYSAGHLDMLGRIKSLQTRVDQIVGRG--PGDRKAREKGDKGPSDAEVVDEISMMGRV 619

Qy        563 VKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFECEQTSDYQSPVDSKDL 622
              |||||||||| ||| ||  | : || |::  :| : |:| |: : |||| |||| :|:
Db        620 VKVEKQVQSIEHKLDLLLGFYSRCLRSGTSA--SLGAVQVPLFDPDITSDYHSPVDHEDI 677

Qy        623 SGSAQNSGCLSRSTSANI 640
              | |||    :||| | |:
Db        678 SVSAQTLS-ISRSVSTNM 694


RESULT 11
US-09-810-796-15
; Sequence 15, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
;  APPLICANT: Jegla, Timothy James
;  APPLICANT:  ICAgen, Inc.
;  TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
;  FILE REFERENCE: 018512-005010US
;  CURRENT APPLICATION NUMBER: US/09/810,796
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: US 60/190,954
;  PRIOR FILING DATE: 2000-03-21
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: human KCNQ4
US-09-810-796-15

  Query Match             43.7%;  Score 1985;  DB 9;  Length 695;
  Best Local Similarity   60.3%;  Pred. No. 3.2e-137;
  Matches  409;  Conservative   76;  Mismatches  101;  Indels   92;  Gaps   13;

Qy         35 GGGGGLRESRRGKQGARMSLLGKPL----------SYTSSQSCRRNVKYRRVQNYL 80
              ||||  |         |: ||| ||              |    :|   : :|||:||::
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Db         37 GGGGSPR---------RLGLLGSPLPPGAPLPGPGSGSGSACGQRSSAAHKRYRRLQNWV 87

Qy         81 YNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEF 140
              |||||||||||:|| |:||||| ||:||| ||| || :||: |||||||||||||||:
Db         88 YNVLERPRGWAFVYHVFIFLLVFSCLVLSVLSTIQEHQELANECLLILEFVMIVVFGLEY 147

Qy        141 IIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLR 200
              |:|:|||||||||||||| |||||||||| || :||:||::| |||||||||||||:|
Db        148 IVRVWSAGCCCRYRGWQGRFRFARKPFCVIDFIVFVASVAVIAAGTQGNIFATSALRSMR 207

Qy        201 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKEF 260
              |||||||||||||||||||||||||||||||||||||||||||:|||||| ||||| :|
Db        208 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFASFLVYLAEKDANSDF 267

Qy        261 STYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQ 320
              |:|||:|||||||||||||||| |||||:|:|||||||||||||||||||||||||||||
Db        268 SSYADSLWWGTITLTTIGYGDKTPHTWLGRVLAAGFALLGISFFALPAGILGSGFALKVQ 327

Qy        321 EQHRQKHFEKRRNPAANLIQCVWRSYAAD-EKSVSIATW---------------------- 358
              |||||||||||| ||||||| || |: |  ::   |||
Db        328 EQHRQKHFEKRRMPAANLIQAAWRLYSTDMSRAYLTATWYYYDSILPSFRELALLFEHVQ 387

Qy        359 -----------------------KPHLKALHT------CSPTNQKLSFKERVRMASPRG 388
                                    | :  |       |   : ::  |:|:|| | :
Db        388 RARNGGLRPLEVRRAPVPDGAPSRYPPVATCHRPGSTSFCPGESSRMGIKDRIRMGSSQR 447

Qy        389 QSIKSRQ--ASVGDRRSPSTDITAEG-SPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVID 445
              ::  |:|  |      |||::   |  ||||||||||||||||| ||||     ||
Db        448 RTGPSKQQLAPPTMPTSPSSEQVGEATSPTKVQKSWSFNDRTRFRASLRL-----KPRTS 502

Qy        446 ADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDV 505
              |: |  :::| :||  ||:::|:|: | :|||||:|||:|| ||||||||||||||||||
Db        503 AEDA-PSEEVAEEKSYQCELTVDDIMPAVKTVIRSIRILKFLVAKRKFKETLRPYDVKDV 561

Qy        506 IEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSRE---KITAEHETTDDLSMLGRV 562
              |||||||||||| ||||||||||||:|:|    |:|:||   |  :: |  |::||:|||
Db        562 IEQYSAGHLDMLGRIKSLQTRVDQIVGRG--PGDRKAREKGDKGPSDAEVVDEISMMGRV 619

Qy        563 VKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFECEQTSDYQSPVDSKDL 622
              |||||||||||| ||| ||  | : || |:::  :| : |:| |: : |||| |||| :|:
Db        620 VKVEKQVQSIEHKLDLLLGFYSRCLRSGTSA--SLGAVQVPLFDPDITSDYHSPVDHEDI 677

Qy        623 SGSAQNSGCLSRSTSANI 640
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Db        678 SVSAQTLS-ISRSVSTNM 694
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RESULT 12
US-10-353-690-56
; Sequence 56, Application US/10353690
; Publication No. US20030215840A1
; GENERAL INFORMATION:
;  APPLICANT: Logan, Thomas Joseph
;  APPLICANT:  Chun, Miyoung
;  APPLICANT:  Galvin, Katherine M.
;  APPLICANT:  Healy, Aileen
;  APPLICANT:  Acton, Susan L.
;  APPLICANT:  Donoghue, Mary
;  APPLICANT:  Stagliano, Nancy
;  APPLICANT:  Perodin, Jacquelin
;  APPLICANT:  Rodrigue-Way, Amelie
;  TITLE OF INVENTION: Methods and compositions for treating
;  TITLE OF INVENTION:  cardiovascular disease using 1682, 6169, 6193, 7771, 14395,
;  TITLE OF INVENTION:  29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 1720,
;  TITLE OF INVENTION:  9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
;  TITLE OF INVENTION:  14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,
;  TITLE OF INVENTION:  10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,
;  TITLE OF INVENTION:  283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
;  TITLE OF INVENTION:  51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,
;  TITLE OF INVENTION:  9792, 15400, 1452 or 6585 molecules
;  FILE REFERENCE: MPI02-018P1RNOMNIM
;  CURRENT APPLICATION NUMBER: US/10/353,690
;  CURRENT FILING DATE:  2003-01-29
;  PRIOR APPLICATION NUMBER: 60/353,224
;  PRIOR FILING DATE: 2002-02-01
;  PRIOR APPLICATION NUMBER: 60/364,529
;  PRIOR FILING DATE: 2002-03-15
;  PRIOR APPLICATION NUMBER: 60/373,861
;  PRIOR FILING DATE: 2002-04-19
;  PRIOR APPLICATION NUMBER: 60/376,287
;  PRIOR FILING DATE: 2002-04-29
;  PRIOR APPLICATION NUMBER: 60/388,080
;  PRIOR FILING DATE: 2002-06-12
;  PRIOR APPLICATION NUMBER: 60/390,971
;  PRIOR FILING DATE: 2002-06-24
;  PRIOR APPLICATION NUMBER: 60/394,130
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: 60/394,797
;  PRIOR FILING DATE: 2002-07-10
;  PRIOR APPLICATION NUMBER: 60/404,904
;  PRIOR FILING DATE: 2002-08-21
;  PRIOR APPLICATION NUMBER: 60/405,450
;  PRIOR FILING DATE: 2002-08-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 56
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-353-690-56

  Query Match             43.7%;  Score 1985;  DB 15;  Length 695;
  Best Local Similarity   60.3%;  Pred. No. 3.2e-137;
  Matches  409;  Conservative   76;  Mismatches  101;  Indels   92;  Gaps   13;

Qy         35 GGGGGLRESRRGKQGARMSLLGKPL-------------SYTSSQSCRRNVKYRRVQNYL 80
              ||||  |          |: ||| ||              |    :|   : :|||:||::
Db         37 GGGGSPR---------RLGLLGSPLPPGAPLPGPGSGSGSACGQRSSAAHKRYRRLQNWV 87

Qy         81 YNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEF 140
              |||||||||||:|| |:||||| ||:||| ||| || :||: |||||||||||||||:
Db         88 YNVLERPRGWAFVYHVFIFLLVFSCLVLSVLSTIQEHQELANECLLILEFVMIVVFGLEY 147

Qy        141 IIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLR 200
              |:|:|||||||||||||| |||||||||| || :||:||::| |||||||||||||:|
Db        148 IVRVWSAGCCCRYRGWQGRFRFARKPFCVIDFIVFVASVAVIAAGTQGNIFATSALRSMR 207

Qy        201 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKEF 260
              |||||||||||||||||||||||||||||||||||||||||||:|||||| ||||| :|
Db        208 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFASFLVYLAEKDANSDF 267

Qy        261 STYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQ 320
              |:|||:|||||||||||||||| |||||:|:|||||||||||||||||||||||||||||
Db        268 SSYADSLWWGTITLTTIGYGDKTPHTWLGRVLAAGFALLGISFFALPAGILGSGFALKVQ 327

Qy        321 EQHRQKHFEKRRNPAANLIQCVWRSYAAD-EKSVSIATW---------------------- 358
              |||||||||||| ||||||| || |: |  ::   |||
Db        328 EQHRQKHFEKRRMPAANLIQAAWRLYSTDMSRAYLTATWYYYDSILPSFRELALLFEHVQ 387

Qy        359 -----------------------KPHLKALHT------CSPTNQKLSFKERVRMASPRG 388
                                    | :  |       |   : ::  |:|:|| | :
Db        388 RARNGGLRPLEVRRAPVPDGAPSRYPPVATCHRPGSTSFCPGESSRMGIKDRIRMGSSQR 447

Qy        389 QSIKSRQ--ASVGDRRSPSTDITAEG-SPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVID 445
              ::  |:|  |      |||::   |  ||||||||||||||||| ||||     ||
Db        448 RTGPSKQQLAPPTMPTSPSSEQVGEATSPTKVQKSWSFNDRTRFRASLRL-----KPRTS 502

Qy        446 ADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDV 505
              |: |  :::| :||  ||:::|:|: | :|||||:|||:|| ||||||||||||||||||
Db        503 AEDA-PSEEVAEEKSYQCELTVDDIMPAVKTVIRSIRILKFLVAKRKFKETLRPYDVKDV 561

Qy        506 IEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSRE---KITAEHETTDDLSMLGRV 562
              |||||||||||| ||||||||||||:|:|    |:|:||   |  :: |  |::||:|||
Db        562 IEQYSAGHLDMLGRIKSLQTRVDQIVGRG--PGDRKAREKGDKGPSDAEVVDEISMMGRV 619
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Qy        563 VKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFECEQTSDYQSPVDSKDL 622
              |||||||||||| ||| ||  | : || |:::  :| : |:| |: : |||| |||| :|:
Db        620 VKVEKQVQSIEHKLDLLLGFYSRCLRSGTSA--SLGAVQVPLFDPDITSDYHSPVDHEDI 677

Qy        623 SGSAQNSGCLSRSTSANI 640
              | |||    :||| | |:
Db        678 SVSAQTLS-ISRSVSTNM 694
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RESULT 13
US-10-661-629-6
; Sequence 6, Application US/10661629
; Publication No. US20040180405A1
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANN
; FILE REFERENCE: 2815-0236P
; CURRENT APPLICATION NUMBER: US/10/661,629
; CURRENT FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-661-629-6

Query Match 43.7%; Score 1985; DB 16; Length 695;
Best Local Similarity 60.3%; Pred. No. 3.2e-137;
Matches 409; Conservative 76; Mismatches 101; Indels 92; Gaps 13;

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Qy         35 GGGGGLRESRRGKQGARMSLLGKPL-------------SYTSSQSCRRNVKYRRVQNYL 80
              ||||  |          |: ||| ||              |    :|   : :|||:||::
Db         37 GGGGSPR---------RLGLLGSPLPPGAPLPGPGSGSGSACGQRSSAAHKRYRRLQNWV 87

Qy         81 YNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEF 140
              |||||||||||:|| |:||||| ||:||| ||| || :||: |||||||||||||||:
Db         88 YNVLERPRGWAFVYHVFIFLLVFSCLVLSVLSTIQEHQELANECLLILEFVMIVVFGLEY 147

Qy        141 IIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLR 200
              |:|:|||||||||||||| |||||||||| || :||:||::| |||||||||||||:|
Db        148 IVRVWSAGCCCRYRGWQGRFRFARKPFCVIDFIVFVASVAVIAAGTQGNIFATSALRSMR 207

Qy        201 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKEF 260
              |||||||||||||||||||||||||||||||||||||||||||:|||||| ||||| :|
Db        208 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFASFLVYLAEKDANSDF 267

Qy        261 STYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQ 320
              |:|||:|||||||||||||||| |||||:|:||||||||||||||||||||||||||||
Db        268 SSYADSLWWGTITLTTIGYGDKTPHTWLGRVLAAGFALLGISFFALPAGILGSGFALKVQ 327

Qy        321 EQHRQKHFEKRRNPAANLIQCVWRSYAAD-EKSVSIATW---------------------- 358
              |||||||||||| |||||||  || |: |  ::   |||
Db        328 EQHRQKHFEKRRMPAANLIQAAWRLYSTDMSRAYLTATWYYYDSILPSFRELALLFEHVQ 387

Qy        359 -----------------------KPHLKALHT------CSPTNQKLSFKERVRMASPRG 388
                                    | :   |       |   : ::  |:|:|| | :
Db        388 RARNGGLRPLEVRRAPVPDGAPSRYPPVATCHRPGSTSFCPGESSRMGIKDRIRMGSSQR 447

Qy        389 QSIKSRQ--ASVGDRRSPSTDITAEG-SPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVID 445
              ::  |:|  |      |||::   |  |||||||||||||||| ||||     ||
Db        448 RTGPSKQQLAPPTMPTSPSSEQVGEATSPTKVQKSWSFNDRTRFRASLRL-----KPRTS 502

Qy        446 ADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDV 505
              |: |  :::| :||  ||:::|:|: | :|||||:|||:|| ||||||||||||||||
Db        503 AEDA-PSEEVAEEKSYQCELTVDDIMPAVKTVIRSIRILKFLVAKRKFKETLRPYDVKDV 561

Qy        506 IEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSRE---KITAEHETTDDLSMLGRV 562
              |||||||||||| ||||||||||:|:|    |:|:||   |  :: |  |::||:|||
Db        562 IEQYSAGHLDMLGRIKSLQTRVDQIVGRG--PGDRKAREKGDKGPSDAEVVDEISMMGRV 619

Qy        563 VKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFECEQTSDYQSPVDSKDL 622
              |||||||||||| ||| ||  | : || |:::  :| : |:| |: : |||| |||| :|:
Db        620 VKVEKQVQSIEHKLDLLLGFYSRCLRSGTSA--SLGAVQVPLFDPDITSDYHSPVDHEDI 677

Qy        623 SGSAQNSGCLSRSTSANI 640
              | |||    :||| | |:
Db        678 SVSAQTLS-ISRSVSTNM 694
```

RESULT 14
US-10-850-928-2
; Sequence 2, Application US/10850928
; Publication No. US20050037460A1
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas J.
; TITLE OF INVENTION: POTASSIUM CHANNELS AND GENES ENCODING THESE
; TITLE OF INVENTION: POTASSIUM CHANNELS
; FILE REFERENCE: 2815-127PUS2
; CURRENT APPLICATION NUMBER: US/10/850,928
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: 09/492,361
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-850-928-2

Query Match 43.7%; Score 1985; DB 17; Length 695;
Best Local Similarity 60.3%; Pred. No. 3.2e-137;
Matches 409; Conservative 76; Mismatches 101; Indels 92; Gaps 13;

```
Qy         35 GGGGGLRESRRGKQGARMSLLGKPL-------------SYTSSQSCRRNVKYRRVQNYL 80
              ||||  |          |: ||| ||              |    :|   : :|||:||::
Db         37 GGGGSPR---------RLGLLGSPLPPGAPLPGPGSGSGSACGQRSSAAHKRYRRLQNWV 87

Qy         81 YNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEF 140
              |||||||||||:|| |:||||| ||:||| ||| || :||: |||||||||||||||:
Db         88 YNVLERPRGWAFVYHVFIFLLVFSCLVLSVLSTIQEHQELANECLLILEFVMIVVFGLEY 147

Qy        141 IIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLR 200
              |:|:|||||||||||||| |||||||||| || :||:||::| |||||||||||||:|
Db        148 IVRVWSAGCCCRYRGWQGRFRFARKPFCVIDFIVFVASVAVIAAGTQGNIFATSALRSMR 207

Qy        201 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKEF 260
              |||||||||||||||||||||||||||||||||||||||||||:|||||| ||||| :|
Db        208 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFASFLVYLAEKDANSDF 267

Qy        261 STYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQ 320
              |:|||:|||||||||||||||| |||||:|:||||||||||||||||||||||||||||
Db        268 SSYADSLWWGTITLTTIGYGDKTPHTWLGRVLAAGFALLGISFFALPAGILGSGFALKVQ 327

Qy        321 EQHRQKHFEKRRNPAANLIQCVWRSYAAD-EKSVSIATW---------------------- 358
              |||||||||||| |||||||  || |: |  ::   |||
Db        328 EQHRQKHFEKRRMPAANLIQAAWRLYSTDMSRAYLTATWYYYDSILPSFRELALLFEHVQ 387

Qy        359 -----------------------KPHLKALHT------CSPTNQKLSFKERVRMASPRG 388
                                    | :   |       |   : ::  |:|:|| | :
Db        388 RARNGGLRPLEVRRAPVPDGAPSRYPPVATCHRPGSTSFCPGESSRMGIKDRIRMGSSQR 447

Qy        389 QSIKSRQ--ASVGDRRSPSTDITAEG-SPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVID 445
              ::  |:|  |      |||::   |  |||||||||||||||| ||||     ||
Db        448 RTGPSKQQLAPPTMPTSPSSEQVGEATSPTKVQKSWSFNDRTRFRASLRL-----KPRTS 502

Qy        446 ADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDV 505
              |: |  :::| :||  ||:::|:|: | :|||||:|||:|| ||||||||||||||||
Db        503 AEDA-PSEEVAEEKSYQCELTVDDIMPAVKTVIRSIRILKFLVAKRKFKETLRPYDVKDV 561

Qy        506 IEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSRE---KITAEHETTDDLSMLGRV 562
              |||||||||||| ||||||||||:|:|    |:|:||   |  :: |  |::||:|||
Db        562 IEQYSAGHLDMLGRIKSLQTRVDQIVGRG--PGDRKAREKGDKGPSDAEVVDEISMMGRV 619

Qy        563 VKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFECEQTSDYQSPVDSKDL 622
```

```
                ||||||||||| ||| ||  | : || |:::  :| : |:| |: : |||| |||| :|:
Db        620 VKVEKQVQSIEHKLDLLLGFYSRCLRSGTSA--SLGAVQVPLFDPDITSDYHSPVDHEDI 677

Qy        623 SGSAQNSGCLSRSTSANI 640
              | |||    :||| | |:
Db        678 SVSAQTLS-ISRSVSTNM 694


RESULT 15
US-10-948-493-31
; Sequence 31, Application US/10948493
; Publication No. US20050064491A1
; GENERAL INFORMATION:
;  APPLICANT: DWORETZKY, STEVEN I
;  APPLICANT:  RAMANATHAN, CHANDRA S
;  APPLICANT:  TROJNACKI, JOANNE T
;  APPLICANT:  BOISSARD, CHRISTOPHER G
;  APPLICANT:  GRIBKOFF, VALENTIN K
;  TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: D0023 DIV
;  CURRENT APPLICATION NUMBER: US/10/948,493
;  CURRENT FILING DATE:  2004-09-23
;  PRIOR APPLICATION NUMBER: 60/207,389
;  PRIOR FILING DATE: 2000-05-26
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
;   LENGTH: 695
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-948-493-31

  Query Match           43.7%;  Score 1985;  DB 17;  Length 695;
  Best Local Similarity   60.3%;  Pred. No. 3.2e-137;
  Matches  409;  Conservative   76;  Mismatches  101;  Indels   92;  Gaps   13;

Qy         35 GGGGGLRESRRGKQGARMSLLGKPL----------SYTSSQSCRRNVKYRRVQNYL 80
              ||||  |         |: ||| ||              |    :|   : :|||:||::
Db         37 GGGGSPR---------RLGLLGSPLPPGAPLPGPGSGSGSACGQRSSAAHKRYRRLQNWV 87

Qy         81 YNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEF 140
              ||||||||||||:|| |:||||| ||:||| ||| || :||: |||||||||||||||:
Db         88 YNVLERPRGWAFVYHVFIFLLVFSCLVLSVLSTIQEHQELANECLLILEFVMIVVFGLEY 147

Qy        141 IIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLR 200
              |:|:|||||||||||||| |||||||||| || :||:||::| |||||||||||||:|
Db        148 IVRVWSAGCCCRYRGWQGRFRFARKPFCVIDFIVFVASVAVIAAGTQGNIFATSALRSMR 207

Qy        201 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKEF 260
              ||||||||||||||||||||||||||||||||||||||||||||:|||||| ||||| :|
Db        208 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFASFLVYLAEKDANSDF 267

Qy        261 STYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQ 320
              |:|||:|||||||||||||||| |||||:|:|||||||||||||||||||||||||||||
Db        268 SSYADSLWWGTITLTTIGYGDKTPHTWLGRVLAAGFALLGISFFALPAGILGSGFALKVQ 327

Qy        321 EQHRQKHFEKRRNPAANLIQCVWRSYAAD-EKSVSIATW---------------------- 358
              |||||||||||| |||||||  || |: |  ::   |||
Db        328 EQHRQKHFEKRRMPAANLIQAAWRLYSTDMSRAYLTATWYYYDSILPSFRELALLFEHVQ 387

Qy        359 ------------------------KPHLKALHT------CSPTNQKLSFKERVRMASPRG 388
                                     | :   |       |   : ::  |:|:|| | :
Db        388 RARNGGLRPLEVRRAPVPDGAPSRYPPVATCHRPGSTSFCPGESSRMGIKDRIRMGSSQR 447

Qy        389 QSIKSRQ--ASVGDRRSPSTDITAEG-SPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVID 445
              ::  |:|  |      |||::   |  |||||||||||||||| ||||     ||
Db        448 RTGPSKQQLAPPTMPTSPSSEQVGEATSPTKVQKSWSFNDRTRFRASLRL-----KPRTS 502

Qy        446 ADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDV 505
              |: |  :::| :||  ||:::|:|: | :|||||:|||:|| ||||||||||||||||||
Db        503 AEDA-PSEEVAEEKSYQCELTVDDIMPAVKTVIRSIRILKFLVAKRKFKETLRPYDVKDV 561

Qy        506 IEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSRE---KITAEHETTDDLSMLGRV 562
              |||||||||||| ||||||||||||:|:|    |:|:||   |  :: |  |::||:|||
Db        562 IEQYSAGHLDMLGRIKSLQTRVDQIVGRG--PGDRKAREKGDKGPSDAEVVDEISMMGRV 619

Qy        563 VKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFECEQTSDYQSPVDSKDL 622
              |||||||||||  ||| ||  | : || |:::  :| : |:| |: : |||| |||| :|:
Db        620 VKVEKQVQSIEHKLDLLLGFYSRCLRSGTSA--SLGAVQVPLFDPDITSDYHSPVDHEDI 677

Qy        623 SGSAQNSGCLSRSTSANI 640
              | |||    :||| | |:
Db        678 SVSAQTLS-ISRSVSTNM 694


Search completed: April  8, 2005, 16:46:17
Job time : 155 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 8, 2005, 16:32:30 ; Search time 50 Seconds
(without alignments)
1708.810 Million cell updates/sec

Title: US-09-810-796-5
Perfect score: 4547
Sequence: 1 MKDVESGRGRVLLNSAAARG.....SICKAGESTDALSLPHVKLK 888

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1226.5	27.0	393	2	JC5275	voltage-gated pota
2	1226	27.0	744	2	T34116	voltage-gated pota
3	950	20.9	645	2	T27186	hypothetical prote
4	423.5	9.3	664	2	T28852	probable potassium
5	291.5	6.4	858	2	S31761	potassium channel
6	289	6.4	853	1	CHRTD1	potassium channel
7	279	6.1	857	2	I56529	potassium channel
8	272	6.0	802	2	JH0595	potassium channel
9	248.5	5.5	528	2	T34417	delayed rectifier
10	248.5	5.5	924	2	B41359	potassium channel
11	245	5.4	484	2	T24238	hypothetical prote
12	245	5.4	581	2	S17150	potassium channel
13	242.5	5.3	490	2	T26983	hypothetical prote
14	242	5.3	613	2	A39402	potassium channel
15	242	5.3	624	2	S22703	voltage-gated pota
16	241.5	5.3	344	2	E90564	potassium channel
17	241	5.3	263	2	AI2384	hypothetical prote
18	238	5.2	654	2	S11049	potassium channel
19	237	5.2	523	2	A38101	potassium channel
20	237	5.2	525	2	A43531	potassium channel
21	235.5	5.2	625	2	S13919	potassium channel
22	235.5	5.2	660	2	S24125	potassium channel
23	235	5.2	924	2	S12746	potassium channel
24	234	5.1	643	2	S00480	potassium channel
25	234	5.1	653	2	A39922	potassium channel
26	233.5	5.1	656	2	JH0193	potassium channel
27	232	5.1	528	2	I84205	potassium channel
28	231.5	5.1	769	2	I56546	Shaw type potassiu
29	230	5.1	280	2	E75470	probable ion trans
30	230	5.1	495	2	B39113	potassium channel
31	229.5	5.0	495	2	I57680	potassium channel
32	228.5	5.0	511	2	A46020	potassium channel
33	228.5	5.0	511	2	S07095	potassium channel
34	228	5.0	651	2	A39372	potassium channel
35	227.5	5.0	630	2	JU0271	voltage-sensitive
36	226.5	5.0	558	2	T23991	hypothetical prote
37	226	5.0	495	2	A40090	potassium channel
38	225.5	5.0	585	2	A39395	delayed rectifier
39	224	4.9	679	2	A42073	potassium channel
40	223.5	4.9	602	2	JH0166	potassium voltage-
41	222.5	4.9	490	2	A35312	potassium channel
42	221.5	4.9	295	2	C72692	probable potassium
43	220.5	4.8	597	2	S51212	BAK5 protein - bov
44	219	4.8	361	2	S19552	potassium channel
45	215.5	4.7	460	2	T27759	hypothetical prote

ALIGNMENTS

RESULT 1
JC5275
voltage-gated potassium channel protein - human
C;Species: Homo sapiens (man)
C;Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: JC5275
R;Yokoyama, M.; Nishi, Y.; Yoshii, J.; Okubo, K.; Matsubara, K.
DNA Res. 3, 311-320, 1996
A;Title: Identification and cloning of neuroblastoma-specific and nerve tissue-specific
A;Reference number: JC5272; MUID:97191543; PMID:9039501
A;Contents: neuroblastma cell
A;Accession: JC5275
A;Molecule type: mRNA
A;Residues: 1-393 <YOK>
A;Cross-references: UNIPROT:O43526; DDBJ:D82346; NID:g1841341; PIDN:BAA11557.1; PID:d101

Query Match 27.0%; Score 1226.5; DB 2; Length 393;
Best Local Similarity 69.2%; Pred. No. 2.1e-73;
Matches 238; Conservative 33; Mismatches 56; Indels 17; Gaps 4;

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Qy         17 AARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLSYTSSQSCRRNVKYRRV 76
              :|   ||:|:|  |       |  | : | |  ||     |||         :|| ||::
Db         34 STRDGALLIAGSEAPK---RGSILSKPRAGGAGA-----GKP--------PKRNAFYRKL 77

Qy         77 QNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVF 136
              ||:|||||||||||||||:|||||| ||:|||||| |: | :   | ||| | ||||
Db         78 QNFLYNVLERPRGWAFIYHAYVFLLVFSCLVLSVFSTIKEYEKSSEGALYILEIVTIVVF 137

Qy        137 GLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSAL 196
              |:|: :|||:||||||||||:|||:|||||||||| :||||||||::| :|||:||||||
Db        138 GVEYFVRIWAAGCCCRYRGWRGRLKFARKPFCVIDIMVLIASIAVLAAGSQGNVFATSAL 197

Qy        197 RSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDA 256
              |||||||||||:||||||||||||||||||||||:|||||||| || :|||||| ||
Db        198 RSLRFLQILRMIRMDRRGGTWKLLGSVVYAHSKELVTAWYIGFLCLILASFLVYLAEKGE 257

Qy        257 NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFA 316
              |  | |||||||| |||||||||| | || ||||:| | |:|:|||||||||||||||||
Db        258 NDHFDTYADALWWGLITLTTIGYGDKYPQTWNGRLLAATFTLIGVSFFALPAGILGSGFA 317

Qy        317 LKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSI-ATWK 359
              |||||||||||||||||| |||  || || :     : :||:
Db        318 LKVQEQHRQKHFEKRRNPAAGLIQSAWRFYATNLSRTDLHSTWQ 361
```

RESULT 2
T34116
voltage-gated potassium channel klq-1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C;Accession: T34116
R;Wilcox, L.

submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid C25B8.
A;Reference number: Z21479
A;Accession: T34116
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-744 <WIL>
A;Cross-references: EMBL:U41556; PIDN:AAC70874.1; GSPDB:GN00028; CESP:C25B8.1
A;Experimental source: strain Bristol N2; clone C25B8
C;Genetics:
A;Gene: klq-1; CESP:C25B8.1
A;Map position: X
A;Introns: 31/3; 64/1; 81/3; 131/2; 161/3; 204/1; 262/3; 304/3; 341/3; 402/2; 426/1; 477

Query Match 27.0%; Score 1226; DB 2; Length 744;
Best Local Similarity 41.1%; Pred. No. 5.9e-73;
Matches 276; Conservative 121; Mismatches 184; Indels 90; Gaps 17;

```
Qy         40 LRESRRGKQGARMSLLGKPLSYTSSQSCRRNVKYRRVQNYLYNVLERPRGW-AFIYHAFV 98
              |  :|   | :  :|||:||||:|   :: | : ::||:|| ::| ||||||| |  ||  |
Db         77 LHDSEEGNR--KMSLVGKPLTY---KNYRTDQRFRRMQNKMHNFLERPRGWKAATYHLAV 131

Qy         99 FLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQG 158
                :|  || ||||||:|:|    |:  |  || | ::    |:| |:|||||  ||||  |
Db        132 LFMVLMCLALSVFSTMPDFEVNATIVLYYLEIVFVIWLATEYICRVWSAGCRSRYRGISG 191

Qy        159 RLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWK 218
              |:|||   :|||| ||::||| |:     | :|| ||:| ||| |||||:|:||| ||||
Db        192 RIRFATSAYCVIDIIVILASITVLCIGATGQVFAASAIRGLRFFQILRMLRIDRRAGTWK 251

Qy        219 LLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIG 278
              ||||||:|| :||:|  |||| |||||||||| ||: | :: |:|||||| |||:|:|
Db        252 LLGSVVWAHRQELLTTVYIGFLGLIFSSFLVYLCEKNTNDKYQTFADALWWGVITLSTVG 311

Qy        279 YGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANL 338
              |||||| || |::::|  |||||||||||||||||||||||:  ||||  :|| ||| |
Db        312 YGDKTPETWPGKIIAAFCALLGISFFALPAGILGSGFALKVQQHQRQKHLIRRRVPAAKL 371

Qy        339 IQCVWRSYAADEKSVSIATWKPHLK------ALHTCSPTNQKLSFKERVRMASPRGQSIK 392
              |||:|| |:|  :| |:|||| ||       | : :|       |:| :: |  ::
Db        372 IQCLWRHYSAAPESTSLATWKIHLARELPPIVKLTPNGSNNATGLINRLRQSTKRTPNLN 431

Qy        393 SRQASVGDRRS----------------PSTDITAEGSPTKVQKSWSFNDRTRFRPSLR-- 434
              ::  :|  : :                ::||:       :  |  :  :::: | :
Db        432 NQNLAVNSQATSKNLSVPRVHDTISLVSTSDISEIEQLGALGFSLGWKSKSKYGGSKKAT 491

Qy        435 ----LKSSQPKPV---IDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFH 487
                  |:|     |    :| : |:|    | :      ::|: || ||  :|||| ::
Db        492 DDSVLQSRMLAPSNAHLDEEEAVG----YQPQ------TIEEFTPALKNCVRAIRRIQLL 541

Qy        488 VAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSREKIT 547
              ||:|||| |:|||||||||||||:|:  |:|::| ::| | |          |: |||
Db        542 VARKKFKEALKPYDVKDVIEQYSAGHVDLQSRVKTVQAKLDFICG--------KNIEKIE 593

Qy        548 AEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFEC 607
               :      :||  |:  :|  |  :: ||| ::::      |  ::  : |     |
Db        594 PK------ISMFTRIATLETTVGKMDKKLDLMVEMLM-----GRQASQRVFSQNTSP--- 639

Qy        608 EQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPNEFSAQTFYALSPTMHS 667
                 ::  |  ::           |:||  : :|  ::       ::|::    || |
Db        640 --RGEFSEPTSARQ---------DLTRSRRSMVSTDMEM------YTARSH---SPGYHG 679

Qy        668 QATQVPISQSD 678
                |  : |:| |
Db        680 DARPI-IAQID 689
```

RESULT 3
T27186
hypothetical protein Y54G9A.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27186

R;Smye, R.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z20324
A;Accession: T27186
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-645 <WIL>
A;Cross-references: UNIPROT:Q9XWG9; EMBL:AL032648; PIDN:CAA21699.1; GSPDB:GN00020; CESP:
A;Experimental source: clone Y54G9A
C;Genetics:
A;Gene: CESP:Y54G9A.3
A;Map position: 2
A;Introns: 56/3; 100/2; 148/1; 411/2; 541/2; 575/3

Query Match 20.9%; Score 950; DB 2; Length 645;
Best Local Similarity 36.2%; Pred. No. 8.2e-55;
Matches 247; Conservative 92; Mismatches 175; Indels 168; Gaps 22;

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Qy         73 YRRVQNYLYNVLERPRGW-AFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFV 131
              || :   :|| |||| ||  |:||  |||:|  |||||| ||: ||:  |:  | ||| |
Db          3 YRAM---IYNCLERPTGWKCFLYHFSVFLIVLICLILSVLSTVEEHSHFAAELLYILEIV 59

Qy        132 MIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVI---------------------- 170
              ::| | :|||:|:|||||  :| |  |||:| |||  :|
Db         60 LVVFFSVEFIVRLWSAGCRSKYIGVYGRLKFVRKPITLIGRFGGRHLQLIRDMLRHGGPS 119

Qy        171 --------DTI-----------------VLIASIAVVS--AKTQGNIFATSA------L 196
                     ||:                  : |: |  :      :  ||   |
Db        120 FCGKRDAGDTVSADSEDAPRRSAGWHMVEIRISKIPKIEIFKSLKIGIFKNFANWNFQQF 179

Qy        197 RSLRFLQILR------------------------MVRMDRRGGTWKLLGSVVYAHSKE 230
              | | | :||:                      :: :     :||||||: | :|
Db        180 RKLEFSKILKKNLAGRVHYWGSATPSSGPDPLDVGCFPKLHQLASFRRLLGSVVFIHRQE 239

Qy        231 LITAWYIGFLVLIFSSFLVYLVEK-----DANKEFSTYADALWWGTITLTTIGYGDKTPL 285
              |||  ||||| |||||: ||| ||      |  : |::|||||||| ||:|||||  |
Db        240 LITTLYIGFLGLIFSSYFVYLAEKDHIGVDGRQAFTSYADALWWGVITMTTIGYGDVVPQ 299

Qy        286 TWLGRLLSAGFALLGISFFALPAGILGSGFALKVQEQHRQKHFNRQIPAAATLIQCLWRC 345
              |||||:::: |::  |||||||||||||||||:: ||||| ::    || ||||:||
Db        300 TWLGRIVASCFSIFAISFFALPAGILGSGFALKVQQKQRQKHFNRQIPAAATLIQCLWRC 359

Qy        346 YAADEKSVSIATWKPHLKAL-HTCSPTNQKLSFKERVRMAS---PRGQSIKSRQASVGD- 400
              :|| || || |||  |:  | |    |:      |    | |    | : :  :|:|: :
Db        360 HAA-EKKVS-ATWNAHIDPLAHETKETHHWNGKKHASSMDSNNLTRKRQLFKKQSSLVNT 417

Qy        401 ---RRSPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDD--- 454
                 : |||||:                      :   | : ::  :    |||
Db        418 FRRKGSPSTDV-----------------------EMGELQQERLLRHERNSDTDDEKR 452

Qy        455 VYDEKGCQCDVSVE-----------------DLTPPLKTVIRAIRIMKFHVAKRKFKET 496
              :|   |  ::  |                  :||   :  |||||  :|: ||:|:|::
Db        453 IY-RVGADIEIDYETEEPTTPTRPQGHISHVCELTDAHRNAIRAIRRVKYFVARRRFQQA 511

Qy        497 LRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSREKITAEHETTDDL 556
               :||||:|||||| |||:|: ||| || |:|| |||       | ||:    |  |
Db        512 RKPYDVRDVIEQYSQGHLNMMVRIKELQRRLDQTLGKPGQYDGKGSRK----GHPVT--- 564

Qy        557 SMLGRVVKVEKQVQSIESKLD----CLLDIYQQVLRKG----SASALALASFQIPPFECE 608
               :  |: ::| |: |:: |::      |  :|: :  :      | |  || |  : |  |
Db        565 -IGSRLSRLELQMSSLDRKVESSNRTLNALYRLMADRNSLTISPSPPALISRPVSPAACL 623

Qy        609 QTSDYQSPVDSKDLSGSAQNSG 630
                |  ||      | |:| ||
Db        624 SPRDQLSPT-----SISSQRSG 640
```

RESULT 4
T28852
probable potassium channel - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C;Accession: T28852

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R;Stellyes, L.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid M60.
A;Reference number: Z20532
A;Accession: T28852
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-664 <STE>
A;Cross-references: EMBL:U39995; PIDN:AAC48062.1; GSPDB:GN00028; CESP:klq-2
A;Experimental source: strain Bristol N2; clone M60
C;Genetics:
A;Gene: CESP:klq-2
A;Map position: X
A;Introns: 72/2; 99/1; 158/1; 201/3; 226/2; 271/1; 328/1; 404/2; 454/3; 520/3; 609/2

  Query Match             9.3%;  Score 423.5;  DB 2;  Length 664;
  Best Local Similarity   25.8%;  Pred. No. 5.2e-20;
  Matches  146;  Conservative   99;  Mismatches  235;  Indels   85;  Gaps   16;

Qy         68 RRNVKYRRVQNYLYNVLERPRGWAFI-YHAFVFLLVFGCLILSVFSTIPEHTKLASSCLL 126
Db         69 QRQRNLRRIRLKVYNFLEKPLNAASAPYHFFIFGLVIANIILGAATN--DNDSTVSKIHF 126

Qy        127 ILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKT 186
Db        127 FLEIFMIVFFILEFAVRLWSVRADAKYRTKYGRLYYLFHTVTLIDILIIPATILLLVFK- 185

Qy        187 QGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSS 246
Db        186 -GHDVDGSTLDTLRFIQILRLFHVDRQMATWKLLRKMIILGKWQLMATYYITLVVGLSLA 244

Qy        247 FLVY----------------LVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGR 290
Db        245 TIVYSTEALAQGIQDNGYGLIVPEGTNATFPTMAHSWWFTAVTVMTVGYGDIYPVGALTK 304

Qy        291 LLSAGFALLGISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADE 350
Db        305 FLVCVLGFIAFCTFQAANTQISVGLTLMMEEENKNQQTNRLRNLAASTIQCWWRYHLA-- 362

Qy        351 KSVSIATWKP---HLKALHTC-------SPTNQKLSFKERVRMASPRGQSIKSRQASVGD 400
Db        363 -----TNWKPPRRYTYFVHVCYKLYVTEERINQNRVLAKKLREKLEKKRPIKKK--SLTH 415

Qy        401 RRSPSTDITAEG----SPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVY 456
Db        416 QNSVTAEILKFGFKGMAKPMLEKQDSF-DKAERKISLR---RTRKRVLFAEAR--NSSVE 469

Qy        457 DEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKET-------LRPYDVKDVIEQY 509
Db        470 TSMSSSVDVS------ELETQFEITNFLEQNVDELSSKGNQSGRSLLWKPQGSTLAQTQR 523

Qy        510 SAGHLDML------------CRIKSLQTRVDQILGKGQITSDKKSREKITAEHETTDDLS 557
Db        524 IAGQLLMIEAEIAERENQRNQKMKELEAAILELTGKPTVSPFDDSGQK----------LS 573

Qy        558 MLGRVVKVEKQVQSIESKLDCLLDI 582
Db        574 IIERLEFCEKRMEDLERKTDALNEI 598


RESULT 5
S31761
potassium channel protein DRK1 - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S31761
R;Albrecht, B.; Lorra, C.; Stocker, K.; Pongs, O.
submitted to the EMBL Data Library, September 1992
A;Description: Cloning, expression and chromosomal localization of the delayed rectifier
A;Reference number: S31761
A;Accession: S31761
A;Molecule type: DNA
A;Residues: 1-858 <ALB>
A;Cross-references: UNIPROT:Q14721; EMBL:X68302; NID:g30892; PIDN:CAA48374.1; PID:g30893
C;Genetics:
A;Gene: GDB:KCNB1; KV2.1; DRK1
A;Cross-references: GDB:128081; OMIM:600397
A;Map position: 20q13.2-20q13.2
C;Superfamily: potassium channel protein drk1

  Query Match             6.4%;  Score 291.5;  DB 2;  Length 858;
  Best Local Similarity   20.2%;  Pred. No. 4e-11;
  Matches  176;  Conservative  127;  Mismatches  301;  Indels  267;  Gaps   33;

Qy         80 LYNVLERPRGWA---FIYHAFVFLLVFGCLILSVFSTIPEHTKL-------ASSCLLILE 129
Db        175 LWDLLEKPNSSVAAKILAIISIMFIVLSTIALSL-NTLPELQSLDEFGQSTDNPQLAHVE 233

Qy        130 FVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGN 189
Db        234 AVCIAWFTMEYLLRFLSSP-----KKW----KFFKGPLNAIDLLAILPYYV--------T 276

Qy        190 IFATSALRSL------------RFLQILRMVRMDRRGGTWKLLGSVVYAHSKEL-ITAW 235
Db        277 IFLTESNKSVLQFQNVRRVVQIFRIMRILRILKLARHSTGLQSLGFTLRRSYNELGLLIL 336

Qy        236 YIGFLVLIFSSFLVYLVEKDA-NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSA 294
Db        337 FLAMGIMIFSS-LVFFAEKDEDDTKFKSIPASFWWATITMTTVGYGDIYPKTLLGKIVGG 395

Qy        295 GFALLGISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVS 354
Db        396 LCCIAGVLVIALPIPIIVNNFSEFYKEQKRQEKAIKRR-----------EALERAKRNGS 444

Qy        355 IATWKPHLKALHTCSPTNQKLSFKERVRM----ASPRGQSIKSRQASVGDRRSPSTDITA 410
Db        445 IVS-------------MNMKDAFARSIEMMDIVVEKNGENMGKKDKVQDNHLSPNKWKWT 491

Qy        411 EGSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDL 470
Db        492 KRTLSETSSSKSFETKEQGSPEKARSSSSPQHL----NVQQLEDMYNKMA---------- 537

Qy        471 TPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQI 530
Db        538 ----KTQSQPILNTKESAAQSKPKEELEMESIPS-------------PVAPLPTRTEGV 579

Qy        531 LGKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKG 590
Db        580 I-------DMRS-------------------------MSSIDSFISCATD-FPEATRFS 605

Qy        591 SASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTP 650
Db        606 HSPLTSLPS---------KTGGSTAP--EVGWRGALGASG--GRFVEANPS--------P 644

Qy        651 NEFSAQTFYALSP--------TMHSQATQVPISQSD-----------------GSAVAA 684
Db        645 DASQHSSFFIESPKSSMKTNNPLKLRALKVNFMEGDPSPLLPVLGMYHDPLRNRGSAAAA 704

Qy        685 T-----NTIANQINTAPKPAAPTTLQIPPPLPAIKHLPRPETLHPN-----PAGLQESIS 734
Db        705 VAGLECATLLDKAVLSPESSIYTTASAKTP-------PRSPEKHTAIAFNFEAGVHQYI- 756

Qy        735 DVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETLLSVCPMVPKDLGKSLSVQNLIRS 794
Db        757 DADT-------------------------DDEGQLLYSVDSSPPKSLPGSTSPK----- 785

Qy        795 TEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEEVGPEETETDTFDAAPQPAREAAF 854
Db        786 -----------FSTGTRSEKNHF-------------------ESSPLPTSPKFLRQNCI 814

Qy        855 ASDSLRTGRSRSSQSICKAGE--STDALSLP 883
Db        815 YSTEALTGKGPSGQEKCKLENHISPDVRVLP 845


RESULT 6
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```
CHRTD1
potassium channel protein drk1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S05448; A44838
R;Frech, G.C.; VanDongen, A.M.J.; Schuster, G.; Brown, A.M.; Joho, R.H.
Nature 340, 642-645, 1989
A;Title: A novel potassium channel with delayed rectifier properties isolated from rat b
A;Reference number: S05448; MUID:89365157; PMID:2770868
A;Accession: S05448
A;Molecule type: mRNA
A;Residues: 1-853 <FRE>
A;Cross-references: UNIPROT:P15387; EMBL:X16476; NID:g57785; PIDN:CAA34497.1; PID:g57786
A;Note: it is uncertain whether Met-1 or Met-17 is the initiator
R;Drewe, J.A.; Verma, S.; Frech, G.; Joho, R.H.
J. Neurosci. 12, 538-548, 1992
A;Title: Distinct spatial and temporal expression patterns of K+ channel mRNAs from diff
A;Reference number: A44838; MUID:92156897; PMID:1740690
A;Accession: A44838
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 'MPAG',1-571 <DRE>
A;Cross-references: GB:M81783; NID:g205038
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:81768)
C;Genetics:
A;Gene: drk1
C;Superfamily: potassium channel protein drk1
C;Keywords: glycoprotein; ion channel; phosphoprotein; potassium channel; transmembrane
F;1-182/Domain: intracellular #status predicted <INT1>
F;183-204/Domain: transmembrane #status predicted <TM1>
F;225-245/Domain: transmembrane #status predicted <TM2>
F;256-276/Domain: transmembrane #status predicted <TM3>
F;291-312/Domain: transmembrane #status predicted <TM4>
F;327-348/Domain: transmembrane #status predicted <TM5>
F;389-410/Domain: transmembrane #status predicted <TM6>
F;411-853/Domain: intracellular #status predicted <INT2>
F;279/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             6.4%;  Score 289;  DB 1;  Length 853;
  Best Local Similarity   19.7%;  Pred. No. 5.8e-11;
  Matches  176;  Conservative  134;  Mismatches  269;  Indels  316;  Gaps   37;

Qy         80 LYNVLERPRGWA---FIYHAFVFLLVFGCLILSVFSTIPEHTKL-------ASSCLLILE 129
Db        171 LWDLLEKPNSSVAAKILAIISIMFIVLSTIALSL-NTLPELQSLDEFGQSTDNPQLAHVE 229

Qy        130 FVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGN 189
Db        230 AVCIAWFTMEYLLRFLSSP-----KKW----KFFKGPLNAIDLLAILPYYV--------T 272

Qy        190 IFATSALRSL-------------RFLQILRMVRMDRRGGTWKLLGSVVYAHSKEL-ITAW 235
Db        273 IFLTESNKSVLQFQNVRRVVQIFRIMRILRILKLARHSTGLQSLGFTLRRSYNELGLLIL 332

Qy        236 YIGFLVLIFSSFLVYLVEKDA-NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSA 294
Db        333 FLAMGIMIFSS-LVFFAEKDEDDTKFKSIPASFWWATITMTTVGYGDIYPKTLLGKIVGG 391

Qy        295 GFALLGISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVS 354
Db        392 LCCIAGVLVIALPIPIIVNNFSEFYKEQKRQEKAIKRR---------------------- 429

Qy        355 IATWKPHLKALHTCSPTNQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAEGSP 414
Db        430 ------------------------EALERAKRNGSIV---------------------- 442

Qy        415 TKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLTPPL 474
Db        443 -------SMNMKDAFARSIEM----------------MDIVVEKNG-------------- 465

Qy        475 KTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKG 534
Db        466 ESIAKKDKVQDNHLSPNKWKWT------KRALSETSSS--------KSFETK-------- 503

Qy        535 QITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASA 594
Db        504 EQGSPEKARSSSSPQH---------------LNVQQLE-------DMYSKMAKTQSQPI 540

Qy        595 L---ALASFQIPPPECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 651
Db        541 LNTKEMAPQSKPPEELEMSS-MPSPVAPL----PARTEGVIDMRSMSSID---SFISCAT 592

Qy        652 EFSAQTFYALSP--TMHSQATQVPISQ--------SDGSAVAATNTIANQINT-----AP 696
Db        593 DFPEATRFSHSPLASLSSKAGSSTAPEVGWRGALGASGGRLTETNPIPETSRSGFFVESP 652

Qy        697 KPAAPTTLQIP----------PPLPAIKHLPRPETLHPNP-----------AGLQESIS 734
Db        653 RSSMKTNNPLKLRALKVNFVEGDPTPLLPSL----GLYHDPLRNRGGAAAAVAGL-ECAS 707

Qy        735 DVTTCLVASKENVQVAQSNLTKDRSMRK------SFDMG-----------GETLLSVCP 776
Db        708 LLDKPVLSPESSIYTTASARTPPRSPEKHTAIAFNFEAGVHHYIDTDTDDEGQLLYSVDS 767

Qy        777 MVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEEVGPEE 836
Db        768 SPPKSLHGSTSPK----------------FSTGAR---------------------- 786

Qy        837 TETDTFDAAPQPAR------EAAFASDSLRTGRSRSSQSICKAGEST--DALSLP 883
Db        787 TEKNHFESSPLPTSPKFLRPNCVYSSEGL-TGKGPGAQEKCKLENHTPPDVHMLP 840


RESULT 7
I56529
potassium channel protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I56529
R;Pak, M.D.; Covarrubias, M.; Ratcliffe, A.; Salkoff, L.
J. Neurosci. 11, 869-880, 1991
A;Title: A mouse brain homolog of the Drosophila Shab K+ channel with conserved delayed-r
A;Reference number: I56529; MUID:91162315; PMID:2002364
A;Accession: I56529
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-857 <RES>
A;Cross-references: UNIPROT:Q03717; GB:M64228; NID:g200975; PIDN:AAA40112.1; PID:g200976
C;Genetics:
A;Gene: Shab
C;Superfamily: potassium channel protein drk1

  Query Match             6.1%;  Score 279;  DB 2;  Length 857;
  Best Local Similarity   20.4%;  Pred. No. 2.7e-10;
  Matches  181;  Conservative  124;  Mismatches  280;  Indels  304;  Gaps   37;

Qy         80 LYNVLERPRGWA---FIYHAFVFLLVFGCLILSVFSTIPEHTKL-------ASSCLLILE 129
Db        175 LWDLLEKPNSSVAAKILAIISIMFIVLSTIALSL-NTLPELQSLDEFGQSTDNPQLAHVE 233

Qy        130 FVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGN 189
Db        234 AVCIAWFTMEYLLRFLSSP-----KKW----KFFKGPLNAIDLLAILPYYV--------T 276

Qy        190 IFATSALRSL-------------RFLQILRMVRMDRRGGTWKLLGSVVYAHSKEL-ITAW 235
Db        277 IFLTESNKSVLQFQNVRRVVQIFRIMRILRILKLARHSTGLQSLGFTLRRSYNELGLLIL 336

Qy        236 YIGFLVLIFSSFLVYLVEKDA-NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSA 294
Db        337 FLAMGIMIFSS-LVFFAEKDEDDTKFKSIPASFWWATITMTTVGYGDIYPKTLLGKIVGG 395

Qy        295 GFALLGISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVS 354
Db        396 LCCIAGVLVIALPIPIIVNNFSEFYKEQKRQEKAIKRR----------EALERAKRNGS 444
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```
Qy        355 IATWKPHLKALHTCSPTNQKLSFKERVRM----ASPRGQSIKSRQASVGDRRSPSTDITA 410
Db        445 IVS-------------MNMKDAFARSIEMMDIVVEKNGEGVAKKDKVQDNHLSPNKWKWT 491

Qy        411 EGSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDL 470
Db        492 KRALSETSSSKSFETKEQGSPEKARSSSSPQHL----NVQQLQDMYSK-----MAKTQS 541

Qy        471 TPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQI 530
Db        542 QPILNT----------------KEMAPQSQPQEELEMGS-----MPSPVAPLPTRTEGV 579

Qy        531 LGKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKG 590
Db        580 I-------DMRS-------------------------MSSIDSFISCATDF-------- 598

Qy        591 SASALALASFQIPPPFECEQTSDYQSPVDSKDLSGSAQNS--------GCLSRSTSANISR 642
Db        599 ----------------PEATRFSHSPLAS--LSGKSGGSTAPEVGWRGALGASGGR---- 636

Qy        643 GLQFILTPN---EFSAQTFYALSP--------TMHSQATQVPISQSDGSAVAATNTIANQ 691
Db        637 ----LMETNPIPEASRSGFFVESPRSSMKTHNPMKLRALKVNFLEGD------------- 679

Qy        692 INTAPKPAAPTTLQIPPPLPAIKHLPRPETLHPNP----------AGLQESISDVTTCL 740
Db        680 ---------PT-----PLLPAL-------GLYHDPLRNRGGARAAVAGL-ECASLLDKPV 717

Qy        741 VASKENVQVAQSNLTKDRSMRK------SFDMG-----------GETLLSVCPMVPKDL 782
Db        718 LSPESSIYTTASARTPPRSPEKHTAIAFNFEAGVHQYITDTDTDDEGQLLYSVDSSLPKSL 777

Qy        783 GKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEEVGPEETETDTF 842
Db        778 HGSTSPK----------------FSLGAR-------------------------TEKNHF 796

Qy        843 DAAPQPAR------EAAFASDSLRTGRSRSSQSICKAGEST--DALSLP 883
Db        797 ESSPLPTSPKFLRPNCVYASEGL-PGKGPGAQEKCKLENHTSPDVHMLP 844


RESULT 8
JH0595
potassium channel protein cdrK - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 20-Aug-1999
C;Accession: JH0595
R;Hwang, P.M.; Glatt, C.E.; Bredt, D.S.; Yellen, G.; Snyder, S.H.
Neuron 8, 473-481, 1992
A;Title: A novel K+ channel with unique localizations in mammalian brain: molecular clon
A;Reference number: JH0595; MUID:92198655; PMID:1550672
A;Accession: JH0595
A;Molecule type: mRNA
A;Residues: 1-802 <HWA>
A;Cross-references: GB:M77482; NID:g203395; PIDN:AAA40905.1; PID:g203396
A;Experimental source: circumvallate papillae
C;Superfamily: potassium channel protein drk1
C;Keywords: glycoprotein; phosphoprotein; transmembrane protein
F;191-212/Domain: transmembrane #status predicted <TM1>
F;233-254/Domain: transmembrane #status predicted <TM2>
F;265-286/Domain: transmembrane #status predicted <TM3>
F;299-320/Domain: transmembrane #status predicted <TM4>
F;335-356/Domain: transmembrane #status predicted <TM5>
F;397-418/Domain: transmembrane #status predicted <TM6>
F;187,287,419,446/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;448,500/Binding site: phosphate (Ser) (covalent) #status predicted

  Query Match             6.0%;  Score 272;  DB 2;  Length 802;
  Best Local Similarity   24.4%;  Pred. No. 7e-10;
  Matches  121;  Conservative   82;  Mismatches  191;  Indels  102;  Gaps   21;

Qy         80 LYNVLERPRGWA---FIYHAFVFLLVFGCLILSVFSTIPE-----------HTKLASSC 124
Db        179 LWDLLEKPNSSVAAKILAIVSILFIVLSTIALSL-NTLPELQENDEPGQPSDNRKLAH-- 235

Qy        125 LLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSA 184
Db        236 ---VEAVCIAWFTMEYLLRFLSS---------PNKWKFFKGPLNVIDLLAILPYYV---- 279

Qy        185 KTQGNIFATSALRSL------------RFLQILRMVRMDRRGGTWKLLGSVVYAHSKEL 231
Db        280 ----TIFLTESNKSVLQFQNVRRVVQIFRIMRILRILKLARHSTGLQSLGFTLRRSYNEL 335

Qy        232 -ITAWYIGFLVLIFSSFLVYLVEKDAN-KEFSTYADALWWGTITLTTIGYGDKTPLTWLG 289
Db        336 GLLILFLAMGIMIFSS-LVFFAEKDEDATKFTSIPASFWWATITMTTVGYGDIYPKTLLG 394

Qy        290 RLLSAGFALLGISFFALPAGILGSGFALKVQEQHRQKHFEKRRNP----------AANL 338
Db        395 KIVGGLCCIAGVLVIALPIPIIVNNFSEFYKEQKRQEKAIKRREALERAKRNGSIVSMNL 454

Qy        339 IQCVWRSY----AADEKSVSIATWKPHLKALHTCSPTNQKLSFKERVRMASPRGQSIKSR 394
Db        455 KDAFARSMELIDVAVEKAGESANIKDSVDDNH-LSPSRWKWARKALSETSSNKSYENKYQ 513

Qy        395 QASVGDRRSPSTDITAEGSP--TKVQK-SWSFNDRTRFRPSLRLKSSQPKPVIDADTALG 451
Db        514 EVSQKDSHEQLNN-TSSSSPQHLSAQKLEMLYNEITKTQ-----THSHPNP--DCQEQPE 565

Qy        452 TDDVYDEKGCQCDVSVEDLTPPLKTVIRA----------IRIMKFHVAKRKFKETLRPY 500
Db        566 RPSAYEE-----EIEMEEVVCPQEQLAVAQTEVIVDMKSTSSIDSFTSCATDFTETER-- 618

Qy        501 DVKDVIEQYSAGHLDM 516
Db        619 ---SPLPPPSASHLQM 631


RESULT 9
T34417
delayed rectifier channel protein homolog exp-2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T34417
R;Fulton, B.; Wohldmann, P.
submitted to the EMBL Data Library, July 1998
A;Description: The sequence of C. elegans cosmid F12F3.
A;Reference number: Z21521
A;Accession: T34417
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-528 <FUL>
A;Cross-references: UNIPROT:P91256; EMBL:U80022; PIDN:AAC25887.1; GSPDB:GN00023; CESP:F1
A;Experimental source: strain Bristol N2; clone F12F3
C;Genetics:
A;Gene: exp-2; CESP:F12F3.1
A;Map position: 5
A;Introns: 42/2; 135/3; 173/3; 213/3; 271/3; 469/1

  Query Match             5.5%;  Score 248.5;  DB 2;  Length 528;
  Best Local Similarity   23.5%;  Pred. No. 1.3e-08;
  Matches   72;  Conservative   61;  Mismatches  117;  Indels   57;  Gaps    8;

Qy         75 RVQNYLYNVLERP------RGWAFIYHAFVFLLVFGCLILSVFSTIP---------- 115
Db        226 KLRRRMWTFLERPGSSMQAKAFELSSTLFVAISVMG---LS-FGTIPDFQVTHLMPPHNE 281

Qy        116 --------------EHTKLASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRL 160
Db        282 TVVLPNGTVTVVQKVEQMRVEHPAFVFTERICIAFFTVEYCLRFFAA---------PRKL 332

Qy        161 RFARKPFCVIDTI--------VLIASIAVVSAKTQGNIFATSALRSLRFLQILRMVRMDR 212
Db        333 RFALKPLNLVDLLAIVPFYLELLLTLCGVDDRKLRDLRWAFLVVRILRVLRVIRIIKLGR 392
```

```
Qy        213 RGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKD-ANKEFSTYADALWWGT 271
Db        393 FSSGLQTFGMTLQRSQKQLQMMTIVLLTGVVFFSTMIYFLEKDEEGTPFTSIPAAYWWCI 452

Qy        272 ITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQEQHRQKHFEKR 331
Db        453 VTMTTVGYGDAVPATTMGKIIASAAIMCGVLVLALPITIIVDNF-IKVAQDEQQAEQQKN 511

Qy        332 RNPAANL 338
Db        512 DQQSEQL 518
```

RESULT 10
B41359
potassium channel protein shab11 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 16-Feb-1997
C;Accession: B41359
R;Butler, A.; Wei, A.; Baker, K.; Salkoff, L.
Science 243, 943-947, 1989
A;Title: A family of putative potassium channel genes in Drosophila.
A;Reference number: A41359; MUID:89146139; PMID:2493160
A;Accession: B41359
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-924 <BUT>
A;Cross-references: GB:M32659
C;Genetics:
A;Gene: FlyBase:Shab
A;Cross-references: FlyBase:FBgn0003383
C;Superfamily: potassium channel protein drk1

  Query Match 5.5%; Score 248.5; DB 2; Length 924;
  Best Local Similarity 26.2%; Pred. No. 3.1e-08;
  Matches 98; Conservative 70; Mismatches 153; Indels 53; Gaps 15;

```
Qy         72 KYRRVQNYLYNVLERP------RGWAFIYHAFVFLLVFGCLILSVFSTIPE------HTK 119
Db        413 KFSEYQKYLWELLEKPNTSFAARVIAVISILFIVL----STIALTLNTLPQLQHIDNGTP 468

Qy        120 LASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIA-S 178
Db        469 QDNPQLAMVEAVCITWFTLEYILRFSSS---------PDKWKFFKGGLNIIDLLAILPYF 519

Qy        179 IAVVSAKTQGNIFATSALRSL-------RFLQILRMVRMDRRGGTWKLLGSVVYAHSKEL 231
Db        520 VSLFLLETNKN--ATDQFQDVRRVVQVFRIMRILRVLKLARHSTGLQSLGFTLRNSYKEL 577

Qy        232 -ITAWYIGFLVLIFSSFLVYLVEKD-ANKEFSTYADALWWGTITLTTIGYGDKTPLTWLG 289
Db        578 GLLMLFLAMGVLIFSS-LAYFAEKDEKDTKFVSIPEAFWWAGITMTTVGIRDICPTTALG 636

Qy        290 RLLSAGFALLGISFFALPAGILGSGFALKVQEQHRQKHFEKRRN----PAANLIQCVWRS 345
Db        637 KVIGTVCCICGVLVVALPIPIIVNNFAEFYKNQMRREKALKRREHSIVPSGRGQHCLLPS 696

Qy        346 YAADE---KSVSIATWKPHLKALHTCSPTNQKLSFKERVRMASPR-GQSIKSRQASVGDR 401
Db        697 YQSERSFAKSMDLID-----VIVDTGKQTN--VVHPKGKRQSTPNIGRQTLDVQSAPGHN 749

Qy        402 RSPSTDITAEGSPT 415
Db        750 LSQTDGNSTEGEST 763
```

RESULT 11
T24238
hypothetical protein R186.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24238
R;Barlow, K.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z19861
A;Accession: T24238
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-484 <WIL>
A;Cross-references: UNIPROT:Q22012; EMBL:Z78016; PIDN:CAB01442.1; GSPDB:GN00023; CESP:R18
A;Experimental source: clone R186
C;Genetics:
A;Gene: CESP:R186.5
A;Map position: 5
A;Introns: 30/2; 65/2; 85/3; 128/3; 235/3; 370/3; 409/3; 446/1
C;Superfamily: potassium channel protein drk1

  Query Match 5.4%; Score 245; DB 2; Length 484;
  Best Local Similarity 24.2%; Pred. No. 2e-08;
  Matches 72; Conservative 59; Mismatches 117; Indels 50; Gaps 8;

```
Qy         73 YRRVQNYLYNVLERP---RGWAFIYHAFVFLLVFGCLI------------LSVFSTIPE 116
Db        148 WQKIKPRIWRLFDEPNSSRSAQFIAAISVFFLITAIIVFCLKTHPGLRIPELAPFGNFSR 207

Qy        117 HTKLASS-----------------CLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQG 158
Db        208 NHRSTSSRIHPAQINIDKANSRPHPTFMYIETICNIWFTIEIL---------ARFSSCPS 258

Qy        159 RLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWK 218
Db        259 RFEYLRAPVNIID---IVATLTFYIDLLSSMFGATADLEFFSIIRIMRLFKLTHHNSGLK 315

Qy        219 LLGSVVYAHSKEL-ITAWYIGFLVLIFSSFLVYL--VEKDANKEFSTYADALWWGTITLT 275
Db        316 ILMHTFRASAKELMLLVFFLVLGVVVFASLVYYAERVESNEDNQFVSIPIGLWWAIVTMT 375

Qy        276 TIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQE-QHRQKHFEKRR 332
Db        376 TIGYGDITPHTYLGRLIGSICALAGVLTIALPVPVIVSNFAMFYSHTQARSKMPKKRR 433
```

RESULT 12
S17150
potassium channel protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Feb-2001
C;Accession: S17150
R;Luneau, C.; Wiedmann, R.; Smith, J.S.; Williams, J.B.
FEBS Lett. 288, 163-167, 1991
A;Title: Shaw-like rat brain potassium channel cDNA's with divergent 3' ends.
A;Reference number: S17150; MUID:91348257; PMID:1879548
A;Accession: S17150
A;Molecule type: DNA
A;Residues: 1-581 <LUN>
C;Superfamily: potassium channel protein drk1

  Query Match 5.4%; Score 245; DB 2; Length 581;
  Best Local Similarity 23.3%; Pred. No. 2.6e-08;
  Matches 94; Conservative 79; Mismatches 138; Indels 92; Gaps 17;

```
Qy         35 GGGGGLRESRRGKQGARMSL-----LGKPLSYTSSQSCRRNVKYRRVQNYLYNVLERP-- 87
Db        176 GGDPGDDEDLGGK---RLGIEDAAGLGGPDG--------KSGRWRKLQPRMWALFEDPYS 224

Qy         88 -RGWAFIYHAFVFLLVFG----CL---------------ILSVFSTIPEHTKLASSCLLI 127
Db        225 SRAARFIAFASLFFILVSITTFCLETHEAFNIVKNKTEPVINGTSAVLQYEIETDPALTY 284

Qy        128 LEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLI-----ASIAVV 182
Db        285 VEGVCVVWFTFEFLVRIVFS---------PNKLEFIKNLLNIIDFVAILPFYLEVGLSGL 335

Qy        183 SAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKE-LITAWYIGFLV 241
Db        336 SSKAAKDVL--GFLRVVRFVRILRIFKLTRHFVGLRVLGHTLRASTNEFLLLIIFLALGV 393
```

```
Qy        242 LIFSSFLVYLVEK----------DANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRL 291
              |||:: ::|  |:           : :|        ||  :|:||:||||  | || | |
Db        394 LIFAT-MIYYAERVGAQPNDPSASEHTQFKNIPIGFWWAVVTMTTLGYGDMYPQTWSGML 452

Qy        292 LSAGFALLGISFFALPAGIL----GSGFALKVQEQ----HRQKHF-----------EKR 331
              : |  || |:   |:|  ::     |  ::| : :|     |:||           :
Db        453 VGALCALAGVLTIAMPVPVIVNNFGMYYSLAMAKQKLPRKRKKHIPPAPLASSPTFCKTE 512

Qy        332 RNPAANLIQ---CVWRSYAADEKSVSIATWKPHLKALHTCSPT 371
               | | |  |   |: :     | : |:|:    |: : : | |
Db        513 LNMACNSTQSDTCLGKENRLLEHNRSVAS---TLEPMESTSQT 552


RESULT 13
T26983
hypothetical protein Y48A6B.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26983
R;Gardner, A.
submitted to the EMBL Data Library, June 1998
A;Reference number: Z20295
A;Accession: T26983
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-490 <WIL>
A;Cross-references: UNIPROT:Q9XXD1; EMBL:AL023844; PIDN:CAA19530.1; GSPDB:GN00021; CESP:
A;Experimental source: clone Y48A6B
C;Genetics:
A;Gene: CESP:Y48A6B.6
A;Map position: 3
A;Introns: 34/2; 94/1; 138/1; 175/3; 256/1; 282/1; 365/3; 410/2; 419/1; 429/1; 452/3
C;Superfamily: potassium channel protein drk1

  Query Match             5.3%;  Score 242.5;  DB 2;  Length 490;
  Best Local Similarity   27.1%;  Pred. No. 3e-08;
  Matches   76;  Conservative   63;  Mismatches  110;  Indels   31;  Gaps   10;

Qy         69 RNVKYRRVQNYLYNVLERP----RGWAFIYHAFVFLLV-FGCLILSVFSTIPEHTKLASS 123
              : :::  ::  ::|::| |     :  ||   : ||:|:     |:|      :   ||  ::
Db        192 KTLRFGEIRRCVWNIIEEPASSGKAQAFAVCSVVFVLISISGLVLGSLPELQVATKQRNN 251

Qy        124 ------------CLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLR----FARKP 166
                         |  :|:| || | :|: :::  :    | : ::  |       |  |
Db        252 LTGEEFTEMEPMPILGYIEYVCIVWFTMEYGLKMLVS--AERSKTFRQLLNIIDLLAILP 309

Qy        167 FCVIDTIVLIASIAVVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYA 226
              | :|: ::||  |:    :     |    :| || |:::|:::: |     ::  |  : |
Db        310 F-IIEMLLLIFGISTEQLRDLKGAFL--VIRILRVLRVIRVLKLGRYSSGLQMFGKTLKA 366

Qy        227 HSKELITAWYIGFLVLIFSSFLVYLVEKD--ANKEFSTYADALWWGTITLTTIGYGDKTP 284
                ::|     :    :|| | ||| :|||  |:| | :   | ||  :|:||:|||| ||
Db        367 SFRQLGMMAMVVMTGVIFFSTLVYFLEKDEPASK-FHSIPAACWWCIVTMTTVGYGDLTP 425

Qy        285 LTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQEQHR 324
              :|  |:|:: |    |:   ||| |:   | :|| |  |
Db        426 VTVPGKLVATGAIACGVLVLALPITIIVDNF-MKVAETER 464


RESULT 14
A39402
potassium channel protein IIIA form 1, shaker-type - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 09-Jul-2004
C;Accession: A39402
R;McCormack, T.; Vega-Saenz de Miera, E.C.; Rudy, B.
Proc. Natl. Acad. Sci. U.S.A. 88, 4060, 1991
A;Reference number: A39402; MUID:91219512; PMID:2023956
A;Contents: erratum
A;Accession: A39402
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-613 <MCC>
A;Cross-references: UNIPROT:P22462; GB:M34052; NID:g206913; PIDN:AAA42142.1; PID:g206914
C;Superfamily: potassium channel protein drk1

  Query Match             5.3%;  Score 242;  DB 2;  Length 613;
  Best Local Similarity   24.1%;  Pred. No. 4.5e-08;
  Matches   83;  Conservative   70;  Mismatches  117;  Indels   74;  Gaps   14;

Qy         35 GGGGGLRESRRGKQGARMSL-----LGKPLSYTSSQSCRRNVKYRRVQNYLYNVLERP-- 87
              ||  |  |   ||   |: :     || |          :: ::|::|  :: : | |
Db        176 GGDPGDDEDLGGK---RLGIEDAAGLGGPDG--------KSGRWRKLQPRMWALFEDPYS 224

Qy         88 -RGWAFIYHAFVFLLVFG----CL---------------ILSVFSTIPEHTKLASSCLLI 127
               |   ||  | :| ::      ||               :::  | : ::       |
Db        225 SRAARFIAFASLFFILVSITTFCLETHEAFNIVKNKTEPVINGTSAVLQYEIETDPALTY 284

Qy        128 LEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLI-----ASIAVV 182
              :| | :| |  ||::||  :          :| | :    :|| : ::       :: :
Db        285 VEGVCVVWFTFEFLVRIVFS---------PNKLEFIKNLLNIIDFVAILPFYLEVGLSGL 335

Qy        183 SAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKE-LITAWYIGFLV 241
              |:|   ::     || :||::|||: :: |     ::||  : | : | |:   ::   |
Db        336 SSKAAKDVL--GFLRVVRFVRILRIFKLTRHFVGLRVLGHTLRASTNEFLLLIIFLALGV 393

Qy        242 LIFSSFLVYLVEK----------DANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRL 291
              |||:: ::|  |:           : :|       ||  :|:||:|||| | || | |
Db        394 LIFAT-MIYYAERVGAQPNDPSASEHTQFKNIPIGFWWAVVTMTTLGYGDMYPQTWSGML 452

Qy        292 LSAGFALLGISFFALPAGIL----GSGFALKVQEQ----HRQKH 327
              : |  || |:   |:|  ::    |  ::| : :|     |:||
Db        453 VGALCALAGVLTIAMPVPVIVNNFGMYYSLAMAKQKLPRKRKKH 496


RESULT 15
S22703
voltage-gated potassium channel protein Raw1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-2001
C;Accession: S22703; A45292; S19099
R;Rettig, J.; Wunder, F.; Stocker, M.; Lichtinghagen, R.; Mastiaux, F.; Beckh, S.; Kues,
EMBO J. 11, 2473-2486, 1992
A;Title: Characterization of a shaw-related potassium channel family in rat brain.
A;Reference number: S22702; MUID:92331599; PMID:1378392
A;Accession: S22703
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-624 <RET>
A;Cross-references: EMBL:X62839; NID:g57650; PIDN:CAA44643.1; PID:g57651
R;Rudy, B.; Kentros, C.; Weiser, M.; Fruhling, D.; Serodio, P.; Vega-Saenz de Miera, E.;
Proc. Natl. Acad. Sci. U.S.A. 89, 4603-4607, 1992
A;Title: Region-specific expression of a K+ channel gene in brain.
A;Reference number: A45292; MUID:92262488; PMID:1374908
A;Accession: A45292
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 594-624 <RUD>
A;Note: sequence extracted from NCBI backbone (NCBIN:102300, NCBIP:102305)
C;Superfamily: potassium channel protein drk1
C;Keywords: glycoprotein; ion channel; leucine zipper; transmembrane protein
F;230-248/Domain: transmembrane #status predicted <TM1>
F;282-303/Domain: transmembrane #status predicted <TM2>
F;315-335/Domain: transmembrane #status predicted <TM3>
F;347-365/Domain: transmembrane #status predicted <TM4>
F;382-401/Domain: transmembrane #status predicted <TM5>
F;452-473/Domain: transmembrane #status predicted <TM6>

  Query Match             5.3%;  Score 242;  DB 2;  Length 624;
  Best Local Similarity   24.1%;  Pred. No. 4.6e-08;
  Matches   83;  Conservative   70;  Mismatches  117;  Indels   74;  Gaps   14;

Qy         35 GGGGGLRESRRGKQGARMSL-----LGKPLSYTSSQSCRRNVKYRRVQNYLYNVLERP-- 87
              ||  |  |   ||   |: :     || |          :: ::|::|  :: : | |
Db        176 GGDPGDDEDLGGK---RLGIEDAAGLGGPDG--------KSGRWRKLQPRMWALFEDPYS 224
```

```
Qy          88 -RGWAFIYHAFVFLLVFG----CL---------------ILSVFSTIPEHTKLASSCLLI 127
Db         225 SRAARFIAFASLFFILVSITTFCLETHEAFNIVKNKTEPVINGTSAVLQYEIETDPALTY 284

Qy         128 LEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLI-----ASIAVV 182
Db         285 VEGVCVVWFTFEFLVRIVFS---------PNKLEFIKNLLNIIDFVAILPFYLEVGLSGL 335

Qy         183 SAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKE-LITAWYIGFLV 241
Db         336 SSKAAKDVL--GFLRVVRFVRILRIFKLTRHFVGLRVLGHTLRASTNEFLLLIIFLALGV 393

Qy         242 LIFSSFLVYLVEK----------DANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRL 291
Db         394 LIFAT-MIYYAERVGAQPNDPSASEHTQFKNIPIGFWWAVVTMTTLGYGDMYPQTWSGML 452

Qy         292 LSAGFALLGISFFALPAGIL----GSGFALKVQEQ----HRQKH 327
Db         453 VGALCALAGVLTIAMPVPVIVNNFGMYYSLAMAKQKLPRKRKKH 496
```

Search completed: April 8, 2005, 16:42:50
Job time : 54 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 8, 2005, 16:24:15 ; Search time 187 Seconds
(without alignments)
2431.692 Million cell updates/sec

Title: US-09-810-796-5
Perfect score: 4547
Sequence: 1 MKDVESGRGRVLLNSAAARG.....SICKAGESTDALSLPHVKLK 888

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4527.5	99.6	897	1	CIQ5_HUMAN	Q9nr82 homo sapien
2	4227.5	93.0	878	1	CIQ5_MOUSE	Q9jk45 mus musculu
3	2655.5	58.4	572	2	Q8BSF6	Q8bsf6 mus musculu
4	1985	43.7	695	1	CIQ4_HUMAN	P56696 homo sapien
5	1930	42.4	427	2	Q86W40	Q86w40 homo sapien
6	1803.5	39.7	852	1	CIQ2_RAT	O88943 rattus norv
7	1799.5	39.6	870	2	Q8R498	Q8r498 mus musculu
8	1783	39.2	872	1	CIQ2_HUMAN	O43526 homo sapien
9	1754	38.6	759	1	CIQ2_MOUSE	Q9z351 mus musculu
10	1587.5	34.9	872	1	CIQ3_HUMAN	O43525 homo sapien
11	1556.5	34.2	866	1	CIQ3_BOVIN	P58126 bos taurus
12	1556.5	34.2	873	2	Q8K3F6	Q8k3f6 mus musculu
13	1555.5	34.2	873	1	CIQ3_RAT	O88944 rattus norv
14	1525.5	33.5	523	2	Q8C9Y6	Q8c9y6 mus musculu
15	1364.5	30.0	840	2	Q8IGU8	Q8igu8 drosophila
16	1354	29.8	807	2	Q9V5H6	Q9v5h6 drosophila
17	1329.5	29.2	649	2	Q8IT87	Q8it87 drosophila
18	1321.5	29.1	992	2	Q9V5H7	Q9v5h7 drosophila
19	1226	27.0	692	2	Q967F8	Q967f8 caenorhabdi
20	1226	27.0	740	2	Q8MQC5	Q8mqc5 caenorhabdi
21	1198.5	26.4	459	2	Q7PP97	Q7pp97 anopheles g
22	1181	26.0	409	2	Q9BX08	Q9bx08 homo sapien
23	1145	25.2	621	2	Q9XWG9	Q9xwg9 caenorhabdi
24	1106.5	24.3	512	2	Q7QHB3	Q7qhb3 anopheles g
25	1102	24.2	676	1	CIQ1_HUMAN	P51787 homo sapien
26	1100.5	24.2	668	1	CIQ1_MOUSE	P97414 mus musculu
27	1097.5	24.1	669	1	CIQ1_RAT	Q9z0n7 rattus norv
28	1083.5	23.8	660	1	CIQ1_SQUAC	O73925 squalus aca
29	1064.5	23.4	294	2	Q9BX07	Q9bx07 homo sapien
30	957.5	21.1	612	2	Q8K3P3	Q8k3p3 rattus norv
31	910.5	20.0	440	2	Q8CJG2	Q8cjg2 mus musculu
32	899.5	19.8	377	1	CIQ1_XENLA	P70057 xenopus lae
33	716	15.7	296	2	Q6DKP7	Q6dkp7 cavia porce
34	702	15.4	284	2	Q6DKP6	Q6dkp6 cavia porce
35	647	14.2	276	1	CIQ4_MOUSE	Q9jk97 mus musculu
36	591.5	13.0	172	1	CIQ1_FELCA	O97531 felis silve
37	549.5	12.1	392	2	Q96AI9	Q96ai9 homo sapien
38	538.5	11.8	169	1	CIQ1_CAVPO	O70344 cavia porce
39	486.5	10.7	155	1	CIQ1_RABIT	Q9mys6 oryctolagus
40	452.5	10.0	363	2	Q9BQU4	Q9bqu4 homo sapien
41	446.5	9.8	168	1	CIQ4_RAT	Q9jk96 rattus norv
42	441	9.7	145	2	Q6DKQ1	Q6dkq1 cavia porce
43	437	9.6	97	2	Q9CTU2	Q9ctu2 mus musculu
44	430	9.5	675	2	Q9GYM8	Q9gym8 caenorhabdi
45	424.5	9.3	399	2	Q9BQU5	Q9bqu5 homo sapien

ALIGNMENTS

RESULT 1
CIQ5_HUMAN
ID CIQ5_HUMAN STANDARD; PRT; 897 AA.
AC Q9NR82; Q9NRN0; Q9NYA6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily KQT member 5 (Voltage-gated
DE potassium channel subunit Kv7.5) (Potassium channel alpha subunit
DE KvLQT5) (KQT-like 5).
GN Name=KCNQ5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=20357367; PubMed=10787416; DOI=10.1074/jbc.M002378200;
RA Lerche C., Scherer C.R., Seebohm G., Derst C., Wei A.D., Busch A.E.,
RA Steinmeyer K.;
RT "Molecular cloning and functional expression of KCNQ5, a potassium
RT channel subunit that may contribute to neuronal M-current diversity.";
RL J. Biol. Chem. 275:22395-22400(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC TISSUE=Brain;
RX MEDLINE=20379054; PubMed=10816588; DOI=10.1074/jbc.M003245200;
RA Schroeder B.C., Hechenberger M., Weinreich F., Kubisch C.,
RA Jentsch T.J.;
RT "KCNQ5, a novel potassium channel broadly expressed in brain, mediates
RT M-type currents.";
RL J. Biol. Chem. 275:24089-24095(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Kananura C., Biervert B., Hechenberger M., Engels H., Steinlein O.K.;
RT "The new voltage gated potassium channel KCNQ5 and early infantile
RT convulsions.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE OF 37-897 FROM N.A. (ISOFORM 1).
RC TISSUE=Brain, and Retina;
RA Kniazeva M., Han M.;
RT "A new gene of the voltage-gated potassium channel KCNQ family, KCNQ5,
RT is a candidate gene for retinal disorders.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP CHARACTERIZATION, AND ACTIVATION BY RETICABINE.
RX MEDLINE=21095345; PubMed=11159685;
RA Wickenden A.D., Zou A., Wagoner P.K., Jegla T.;
RT "Characterization of KCNQ5/Q3 potassium channels expressed in
RT mammalian cells.";
RL Br. J. Pharmacol. 132:381-384(2001).
CC -!- FUNCTION: Probably important in the regulation of neuronal

```
CC       excitability. Associates with KCNQ3 to form a potassium channel
CC       which contributes to m-type current, a slowly activating and
CC       deactivating potassium conductance which plays a critical role in
CC       determining the subthreshold electrical excitability of neurons.
CC       May contribute, with other potassium channels, to the molecular
CC       diversity of an heterogeneous population of M-channels, varying in
CC       kinetic and pharmacological properties, which underly this
CC       physiologically important current. Insensitive to
CC       tetraethylammonium, but inhibited by barium, linopirdine and
CC       XE991. Activated by niflumic acid and the anticonvulsant
CC       retigabine. Muscarine suppresses KCNQ5 current in Xenopus oocytes
CC       in which cloned KCNQ5 channels were coexpressed with M(1)
CC       muscarinic receptors.
CC   -!- SUBUNIT: Heteromultimer with KCNQ3.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=1;
CC         IsoId=Q9NR82-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q9NR82-2; Sequence=VSP_001014;
CC       Name=3;
CC         IsoId=Q9NR82-3; Sequence=VSP_001015;
CC   -!- TISSUE SPECIFICITY: Strongly expressed in brain and skeletal
CC       muscle. In brain, expressed in cerebral cortex, occipital pole,
CC       frontal lobe and temporal lobe. Lower levels in hippocampus and
CC       putamen. Low to undetectable levels in medulla, cerebellum and
CC       thalamus.
CC   -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC       characterized by a series of positively charged amino acids at
CC       every third position (By similarity).
CC   -!- SIMILARITY: Belongs to the potassium channel family. KQT
CC       subfamily.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF249278; AAF91335.1; ALT_INIT.
DR   EMBL; AF202977; AAF69797.1; -.
DR   EMBL; AJ272506; CAC88112.1; -.
DR   EMBL; AJ272507; CAC88112.1; JOINED.
DR   EMBL; AJ272508; CAC88112.1; JOINED.
DR   EMBL; AJ272509; CAC88112.1; JOINED.
DR   EMBL; AJ272510; CAC88112.1; JOINED.
DR   EMBL; AJ272511; CAC88112.1; JOINED.
DR   EMBL; AJ272512; CAC88112.1; JOINED.
DR   EMBL; AJ272513; CAC88112.1; JOINED.
DR   EMBL; AJ272514; CAC88112.1; JOINED.
DR   EMBL; AJ272515; CAC88112.1; JOINED.
DR   EMBL; AJ272516; CAC88112.1; JOINED.
DR   EMBL; AJ272517; CAC88112.1; JOINED.
DR   EMBL; AJ272518; CAC88112.1; JOINED.
DR   EMBL; AJ272519; CAC88112.1; JOINED.
DR   EMBL; AF263835; AAF73446.1; -.
DR   HSSP; Q54397; 1JVM.
DR   Genew; HGNC:6299; KCNQ5.
DR   MIM; 607357; -.
DR   GO; GO:0008076; C:voltage-gated potassium channel complex; TAS.
DR   GO; GO:0005242; F:inward rectifier potassium channel activity; TAS.
DR   GO; GO:0007268; P:synaptic transmission; TAS.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003091; K_channel.
DR   InterPro; IPR003937; KCNQ_channel.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF03520; KCNQ_channel; 1.
DR   PRINTS; PR00169; KCHANNEL.
KW   Alternative splicing; Ion transport; Ionic channel; Multigene family;
KW   Potassium; Potassium channel; Potassium transport; Transmembrane;
KW   Transport; Voltage-gated channel.
FT   TRANSMEM     91    111       Segment S1 (Potential).
FT   TRANSMEM    122    142       Segment S2 (Potential).
FT   TRANSMEM    166    186       Segment S3 (Potential).
FT   TRANSMEM    195    217       Segment S4 (Potential).
FT   TRANSMEM    232    252       Segment S5 (Potential).
FT   TRANSMEM    291    311       Segment S6 (Potential).
FT   DOMAIN      264    284       Segment H5 (pore-forming) (Potential).
FT   SITE        276    281       Selectivity filter (By similarity).
FT   VARSPLIC    372    381       KKEQGEASSS -> N (in isoform 2).
FT                                /FTId=VSP_001014.
FT   VARSPLIC    372    381       KKEQGEASSS -> NKFCSNKQKLFRMYTSRKQS (in
FT                                isoform 3).
FT                                /FTId=VSP_001015.
FT   CONFLICT     57     58       KP -> SR (in Ref. 1).
FT   CONFLICT     94     94       Y -> H (in Ref. 4).
FT   CONFLICT    692    692       A -> V (in Ref. 4).
FT   CONFLICT    764    764       T -> P (in Ref. 4).
FT   CONFLICT    822    822       S -> R (in Ref. 4).
FT   CONFLICT    874    874       R -> Q (in Ref. 4).
SQ   SEQUENCE   897 AA;  99024 MW;  0FD7C7731C1D8D11 CRC64;

  Query Match             99.6%;  Score 4527.5;  DB 1;  Length 897;
  Best Local Similarity   98.9%;  Pred. No. 8.8e-244;
  Matches  887;  Conservative    1;  Mismatches    0;  Indels    9;  Gaps    1;

Qy          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60

Qy         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120

Qy        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180

Qy        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300

Qy        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360

Qy        361 HLKALHTCSPT---------NQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 411
              |||||||||||         :||||||||||||||||||||||||||||||||||||||
Db        361 HLKALHTCSPTKKEQGEASSSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAE 420

Qy        412 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLT 480

Qy        472 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy        532 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGS 600

Qy        592 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 651
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPN 660

Qy        652 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 711
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 EFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLP 720

Qy        712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 771
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETL 780

Qy        772 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 831
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LSVCPMVPKDLGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEE 840

Qy        832 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 888
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 VGPEETETDTFDAAPQPAREAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKLK 897


RESULT 2
CIQ5_MOUSE
ID   CIQ5_MOUSE     STANDARD;      PRT;   878 AA.
AC   Q9JK45;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Potassium voltage-gated channel subfamily KQT member 5 (Voltage-gated
DE   potassium channel subunit Kv7.5) (Potassium channel alpha subunit
DE   KvLQT5) (KQT-like 5) (Fragment).
GN   Name=Kcnq5;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Brain;
RA   Kniazeva M., Han M.;
RT   "A new gene of the voltage-gated potassium channel KCNQ family, KCNQ5,
RT   is a candidate gene for retinal disorders.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Probably important in the regulation of neuronal
CC       excitability. Associates with KCNQ3 to form a potassium channel
CC       which contributes to m-type current, a slowly activating and
CC       deactivating potassium conductance which plays a critical role in
CC       determining the subthreshold electrical excitability of neurons.
CC       May contribute, with other potassium channels, to the molecular
CC       diversity of an heterogeneous population of M-channels, varying in
CC       kinetic and pharmacological properties, which underly this
CC       physiologically important current (By similarity).
CC   -!- SUBUNIT: Heteromultimer with KCNQ3 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC       characterized by a series of positively charged amino acids at
CC       every third position (By similarity).
CC   -!- SIMILARITY: Belongs to the potassium channel family. KQT
CC       subfamily.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF263836; AAF73447.1; -.
DR   HSSP; Q54397; 1JVM.
DR   MGD; MGI:1924937; Kcnq5.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003091; K_channel.
DR   InterPro; IPR003937; KCNQ_channel.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF03520; KCNQ_channel; 1.
DR   PRINTS; PR00169; KCHANNEL.
KW   Ion transport; Ionic channel; Multigene family; Potassium;
KW   Potassium channel; Potassium transport; Transmembrane; Transport;
KW   Voltage-gated channel.
FT   NON_TER       1      1
FT   TRANSMEM     72     92       Segment S1 (Potential).
FT   TRANSMEM    103    123       Segment S2 (Potential).
FT   TRANSMEM    147    167       Segment S3 (Potential).
FT   TRANSMEM    176    198       Segment S4 (Potential).
FT   TRANSMEM    213    233       Segment S5 (Potential).
FT   TRANSMEM    272    292       Segment S6 (Potential).
FT   DOMAIN      245    265       Segment H5 (pore-forming) (Potential).
FT   SITE        257    262       Selectivity filter (By similarity).
SQ   SEQUENCE   878 AA;  97029 MW;  35779F9C7D630F55 CRC64;

  Query Match             93.0%;  Score 4227.5;  DB 1;  Length 878;
  Best Local Similarity   94.3%;  Pred. No. 4.4e-227;
  Matches  827;  Conservative   14;  Mismatches   27;  Indels    9;  Gaps    1;

Qy         20 GDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLSYTSSQSCRRNVKYRRVQNY 79
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GDGLLLLGTRAAALGGGGGGLRESRRGKQGARMSLLGKPLSYTSSQSCRRNVKYRRVQNY 60

Qy         80 LYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLE 139
              |||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LYNVLERPRGWAFVYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLE 120

Qy        140 FIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSL 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSL 180

Qy        200 RFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKE 259
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        181 RFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFXVLIFSSFLVYLVEKDANKE 240

Qy        260 FSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKV 319
              |||||||||||||||||||||||||||||||||||||||||||||||| ||| |||||||||
Db        241 FSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALXAGIXGSGFALKV 300

Qy        320 QEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKPHLKALHTCSPT-------- 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKPHLKALHTCSPTKKEQGEAS 360

Qy        372 -NQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAEGSPTKVQKSWSFNDRTRFR 430
               :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 SSQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAEGSPTKVQKSWSFNDRTRFR 420

Qy        431 PSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAK 490
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        421 PSLRLKSSQPKPVIDADTALGIDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAK 480

Qy        491 RKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSREKITAEH 550
              ||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db        481 RKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQMTSDKKSREKITAEH 540

Qy        551 ETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFECEQT 610
              ||||| ||| ||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        541 ETTDDPSMLARVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALTLASFQIPPFECEQT 600

Qy        611 SDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPNEFSAQTFYALSPTMHSQAT 670
              ||||||||||||||||||||:|| ||||||||||||||||||||||||||||||||||||||
Db        601 SDYQSPVDSKDLSGSAQNSGCLTRSASANISRGLQFILTPNEFSAQTFYALSPTMHSQAT 660

Qy        671 QVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLPAIKHLPRPETLHPNPAGLQ 730
              |||:||:|||:| ||| ||||| |||||||||||||| ||||| ||| |  || |||
Db        661 QVPMSQNDGSSVVATNNIANQISAAPKPAAPTTLQIPPPLSAIKHLSRPEPLLSNPTGLQ 720

Qy        731 ESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETLLSVCPMVPKDLGKSLSVQN 790
              |||||||||||||:|| |||||||||:|||||||||||||| ||||||||||||||||||
Db        721 ESISDVTTCLVASKESVQFAQSNLTKDRSLRKSFDMGGETLLSVRPMVPKDLGKSLSVQN 780

Qy        791 LIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEEVGPEETETDTFDAAPQPAR 850
              |||||||||:| ||||||||||||||||||||||||||||||| ||||||||  | ||
```

```
Db        781 LIRSTEELNLQFSGSESSGSRGSQDFYPKWRESKLFITDEEVGAEETETDTFDGTPPPAG 840

Qy        851 EAAFASDSLRTGRSRSSQSICKAGESTDALSLPHVKL 887
              ||||:|||||||||||||:||| |:|||||||||||||
Db        841 EAAFSSDSLRTGRSRSSQNICKTGDSTDALSLPHVKL 877


RESULT 3
Q8BSF6
ID   Q8BSF6      PRELIMINARY;      PRT;   572 AA.
AC   Q8BSF6;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Mus musculus adult male cortex cDNA, RIKEN full-length enriched
DE   library, clone:7730402H11 product:potassium voltage-gated channel,
DE   subfamily Q, member 5, full insert sequence. (Fragment).
GN   Name=Kcnq5;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cortex;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cortex;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cortex;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cortex;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cortex;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cortex;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK033079; BAC28145.1; -.
DR   MGD; MGI:1924937; Kcnq5.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR   GO; GO:0006813; P:potassium ion transport; IEA.
DR   InterPro; IPR003937; KCNQ_channel.
DR   Pfam; PF03520; KCNQ_channel; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   572 AA;  62938 MW;  D30FEAF2BECFED9B CRC64;

  Query Match           58.4%;  Score 2655.5;  DB 2;  Length 572;
  Best Local Similarity   91.8%;  Pred. No. 9.1e-140;
  Matches  524;  Conservative   13;  Mismatches   25;  Indels    9;  Gaps    1;

Qy        326 KHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKPHLKALHTCSPT---------NQKLS 376
              |||||||||||||||||||||||||||||||||||||||||||||||         :||||
Db          1 KHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKPHLKALHTCSPTKKEQGEASSSQKLS 60

Qy        377 FKERVRMASPRGQSIKSRQASVGDRRSPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRLK 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FKERVRMASPRGQSIKSRQASVGDRRSPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRLK 120

Qy        437 SSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKET 496
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        121 SSQPKPVIDADTALGIDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKET 180

Qy        497 LRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSREKITAEHETTDDL 556
              |||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db        181 LRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQMTSDKKSREKITAEHETTDDP 240

Qy        557 SMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFECEQTSDYQSP 616
              ||| |||||||||||||||||||||||||||||| |||| ||||||||||||||||||||
Db        241 SMLARVVKVEKQVQSIESKLDCLLDIYQQVLRKGYASALTLASFQIPPFECEQTSDYQSP 300

Qy        617 VDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPNEFSAQTFYALSPTMHSQATQVPISQ 676
              |||||||||||||||:|| ||||||||||||||||||||||||||||||||||||:||
Db        301 VDSKDLSGSAQNSGCLTRSASANISRGLQFILTPNEFSAQTFYALSPTMHSQATQVPMSQ 360

Qy        677 SDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLPAIKHLPRPETLHPNPAGLQESISDV 736
              :|||:| ||| ||||||: |||||||||||||||| ||||| ||| :|  || |||||||||
Db        361 NDGSSVVATNNIANQISAAPKPAAPTTLQIPPPLSAIKHLSRPEPLLSNPTGLQESISDV 420

Qy        737 TTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETLLSVCPMVPKDLGKSLSVQNLIRSTE 796
              |||||||||:|| |||||||||:|||||||||||||| ||||||||||||||||||||||
Db        421 TTCLVASKESVQFAQSNLTKDRSLRKSFDMGGETLLSVRPMVPKDLGKSLSVQNLIRSTE 480

Qy        797 ELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEEVGPEETETDTFDAAPQPAREAAFAS 856
              |||:| |||||||||||||||||||||||||||||||||||| |||||||||  | || ||||:|
Db        481 ELNLQFSGSESSGSRGSQDFYPKWRESKLFITDEEVGAEETETDTFDGTPPPAGEAAFSS 540

Qy        857 DSLRTGRSRSSQSICKAGESTDALSLPHVKL 887
              ||||||||||||:||| |:|| |||||||||
Db        541 DSLRTGRSRSSQNICKTGDSTGALSLPHVKL 571


RESULT 4
CIQ4_HUMAN
ID   CIQ4_HUMAN     STANDARD;      PRT;   695 AA.
AC   P56696; O96025;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Potassium voltage-gated channel subfamily KQT member 4 (Voltage-gated
DE   potassium channel subunit Kv7.4) (Potassium channel alpha subunit
```

```
DE   KvLQT4) (KQT-like 4).
GN   Name=KCNQ4;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANT DFNA2 SER-285.
RC   TISSUE=Retina;
RX   MEDLINE=99148276; PubMed=10025409; DOI=10.1016/S0092-8674(00)80556-5;
RA   Kubisch C., Schroeder B.C., Friedrich T., Luetjohann B.,
RA   El-Amraoui A., Marlin S., Petit C., Jentsch T.J.;
RT   "KCNQ4, a novel potassium channel expressed in sensory outer hair
RT   cells, is mutated in dominant deafness.";
RL   Cell 96:437-446(1999).
RN   [2]
RP   INHIBITION BY M1 MUSCARINIC RECEPTORS.
RX   MEDLINE=20178300; PubMed=10713961;
RA   Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Jentsch T.J.,
RA   Brown D.A.;
RT   "Inhibition of KCNQ1-4 potassium channels expressed in mammalian cells
RT   via M1 muscarinic acetylcholine receptors.";
RL   J. Physiol. (Lond.) 522:349-355(2000).
RN   [3]
RP   PHARMACOLOGICAL CHARACTERIZATION, AND POSSIBLE FUNCTION.
RX   MEDLINE=21143874; PubMed=11245603;
RA   Soegaard R., Ljungstroem T., Pedersen K.A., Oelesen S.-P.,
RA   Jensen B.S.;
RT   "KCNQ4 channels expressed in mammalian cells: functional
RT   characteristics and pharmacology.";
RL   Am. J. Physiol. 280:C859-C866(2001).
RN   [4]
RP   VARIANTS DFNA2 SER-276; CYS-285 AND SER-321.
RX   MEDLINE=99299248; PubMed=10369879; DOI=10.1093/hmg/8.7.1321;
RA   Coucke P.J., Van Hauwe P., Kelley P.M., Kunst H., Schatteman I.,
RA   Van Velzen D., Meyers J., Ensink R.J., Verstreken M., Declau F.,
RA   Marres H., Kastury K., Bhasin S., McGuirt W.T., Smith R.J.H.,
RA   Cremers C.W.R.J., Van de Heyning P., Willems P.J., Smith S.D.,
RA   Van Camp G.;
RT   "Mutations in the KCNQ4 gene are responsible for autosomal dominant
RT   deafness in four DFNA2 families.";
RL   Hum. Mol. Genet. 8:1321-1328(1999).
RN   [5]
RP   VARIANT DFNA2 SER-281.
RX   MEDLINE=20040027; PubMed=10571947;
RX   DOI=10.1002/(SICI)1098-1004(199912)14:6<493::AID-HUMU8>3.0.CO;2-P;
RA   Talebizadeh Z., Kelley P.M., Askew J.W., Beisel K.W., Smith S.D.;
RT   "Novel mutation in the KCNQ4 gene in a large kindred with dominant
RT   progressive hearing loss.";
RL   Hum. Mutat. 14:493-501(1999).
RN   [6]
RP   VARIANT DFNA2 HIS-274.
RX   MEDLINE=20388752; PubMed=10925378;
RX   DOI=10.1002/1096-8628(20000731)93:3<184::AID-AJMG4>3.0.CO;2-5;
RA   Van Hauwe P., Coucke P.J., Ensink R.J., Huygen P., Cremers C.W.R.J.,
RA   Van Camp G.;
RT   "Mutations in the KCNQ4 K+ channel gene, responsible for autosomal
RT   dominant hearing loss, cluster in the channel pore region.";
RL   Am. J. Med. Genet. 93:184-187(2000).
CC   -!- FUNCTION: Probably important in the regulation of neuronal
CC       excitability. May underlie a potassium current involved in
CC       regulating the excitability of sensory cells of the cochlea. KCNQ4
CC       channels are blocked by linopirdin, XE991 and bepridil, whereas
CC       clofilium is without significant effect. Muscarinic agonist
CC       oxotremorine-M strongly suppress KCNQ4 current in CHO cells in
CC       which cloned KCNQ4 channels were coexpressed with M1 muscarinnic
CC       receptors.
CC   -!- SUBUNIT: May form heteromultimers with KCNQ3.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Situated at the
CC       basal membrane of cochlear outer hair cells (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=1;
CC         IsoId=P56696-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=P56696-2; Sequence=VSP_001013;
CC   -!- TISSUE SPECIFICITY: Expressed in the outer, but not the inner,
CC       sensory hair cells of the cochlea. Slightly expressed in heart,
CC       brain and skeletal muscle.
CC   -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC       characterized by a series of positively charged amino acids at
CC       every third position (By similarity).
CC   -!- DISEASE: Defects in KCNQ4 are a cause of nonsyndromic
CC       sensorineural deafness type 2 (DFNA2) [MIM:600101], an autosomal
CC       dominant form of progressive hearing loss.
CC   -!- MISCELLANEOUS: Mutagenesis experiments were carried out by
CC       expressing in Xenopus oocytes KCNQ4 mutants either individually
CC       (homomultimers) or in combination with wild-type KCNQ4 (mut/wt
CC       homomultimers) in a ratio of 1:1, to mimic the situation in a
CC       heterozygous DFNA2 patient.
CC   -!- SIMILARITY: Belongs to the potassium channel family. KQT
CC       subfamily.
CC   -!- DATABASE: NAME=Hereditary hearing loss homepage; NOTE=Gene page;
CC       WWW="http://www.uia.ac.be/dnalab/hhh/".
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF105202; AAD14680.1; -.
DR   EMBL; AF105216; AAD14681.1; -.
DR   EMBL; AF105203; AAD14681.1; JOINED.
DR   EMBL; AF105204; AAD14681.1; JOINED.
DR   EMBL; AF105205; AAD14681.1; JOINED.
DR   EMBL; AF105206; AAD14681.1; JOINED.
DR   EMBL; AF105207; AAD14681.1; JOINED.
DR   EMBL; AF105208; AAD14681.1; JOINED.
DR   EMBL; AF105209; AAD14681.1; JOINED.
DR   EMBL; AF105210; AAD14681.1; JOINED.
DR   EMBL; AF105211; AAD14681.1; JOINED.
DR   EMBL; AF105212; AAD14681.1; JOINED.
DR   EMBL; AF105213; AAD14681.1; JOINED.
DR   EMBL; AF105214; AAD14681.1; JOINED.
DR   EMBL; AF105215; AAD14681.1; JOINED.
DR   HSSP; Q54397; 1JVM.
DR   Genew; HGNC:6298; KCNQ4.
DR   MIM; 603537; -.
DR   MIM; 600101; -.
DR   GO; GO:0005267; F:potassium channel activity; TAS.
DR   GO; GO:0007605; P:perception of sound; TAS.
DR   GO; GO:0006813; P:potassium ion transport; TAS.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003091; K_channel.
DR   InterPro; IPR003937; KCNQ_channel.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF03520; KCNQ_channel; 1.
DR   PRINTS; PR00169; KCHANNEL.
KW   Alternative splicing; Deafness; Disease mutation; Ion transport;
KW   Ionic channel; Multigene family; Potassium; Potassium channel;
KW   Potassium transport; Transmembrane; Transport; Voltage-gated channel.
FT   TRANSMEM     98    118       Segment S1 (Potential).
FT   TRANSMEM    132    152       Segment S2 (Potential).
FT   TRANSMEM    173    193       Segment S3 (Potential).
FT   TRANSMEM    202    224       Segment S4 (Potential).
FT   TRANSMEM    238    258       Segment S5 (Potential).
FT   TRANSMEM    297    317       Segment S6 (Potential).
FT   DOMAIN      271    292       Segment H5 (pore-forming) (Potential).
FT   SITE        283    288       Selectivity filter (By similarity).
FT   VARSPLIC    378    431       Missing (in isoform 2).
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FT                                   /FTId=VSP_001013.
FT   VARIANT      274    274         L -> H (in DFNA2).
FT                                   /FTId=VAR_010936.
FT   VARIANT      276    276         W -> S (in DFNA2).
FT                                   /FTId=VAR_008726.
FT   VARIANT      281    281         L -> S (in DFNA2).
FT                                   /FTId=VAR_010937.
FT   VARIANT      285    285         G -> C (in DFNA2; loss of potassium
FT                                   selectivity of the pore).
FT                                   /FTId=VAR_008727.
FT   VARIANT      285    285         G -> S (in DFNA2).
FT                                   /FTId=VAR_001547.
FT   VARIANT      321    321         G -> S (in DFNA2).
FT                                   /FTId=VAR_008728.
FT   MUTAGEN      285    285         G->S: No current (homomultimers). 90% wt
FT                                   current reduction (mu/wt homomultimers).
SQ   SEQUENCE   695 AA;  77091 MW;  A58737BD845E1A3A CRC64;

  Query Match             43.7%;  Score 1985;  DB 1;  Length 695;
  Best Local Similarity   60.3%;  Pred. No. 2.6e-102;
  Matches  409;  Conservative   76;  Mismatches  101;  Indels   92;  Gaps   13;

Qy         35 GGGGGLRESRRGKQGARMSLLGKPL-------------SYTSSQSCRRNVKYRRVQNYL 80
              ||||  |          |: ||| ||               |   :|   : :|||:||::
Db         37 GGGGSPR---------RLGLLGSPLPPGAPLPGPGSGSGSACGQRSSAAHKRYRRLQNWV 87

Qy         81 YNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLEF 140
              |||||||||||:|| |:|||| ||:||| ||| || :||: |||||||||||||||:
Db         88 YNVLERPRGWAFVYHVFIFLLVFSCLVLSVLSTIQEHQELANECLLILEFVMIVVFGLEY 147

Qy        141 IIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSLR 200
              |:|:|||||||||||||| |||||||||| || :||:||::| |||||||||||||:|
Db        148 IVRVWSAGCCCRYRGWQGRFRFARKPFCVIDFIVFVASVAVIAAGTQGNIFATSALRSMR 207

Qy        201 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKEF 260
              |||||||||||||||||||||||||||||||||||||||||||:|||||| ||||| :|
Db        208 FLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFASFLVYLAEKDANSDF 267

Qy        261 STYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKVQ 320
              |:|||:|||||||||||||||| |||||:|:|||||||||||||||||||||||||||||
Db        268 SSYADSLWWGTITLTTIGYGDKTPHTWLGRVLAAGFALLGISFFALPAGILGSGFALKVQ 327

Qy        321 EQHRQKHFEKRRNPAANLIQCVWRSYAAD-EKSVSIATW---------------------- 358
              |||||||||||| ||||||| || |: |  ::   |||
Db        328 EQHRQKHFEKRRMPAANLIQAAWRLYSTDMSRAYLTATWYYYDSILPSFRELALLFEHVQ 387

Qy        359 ------------------------KPHLKALHT------CSPTNQKLSFKERVRMASPRG 388
                                     | :  |       |   : ::  |:|:|| | :
Db        388 RARNGGLRPLEVRRAPVPDGAPSRYPPVATCHRPGSTSFCPGESSRMGIKDRIRMGSSQR 447

Qy        389 QSIKSRQ--ASVGDRRSPSTDITAEG-SPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVID 445
              ::  |:|  |      |||::   |  ||||||||||||||||| ||||      ||
Db        448 RTGPSKQQLAPPTMPTSPSSEQVGEATSPTKVQKSWSFNDRTRFRASLRL-----KPRTS 502

Qy        446 ADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDV 505
              |: |  :::| :||  ||:::|:|: | :|||||:|||:|| ||||||||||||||||
Db        503 AEDA-PSEEVAEEKSYQCELTVDDIMPAVKTVIRSIRILKFLVAKRKFKETLRPYDVKDV 561

Qy        506 IEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSRE---KITAEHETTDDLSMLGRV 562
              |||||||||||| ||||||||||||:|:|    |:|:||   |  :: |  |::||:|||
Db        562 IEQYSAGHLDMLGRIKSLQTRVDQIVGRG--PGDRKAREKGDKGPSDAEVVDEISMMGRV 619

Qy        563 VKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPPECEQTSDYQSPVDSKDL 622
              |||||||||| ||| ||  | : || |:::  :| : |:| |: : |||| |||| :|:
Db        620 VKVEKQVQSIEHKLDLLLGFYSRCLRSGTSA--SLGAVQVPLFDPDITSDYHSPVDHEDI 677

Qy        623 SGSAQNSGCLSRSTSANI 640
              | |||    :||| | |:
Db        678 SVSAQTLS-ISRSVSTNM 694


RESULT 5
Q86W40
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ID   Q86W40      PRELIMINARY;      PRT;   427 AA.
AC   Q86W40;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RA   Strausberg R.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC050689; AAH50689.1; -.
DR   HSSP; Q54397; 1J95.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR   GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006813; P:potassium ion transport; IEA.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003947; KCNQ2_channel.
DR   InterPro; IPR003937; KCNQ_channel.
DR   InterPro; IPR003091; K_channel.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 1.
DR   PRINTS; PR00169; KCHANNEL.
DR   PRINTS; PR01461; KCNQ2CHANNEL.
DR   PRINTS; PR01459; KCNQCHANNEL.
KW   Hypothetical protein; Ion transport; Ionic channel; Transmembrane;
KW   Transport.
SQ   SEQUENCE   427 AA;  46942 MW;  175F91B7BB48836B CRC64;

  Query Match             42.4%;  Score 1930;  DB 2;  Length 427;
  Best Local Similarity   99.2%;  Pred. No. 1.6e-99;
  Matches  371;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         36 MKDVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLS 95

Qy         61 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 YTSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKL 155

Qy        121 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 180
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 ASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIA 215

Qy        181 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 VVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 275

Qy        241 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 VLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLG 335

Qy        301 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 ISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 395

Qy        361 HLKALHTCSPTNQK 374
                |||||||||||  ::
Db        396 HLKALHTCSPTKKE 409


RESULT 6
CIQ2_RAT
ID   CIQ2_RAT       STANDARD;      PRT;   852 AA.
AC   O88943;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Potassium voltage-gated channel subfamily KQT member 2 (Voltage-gated
DE   potassium channel subunit Kv7.2) (Potassium channel alpha subunit
DE   KvLQT2) (KQT-like 2).
GN   Name=Kcnq2;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM A).
RC   TISSUE=Brain;
RA   Derst C., Preisig-Mueller R., Hennighausen A., Daut J.;
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM A).
RC   TISSUE=Brain;
RX   MEDLINE=20493350; PubMed=11038262; DOI=10.1016/S0169-328X(00)00146-7;
RA   Jow F., Wang K.-W.;
RT   "Cloning and functional expression of rKCNQ2 K(+) channel from rat
RT   brain.";
RL   Brain Res. Mol. Brain Res. 80:269-278(2000).
RN   [3]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Brain, and Sympathetic ganglion;
RX   MEDLINE=21154288; PubMed=11230508;
RA   Pan Z., Selyanko A.A., Hadley J.K., Brown D.A., Dixon J.E.,
RA   McKinnon D.;
RT   "Alternative splicing of KCNQ2 potassium channel transcripts
RT   contributes to the functional diversity of M-currents.";
RL   J. Physiol. (Lond.) 531:347-358(2001).
RN   [4]
RP   TISSUE SPECIFICITY.
RX   MEDLINE=99055398; PubMed=9836639; DOI=10.1126/science.282.5395.1890;
RA   Wang H.-S., Pan Z., Shi W., Brown B.S., Wymore R.S., Cohen I.S.,
RA   Dixon J.E., McKinnon D.;
RT   "KCNQ2 and KCNQ3 potassium channel subunits: molecular correlates of
RT   the M-channel.";
RL   Science 282:1890-1893(1998).
CC   -!- FUNCTION: Probably important in the regulation of neuronal
CC       excitability. Associates with KCNQ3 to form a potassium channel
CC       with essentially identical properties to the channel underlying
CC       the native M-current, a slowly activating and deactivating
CC       potassium conductance which plays a critical role in determining
CC       the subthreshold electrical excitability of neurons as well as the
CC       responsiveness to synaptic inputs. KCNQ2 current is blocked by
CC       barium and tetraethylammonium whereas 4-aminopyrodine and
CC       charybdotoxin have no effect on KCNQ2 current. Tyrosine kinase
CC       inhibitors genistein or herbimycin a markedly down-regulate KCNQ2
CC       current. Muscarinic agonist oxotremorine-M suppress KCNQ2/KCNQ3
CC       current in CHO cells in which cloned KCNQ2/KCNQ3 channels were
CC       coexpressed with human M1 muscarinnic receptors.
CC   -!- SUBUNIT: Heteromultimer with KCNQ3.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=9;
CC         Comment=Splice isoforms fell into three classes, those that
CC         contain an in frame exon 16 (Isoforms A-I) those that contain an
CC         out-of-frame exon 16 due to an alternative splice junction in
CC         exon 14 and those that terminate prematurely to exon 16. Only
CC         the forms containing an in frame exon 16 are able to form
CC         functional channels. A similar splice pattern is also produced
CC         for splice variants that contain an out-of-frame exon 16. A wide
CC         variety of different truncated isoforms were isolated for splice
CC         variants that terminate prematurely to exon 16;
CC       Name=A;
CC         IsoId=O88943-1; Sequence=Displayed;
CC       Name=B;
CC         IsoId=O88943-2; Sequence=VSP_001009, VSP_001011;
CC       Name=C;
CC         IsoId=O88943-3; Sequence=VSP_001007;
CC       Name=D;
CC         IsoId=O88943-4; Sequence=VSP_001008, VSP_001010;
CC       Name=E;
CC         IsoId=O88943-5; Sequence=VSP_001008;
CC       Name=F;
CC         IsoId=O88943-6; Sequence=VSP_001007, VSP_001008, VSP_001010;
CC       Name=G;
CC         IsoId=O88943-7; Sequence=VSP_001011;
CC       Name=H;
CC         IsoId=O88943-8; Sequence=VSP_001007, VSP_001008;
CC       Name=I;
CC         IsoId=O88943-9; Sequence=VSP_001010;
CC   -!- TISSUE SPECIFICITY: Expressed in brain and sympathetic ganglia. In
CC       brain, expressed in cortex, hippocampus, and cerebellum. In
CC       sympathetic ganglia, expressed at lower levels in celiac ganglia
CC       and superior mesenteric ganglia than in superior cervical ganglia.
CC   -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC       characterized by a series of positively charged amino acids at
CC       every third position (By similarity).
CC   -!- MISCELLANEOUS: When coexpressed with KCNQ3 subunit in CHO cells or
CC       Xenopus oocytes, isoform B was found to have significantly
CC       different deactivation-activation kinetics. The kinetics was 2.5
CC       times more slowly than the kinetics of other isoforms. The
CC       presence of exon 15a in isoform B accounts for the slow
CC       deactivation-activation kinetics. Alternative splicing of the
CC       KCNQ2 gene may contribute to the variation in M-current kinetics
CC       seen in vivo.
CC   -!- SIMILARITY: Belongs to the potassium channel family. KQT
CC       subfamily.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AF087453; AAC36722.1; -.
DR   HSSP; Q54397; 1JVM.
DR   RGD; 621504; Kcnq2.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003091; K_channel.
DR   InterPro; IPR003937; KCNQ_channel.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF03520; KCNQ_channel; 1.
DR   PRINTS; PR00169; KCHANNEL.
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KW   Alternative splicing; Ion transport; Ionic channel; Multigene family;
KW   Phosphorylation; Potassium; Potassium channel; Potassium transport;
KW   Transmembrane; Transport; Voltage-gated channel.
FT   TRANSMEM      92    112       Segment S1 (Potential).
FT   TRANSMEM     123    143       Segment S2 (Potential).
FT   TRANSMEM     167    187       Segment S3 (Potential).
FT   TRANSMEM     198    221       Segment S4 (Potential).
FT   TRANSMEM     232    252       Segment S5 (Potential).
FT   TRANSMEM     292    312       Segment S6 (Potential).
FT   DOMAIN       265    285       Segment H5 (pore-forming) (Potential).
FT   SITE         277    282       Selectivity filter (By similarity).
FT   MOD_RES       52     52       Phosphoserine (by PKA) (By similarity).
FT   VARSPLIC     373    382       Missing (in isoform C, isoform F and
FT                                 isoform H).
FT                                 /FTId=VSP_001007.
FT   VARSPLIC     416    416       S -> SKGRPCRGCLCGCRPGHSS (in isoform D,
FT                                 isoform E, isoform F and isoform H).
FT                                 /FTId=VSP_001008.
FT   VARSPLIC     417    428       Missing (in isoform B).
FT                                 /FTId=VSP_001009.
FT   VARSPLIC     491    491       Missing (in isoform D, isoform F and
FT                                 isoform I).
FT                                 /FTId=VSP_001010.
FT   VARSPLIC     571    571       R -> RIDMIVGPPPPSTPRHKKYPTKGPTAPSRESPQYSP
FT                                 R (in isoform B and isoform G).
FT                                 /FTId=VSP_001011.
SQ   SEQUENCE   852 AA;  93949 MW;  82A5FE462A5F259A CRC64;

  Query Match             39.7%;  Score 1803.5;  DB 1;  Length 852;
  Best Local Similarity   49.0%;  Pred. No. 4.4e-92;
  Matches  413;  Conservative   96;  Mismatches  193;  Indels  141;  Gaps   22;

Qy         17 AARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLSYTSSQSCRRNVKYRRV 76
              : |   ||: |: |      |  | : | |  ||     |||           :||  ||::
Db         34 STRDGALLIAGSEAPK---RGSVLSKPRTGGAGA-----GKP--------PKRNAFYRKL 77

Qy         77 QNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVF 136
              ||:||||||||||||||||:|||||| ||:||||||| |: | :   | ||| | ||||
Db         78 QNFLYNVLERPRGWAFIYHAYVFLLVFSCLVLSVFSTIKEYEKSSEGALYILEIVTIVVF 137

Qy        137 GLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSAL 196
              |:|: :|||:||||||||||:|||:|||||||||| :||||||||::| :|||:||||||
Db        138 GVEYFVRIWAAGCCCRYRGWRGRLKFARKPFCVIDIMVLIASIAVLAAGSQGNVFATSAL 197

Qy        197 RSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDA 256
              |||||||||||:|||||||||||||||||||||||:|||||||| || :|||||| ||
Db        198 RSLRFLQILRMIRMDRRGGTWKLLGSVVYAHSKELVTAWYIGFLCLILASFLVYLAEKGE 257

Qy        257 NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFA 316
              |  | ||||||||| |||||||||| | || ||||:| | |:|:|||||||||||||||
Db        258 NDHFDTYADALWWGLITLTTIGYGDKYPQTWNGRLLAATFTLIGVSFFALPAGILGSGFA 317

Qy        317 LKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEKSVSI-ATWK--------------- 359
              |||||||||||||||||| ||| || || :     : :||:
Db        318 LKVQEQHRQKHFEKRRNPAAGLIQSAWRFYATNLSRTDLHSTWQYYERTVTVPMISSQTQ 377

Qy        360 --------PHLKALHTC------------------SPTNQKLSFKERVRMASPRGQSIK 392
                     | | |                      || :||:| |:||  :|||| : |
Db        378 TYGASRLIPPLNQLEMLRNLKSKSGLTFRKEPQPEPSP-SQKVSLKDRV-FSSPRGVAAK 435

Qy        393 SRQASVGD--RRSPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTAL 450
               : :      ||||| | : : ||:|| ||||| ||:| | : |:| :  :   :  :
Db        436 GKGSPQAQTVRRSPSADQSLDDSPSKVPKSWSFGDRSRARQAFRIKGAASRQNSEEASLP 495

Qy        451 GTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYS 510
              | | | | | | |:   ||||| ||  |||: :|:| |:||||||:|||||| |||||||
Db        496 GEDIVEDNKSCNCEFVTEDLTPGLKVSIRAVCVMRFLVSKRKFKESLRPYDVMDVIEQYS 555

Qy        511 AGHLDMLCRIKSLQTRVDQILGKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQ 570
              |||||| ||||||:|||||:|:|   :| | | |  || |  :| ||:||: ||||||
Db        556 AGHLDMLSRIKSLQSRVDQIVGRGPTITD-KDRTKGPAETELPEDPSMMGRLGKVEKQVL 614

Qy        571 SIESKLDCLLDIYQQVLRKGSASALALASFQIPPFEC---------EQTSDYQSPVDSKD 621
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              |:| ||| |: || |  | |           ||| |          |    | || ||:|
Db        615 SMEKKLDFLVSIYTQ--RMG-----------IPPAETEAYFGAKEPEPAPPYHSPEDSRD 661

Qy        622 LSGSAQNSGC---LSRSTSANISRGLQFILTPNEFSAQTFYALSPTMHSQATQVPISQSD 678
                |   ||   : ||||:                :|  ||  | |    : | | |
Db        662 ---HADKHGCIIKIVRSTSS--------------TGQRKYAAPPVM--PPAECPPSTS- 700

Qy        679 GSAVAATNTIANQINTAPKPAAPTTLQIPPPLPAIKHLPRPETLHPNPAGLQESISDVTT 738
                        :  |:|     : ::|||||                ||  : |:|  :
Db        701 ------WQQSHQRHGTSPVGDHGSLVRIPPP---------------PAH-ERSLSAYSG 737

Qy        739 CLVASKENVQVAQSNLTK--DRSMRKSFDMGGETLLSVCPMVPKDLGKSLSVQNLIRSTE 796
                  || | :::  :   :  : ::| |     :| :|:  :  ::| :| |  :: :| |
Db        738 GNRASTEFLRLEGTPACRPSEAALRDS-----DTSISIPSVDHEELERSPSGFSISQSKE 792

Qy        797 ELN 799
                ||
Db        793 NLN 795


RESULT 7
Q8R498
ID   Q8R498      PRELIMINARY;      PRT;   870 AA.
AC   Q8R498;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Potassium channel KCNQ2.
GN   Name=Kcnq2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   PubMed=12223552;
RA   Wen H., Levitan I.B.;
RT   "Calmodulin Is an Auxiliary Subunit of KCNQ2/3 Potassium Channels.";
RL   J. Neurosci. 22:7991-8001(2002).
DR   EMBL; AF490773; AAM09696.1; -.
DR   HSSP; Q54397; 1J95.
DR   MGD; MGI:1309503; Kcnq2.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003947; KCNQ2_channel.
DR   InterPro; IPR003937; KCNQ_channel.
DR   InterPro; IPR003091; K_channel.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF03520; KCNQ_channel; 1.
DR   PRINTS; PR00169; KCHANNEL.
DR   PRINTS; PR01461; KCNQ2CHANNEL.
DR   PRINTS; PR01459; KCNQCHANNEL.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
SQ   SEQUENCE   870 AA;  95741 MW;  9C6106C27CE70C5F CRC64;

  Query Match             39.6%;  Score 1799.5;  DB 2;  Length 870;
  Best Local Similarity   47.9%;  Pred. No. 7.5e-92;
  Matches  408;  Conservative   96;  Mismatches  195;  Indels  153;  Gaps   21;

Qy         17 AARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLSYTSSQSCRRNVKYRRV 76
              : |   ||: |: |      |  | : | |  ||     |||          :||  ||::
Db         34 STRDGALLIAGSEAPK---RGSVLSKPRTGGAGA-----GKP--------PKRNAFYRKL 77

Qy         77 QNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVF 136
              ||:||||||||||||||||:|||||| ||:||||||| |: | :   | ||| | ||||
Db         78 QNFLYNVLERPRGWAFIYHAYVFLLVFSCLVLSVFSTIKEYEKSSEGALYILEIVTIVVF 137

Qy        137 GLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSAL 196
              |:|: :|||:||||||||||:|||:|||||||||| :||||||||::| :|||:||||||
Db        138 GVEYFVRIWAAGCCCRYRGWRGRLKFARKPFCVIDIMVLIASIAVLAAGSQGNVFATSAL 197
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Qy        197 RSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDA 256
              ||||||||||:|||||||||||||||||||||||:|||||||| || :|||||| ||
Db        198 RSLRFLQILRMIRMDRRGGTWKLLGSVVYAHSKELVTAWYIGFLCLILASFLVYLAEKGE 257

Qy        257 NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFA 316
              |  | |||||||||| |||||||||| | || ||||:| | |:|:|||||||||||||||
Db        258 NDHFDTYADALWWGLITLTTIGYGDKYPQTWNGRLLAATFTLIGVSFFALPAGILGSGFA 317

Qy        317 LKVQEQHRQKHFEKRRNPAANLIQCVWRSYAAD-------------EKSVSIATW----- 358
              |||||||||||||||||| |||  || || :             |::|::  :
Db        318 LKVQEQHRQKHFEKRRNPAAGLIQSAWRFYATNLSRTDLHSTWQYYERTVTVPMYSSQTQ 377

Qy        359 ----------------------------------------KPHLKALHTCSP--TNQKL 375
                                                     :|    |✓ | |  ::||:
Db        378 TYGASRLIPPLNQLELLRNLKSKSGLTFRKEPQPEPSPSKGRPCRGCLCGCCPGHSSQKV 437

Qy        376 SFKERVRMASPRGQSIKSRQASVGD--RRSPSTDITAEGSPTKVQKSWSFNDRTRFRPSL 433
              | |:||  :|||| : | : :      ||||| | : : ||:|| ||||| ||:| | :
Db        438 SLKDRV-FSSPRGMAAKGKGSPQAQTVRRSPSADQSLDDSPSKVPKSWSFGDRSRTRQAF 496

Qy        434 RLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKF 493
              |:| :  :   :  :  | | | | | | |:   ||||| ||  |||: :|:| |:||||
Db        497 RIKGAASRQNSEEASLPGEDIVEDNKSCNCEFVTEDLTPGLKVSIRAVCVMRFLVSKRKF 556

Qy        494 KETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSREKITAEHETT 553
              ||:|||||| |||||||||||| ||||||:|||||:|:|   :| | | |  || |
Db        557 KESLRPYDVMDVIEQYSAGHLDMLSRIKSLQSRVDQIVGRGPTITD-KDRTKGPAETELP 615

Qy        554 DDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFEC------ 607
              :| ||:||: |||||| |:| ||| |: || |  | |           ||| |
Db        616 EDPSMMGRLGKVEKQVLSMEKKLDFLVSIYTQ--RMG-----------IPPAETEAYFGA 662

Qy        608 ---EQTSDYQSPVDSKDLSGSAQNSGC---LSRSTSANISRGLQFILTPNEFSAQTFYAL 661
                 |    | || ||:|    |   ||   : ||||:             : |  ||
Db        663 KEPEPAPPYHSPEDSRD---HADKHGCIIKIVRSTSS--------------TGQRNYAA 704

Qy        662 SPTMHSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLPA--------- 712
              |         :| :|  |  :     :  |:|     : ::|||| ||
Db        705 PPA-------IPPAQCPPS--TSWQQSHQRHGTSPVGDHGSLVRIPPP-PAHERSLSAYG 754

Qy        713 --------IKHLPRPETLHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSF 764
                      |       |: | |::| : ::   |   | :: : |  :  :| :::
Db        755 GGNRASTEFLRLEGTPACRPSEAALRDSDTSISIPSV-DHEELERSFSGFSISQS-KENL 812

Qy        765 DMGGETLLSVCP 776
              | |    :| |
Db        813 DALGSCYAAVAP 824
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RESULT 8
CIQ2_HUMAN
ID   CIQ2_HUMAN     STANDARD;      PRT;   872 AA.
AC   O43526; O43796; O75580; O95845; Q96J59; Q99454;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Potassium voltage-gated channel subfamily KQT member 2 (Voltage-gated
DE   potassium channel subunit Kv7.2) (Neuroblastoma-specific potassium
DE   channel alpha subunit KvLQT2) (KQT-like 2).
GN   Name=KCNQ2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 6).
RC   TISSUE=Neuroblastoma;
RX   MEDLINE=97191543; PubMed=9039501;
RA   Yokoyama M., Nishi Y., Yoshii J., Okubo K., Matsubara K.;
RT   "Identification and cloning of neuroblastoma-specific and nerve
RT   tissue-specific genes through compiled expression profiles.";
RL   DNA Res. 3:311-320(1996).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS BFNC1 CYS-284 AND
RP   THR-306.
RC   TISSUE=Brain, Fetal brain, and Temporal cortex;
RX   MEDLINE=98085864; PubMed=9425895;
RA   Singh N.A., Charlier C., Stauffer D., DuPont B.R., Leach R.J.,
RA   Melis R., Ronen G.M., Bjerre I., Quattlebaum T., Murphy J.V.,
RA   McHarg M.L., Gagnon D., Rosales T.O., Peiffer A., Anderson V.E.,
RA   Leppert M.;
RT   "A novel potassium channel gene, KCNQ2, is mutated in an inherited
RT   epilepsy of newborns.";
RL   Nat. Genet. 18:25-29(1998).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RC   TISSUE=Fetal brain;
RX   MEDLINE=98092527; PubMed=9430594; DOI=10.1126/science.279.5349.403;
RA   Biervert C., Schroeder B.C., Kubisch C., Berkovic S.F., Propping P.,
RA   Jentsch T.J., Steinlein O.K.;
RT   "A potassium channel mutation in neonatal human epilepsy.";
RL   Science 279:403-406(1998).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 4).
RX   MEDLINE=99055398; PubMed=9836639; DOI=10.1126/science.282.5395.1890;
RA   Wang H.-S., Pan Z., Shi W., Brown B.S., Wymore R.S., Cohen I.S.,
RA   Dixon J.E., McKinnon D.;
RT   "KCNQ2 and KCNQ3 potassium channel subunits: molecular correlates of
RT   the M-channel.";
RL   Science 282:1890-1893(1998).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 5).
RX   MEDLINE=99043242; PubMed=9827540; DOI=10.1016/S0014-5793(98)01296-4;
RA   Tinel N., Lauritzen I., Chouabe C., Lazdunski M., Borsotto M.;
RT   "The KCNQ2 potassium channel: splice variants, functional and
RT   developmental expression. Brain localization and comparison with
RT   KCNQ3.";
RL   FEBS Lett. 438:171-176(1998).
RN   [6]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC   TISSUE=Brain, and Fetal brain;
RX   MEDLINE=98344027; PubMed=9677360; DOI=10.1074/jbc.273.31.19419;
RA   Yang W.-P., Levesque P.C., Little W.A., Conder M.L., Ramakrishnan P.,
RA   Neubauer M.G., Blanar M.A.;
RT   "Functional expression of two KvLQT1-related potassium channels
RT   responsible for an inherited idiopathic epilepsy.";
RL   J. Biol. Chem. 273:19419-19423(1998).
RN   [7]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Brain;
RX   MEDLINE=21114072; PubMed=11160379;
RA   Smith J.S., Iannotti C.A., Dargis P.G., Christian E.P., Aiyar J.;
RT   "Differential expression of KCNQ2 splice variants: implications to M
RT   current function during neuronal development.";
RL   J. Neurosci. 21:1096-1103(2001).
RN   [8]
RP   SEQUENCE FROM N.A. (ISOFORM 6).
RC   TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [9]
RP MUTAGENESIS OF SER-52; GLY-279 AND TYR-284.
RX MEDLINE=99087323; PubMed=9872318; DOI=10.1038/25367;
RA Schroeder B.C., Kubisch C., Stein V., Jentsch T.J.;
RT "Moderate loss of function of cyclic-AMP-modulated KCNQ2/KCNQ3 K+
RT channels causes epilepsy.";
RL Nature 396:687-690(1998).
RN [10]
RP INVOLVEMENT IN M-LIKE CURRENT.
RX MEDLINE=99410758; PubMed=10479678;
RA Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Delmas P.,
RA Buckley N.J., London B., Brown D.A.;
RT "Two types of K(+) channel subunit, Erg1 and KCNQ2/3, contribute to
RT the M-like current in a mammalian neuronal cell.";
RL J. Neurosci. 19:7742-7756(1999).
RN [11]
RP ASSOCIATION WITH KCNE2.
RX MEDLINE=20487128; PubMed=11034315; DOI=10.1016/S0014-5793(00)01918-9;
RA Tinel N., Diochot S., Lauritzen I., Barhanin J., Lazdunski M.,
RA Borsotto M.;
RT "M-type KCNQ2-KCNQ3 potassium channels are modulated by the KCNE2
RT subunit.";
RL FEBS Lett. 480:137-141(2000).
RN [12]
RP SURFACE EXPRESSION OF HETEROMERS.
RX MEDLINE=20250883; PubMed=10788442; DOI=10.1074/jbc.275.18.13343;
RA Schwake M., Pusch M., Kharkovets T., Jentsch T.J.;
RT "Surface expression and single channel properties of KCNQ2/KCNQ3, M-
RT type K+ channels involved in epilepsy.";
RL J. Biol. Chem. 275:13343-13348(2000).
RN [13]
RP INHIBITION BY M1 MUSCARINIC RECEPTORS.
RX MEDLINE=20150152; PubMed=10684873;
RA Shapiro M.S., Roche J.P., Kaftan E.J., Cruzblanca H., Mackie K.,
RA Hille B.;
RT "Reconstitution of muscarinic modulation of the KCNQ2/KCNQ3 K(+)
RT channels that underlie the neuronal M current.";
RL J. Neurosci. 20:1710-1721(2000).
RN [14]
RP INHIBITION BY M1 MUSCARINIC RECEPTORS.
RX MEDLINE=20178300; PubMed=10713961;
RA Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Jentsch T.J.,
RA Brown D.A.;
RT "Inhibition of KCNQ1-4 potassium channels expressed in mammalian cells
RT via M1 muscarinic acetylcholine receptors.";
RL J. Physiol. (Lond.) 522:349-355(2000).
RN [15]
RP ACTIVATION BY RETICABINE.
RX MEDLINE=20368587; PubMed=10908292;
RA Main M.J., Cryan J.E., Dupere J.R., Cox B., Clare J.J., Burbidge S.A.;
RT "Modulation of KCNQ2/3 potassium channels by the novel anticonvulsant
RT retigabine.";
RL Mol. Pharmacol. 58:253-262(2000).
RN [16]
RP ACTIVATION BY RETICABINE.
RX MEDLINE=20411474; PubMed=10953053;
RA Wickenden A.D., Yu W., Zou A., Jegla T., Wagoner P.K.;
RT "Retigabine, a novel anti-convulsant, enhances activation of KCNQ2/Q3
RT potassium channels.";
RL Mol. Pharmacol. 58:591-600(2000).
RN [17]
RP ACTIVATION BY RETICABINE.
RX MEDLINE=20180045; PubMed=10713399; DOI=10.1016/S0304-3940(00)00866-1;
RA Rundfeldt C., Netzer R.;
RT "The novel anticonvulsant retigabine activates M-currents in Chinese
RT hamster ovary-cells tranfected with human KCNQ2/3 subunits.";
RL Neurosci. Lett. 282:73-76(2000).
RN [18]
RP TISSUE DISTRIBUTION, AND BIOCHEMICAL CHARACTERIZATION.
RX MEDLINE=20243795; PubMed=10781098; DOI=10.1073/pnas.090092797;
RA Cooper E.C., Aldape K.D., Abosch A., Barbaro N.M., Berger M.S.,
RA Peacock W.S., Jan Y.N., Jan L.Y.;
RT "Colocalization and coassembly of two human brain M-type potassium
RT channel subunits that are mutated in epilepsy.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4914-4919(2000).
RN [19]
RP SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
RA Hillman R.T., Green R.E., Brenner S.E.;
RT "An unappreciated role for RNA surveillance.";
RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
RN [20]
RP VARIANT THR-780.
RX MEDLINE=99254826; PubMed=10323247;
RA Biervert C., Steinlein O.K.;
RT "Structural and mutational analysis of KCNQ2, the major gene locus for
RT benign familial neonatal convulsions.";
RL Hum. Genet. 104:234-240(1999).
RN [21]
RP VARIANT BFNC1 TRP-214.
RX MEDLINE=21037661; PubMed=11175290; DOI=10.1038/sj.ejhg.5200570;
RA Miraglia del Giudice E., Coppola G., Scuccimarra G., Cirillo G.,
RA Bellini G., Pascotto A.;
RT "Benign familial neonatal convulsions (BFNC) resulting from mutation
RT of the KCNQ2 voltage sensor.";
RL Eur. J. Hum. Genet. 8:994-997(2000).
CC -!- FUNCTION: Probably important in the regulation of neuronal
CC excitability. Associates with KCNQ3 to form a potassium channel
CC with essentially identical properties to the channel underlying
CC the native M-current, a slowly activating and deactivating
CC potassium conductance which plays a critical role in determining
CC the subthreshold electrical excitability of neurons as well as the

Query Match 39.2%; Score 1783; DB 1; Length 872;
Best Local Similarity 47.9%; Pred. No. 6.2e-91;
Matches 406; Conservative 88; Mismatches 180; Indels 174; Gaps 24;

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Qy      17 AARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLSYTSSQSCRRNVKYRRV 76
           :|   ||:|:|      |  | :| | ||     |||         :||  ||::
Db      34 STRDGALLIAGSEAPK---RGSILSKPRAGGAGA-----GKP--------PKRNAFYRKL 77

Qy      77 QNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVF 136
           ||:||||||||||||||:|||||| ||:||||||| |: | :   | ||| | ||||
Db      78 QNFLYNVLERPRGWAFIYHAYVFLLVFSCLVLSVFSTIKEYEKSSEGALYILEIVTIVVF 137

Qy     137 GLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSAL 196
           |:|: :|||:||||||||||:|||:|||||||||| :|||||||::| :|||:||||||
Db     138 GVEYFVRIWAAGCCCRYRGWRGRLKFARKPFCVIDIMVLIASIAVLAAGSQGNVFATSAL 197

Qy     197 RSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDA 256
           ||||||||||:|||||||||||||||||||||||:|||||||| || :|||||| ||
Db     198 RSLRFLQILRMIRMDRRGGTWKLLGSVVYAHSKELVTAWYIGFLCLILASFLVYLAEKGE 257

Qy     257 NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFA 316
           |  | ||||||||| |||||||||||| | || ||||:| | |:|:|||||||||||||||
Db     258 NDHFDTYADALWWGLITLTTIGYGDKYPQTWNGRLLAATFTLIGVSFFALPAGILGSGFA 317

Qy     317 LKVQEQHRQKHFEKRRNPAANLIQCVWRSYAAD-------------EKSVSIATWK---- 359
           |||||||||||||||||| |||  || || :             |::|::  :
Db     318 LKVQEQHRQKHFEKRRNPAAGLIQSAWRFYATNLSRTDLHSTWQYYERTVTVPMYSSQTQ 377

Qy     360 --------PHLKALHT-----------------------------------CSP--TNQKL 375
                   | |  |                                    | |  ::||:
Db     378 TYGASRLIPPLNQLELLRNLKSKSGLAFRKDPPPEPSPSKGSPCRGPLCGCCPGRSSQKV 437

Qy     376 SFKERVRMASPRGQSIKSRQASVGD--RRSPSTDITAEGSPTKVQKSWSFNDRTRFRPSL 433
           | |:||  :|||| : | : :      |||| | : | ||:|| ||||| ||:| | :
Db     438 SLKDRV-FSSPRGVAAKGKGSPQAQTVRRSPSADQSLEDSPSKVPKSWSFGDRSRARQAF 496

Qy     434 RLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKF 493
           |:| :  :   : : :|  :|: |:| | |:    ||||| ||  ||| :|:| |:|||
Db     497 RIKGAASRQNSE-EASLPGEDIVDDKSCPCEFVTEDLTPGLKVSIRAVCVMRFLVSKRKF 555
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Qy        494 KETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKGQITSDKKSREKITAEHETT 553
              ||:|||||| ||||||||||||||| ||||||:|||||:|:|   :| | | |  || |
Db        556 KESLRPYDVMDVIEQYSAGHLDMLSRIKSLQSRVDQIVGRGPAITD-KDRTKGPAEAELP 614

Qy        554 DDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPFEC------ 607
              :| ||:||: |||||| |:| ||| |::|| |  | |           ||| |
Db        615 EDPSMMGRLGKVEKQVLSMEKKLDFLVNIYMQ--RMG-----------IPPTETEAYFGA 661

Qy        608 ---EQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPNEFSAQTFYALSPT 664
                  |    | || ||::        ||: :   :: | |          |||    |  |
Db        662 KEPEPAPPYHSPEDSRE---HVDRHGCIVKIVRSSSSTG------QKNFSAPP--AAPP- 709

Qy        665 MHSQATQVPISQS--------DGSAVAATNTIANQINTAPKPAAPTTLQI---------- 706
                  | | | |         |   :      : :   | ||   :|
Db        710 -----VQCPPSTSWQPQSHPRQGHGTSPVGDHGSLVRIPPPPAHERSLSAYGGGNRASME 764

Qy        707 -----------PP-----------PLPAIKHLPRPETLHPNPAGLQESISDVTTCLVASK 744
                        ||           :|:: |    | |  : :|   |||         ||
Db        765 FLRQEDTPGCRPPEGNLRDSDTSISIPSVDH----EELERSFSGF--SISQ-------SK 811

Qy        745 ENVQVAQS 752
              ||:   |
Db        812 ENLDALNS 819
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RESULT 9
CIQ2_MOUSE
ID   CIQ2_MOUSE     STANDARD;      PRT;   759 AA.
AC   Q9Z351; Q9QWN9; Q9Z342; Q9Z343; Q9Z344; Q9Z345; Q9Z346; Q9Z347;
AC   Q9Z348; Q9Z349; Q9Z350;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Potassium voltage-gated channel subfamily KQT member 2 (Voltage-gated
DE   potassium channel subunit Kv7.2) (Potassium channel alpha subunit
DE   KvLQT2) (KQT-like 2).
GN   Name=Kcnq2; Synonyms=Kqt2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7; 8; 9; 10 AND 11).
RC   TISSUE=Brain;
RX   MEDLINE=98330948; PubMed=9666519;
RA   Nakamura M., Watanabe H., Kubo Y., Yokoyama M., Matsumoto T.,
RA   Sasai H., Nishi Y.;
RT   "KQT2, a new putative potassium channel family produced by alternative
RT   splicing. Isolation, genomic structure, and alternative splicing of
RT   the putative potassium channels.";
RL   Recept. Channels 5:255-271(1998).
RN   [2]
RP   ROLE IN NEURAL HYPEREXCITABILITY.
RX   MEDLINE=20312851; PubMed=10854243;
RA   Watanabe H., Nagata E., Kosakai A., Nakamura M., Yokoyama M.,
RA   Tanaka K., Sasai H.;
RT   "Disruption of the epilepsy KCNQ2 gene results in neural
RT   hyperexcitability.";
RL   J. Neurochem. 75:28-33(2000).
CC   -!- FUNCTION: Probably important in the regulation of neuronal
CC       excitability. Associates with KCNQ3 to form a potassium channel
CC       with essentially identical properties to the channel underlying
CC       the native M-current, a slowly activating and deactivating
CC       potassium conductance which plays a critical role in determining
CC       the subthreshold electrical excitability of neurons as well as the
CC       responsiveness to synaptic inputs.
CC   -!- SUBUNIT: Heteromultimer with KCNQ3.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=11;
CC       Name=1; Synonyms=MKQT2.1;
CC         IsoId=Q9Z351-1; Sequence=Displayed;
CC       Name=2; Synonyms=MKQT2.2;
CC         IsoId=Q9Z351-2; Sequence=VSP_001001;
CC       Name=3; Synonyms=MKQT2.3;
CC         IsoId=Q9Z351-3; Sequence=VSP_001000;
CC       Name=4; Synonyms=MKQT2.4;
CC         IsoId=Q9Z351-4; Sequence=VSP_001002;
CC       Name=5; Synonyms=MKQT2.5;
CC         IsoId=Q9Z351-5; Sequence=VSP_001003, VSP_001004;
CC       Name=6; Synonyms=MKQT2.6;
CC         IsoId=Q9Z351-6; Sequence=VSP_001005, VSP_001006;
CC       Name=7; Synonyms=MKQT2.7;
CC         IsoId=Q9Z351-7; Sequence=VSP_000997, VSP_000998, VSP_000999;
CC       Name=8; Synonyms=MKQT2.8;
CC         IsoId=Q9Z351-8; Sequence=VSP_000998, VSP_000999;
CC       Name=9; Synonyms=MKQT2.9;
CC         IsoId=Q9Z351-9; Sequence=VSP_000993, VSP_000994;
CC       Name=10; Synonyms=MKQT2.10;
CC         IsoId=Q9Z351-10; Sequence=VSP_000995, VSP_000996;
CC       Name=11; Synonyms=MKQT2.11;
CC         IsoId=Q9Z351-11; Sequence=VSP_000991, VSP_000992;
CC   -!- TISSUE SPECIFICITY: Exclusively expressed in the brain. Expressed
CC       in every neuron-containing regions of the central nervous system
CC       examined, such as the cerebellum, cerebral cortex, occipital pole,
CC       substantia nigra, amygdala, caudate nucleus, hippocampus and
CC       thalamus. Also detected in the cochlea.
CC   -!- DEVELOPMENTAL STAGE: Detected at day 11, 15 and 17 of the
CC       embryonic development. Expression increases by a factor of 2.5 at
CC       1 week after birth. Then the expression level remains stable until
CC       the adult stage. The mRNAs for shorter forms (isoforms 9, 10 and
CC       11) are specifically expressed in an embryo on the 11th day after
CC       gestation.
CC   -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC       characterized by a series of positively charged amino acids at
CC       every third position (By similarity).
CC   -!- SIMILARITY: Belongs to the potassium channel family. KQT
CC       subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB000494; BAA37156.1; -.
DR   EMBL; AB000495; BAA37157.1; -.
DR   EMBL; AB000496; BAA37158.1; -.
DR   EMBL; AB000497; BAA37159.1; -.
DR   EMBL; AB000498; BAA37160.1; -.
DR   EMBL; AB000499; BAA37161.1; -.
DR   EMBL; AB000500; BAA37162.1; -.
DR   EMBL; AB000501; BAA37163.1; -.
DR   EMBL; AB000502; BAA37164.1; -.
DR   EMBL; AB000503; BAA37165.1; -.
DR   EMBL; AB000504; BAA37166.1; -.
DR   MGD; MGI:1309503; Kcnq2.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003091; K_channel.
DR   InterPro; IPR003937; KCNQ_channel.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF03520; KCNQ_channel; 1.
DR   PRINTS; PR00169; KCHANNEL.
KW   Alternative splicing; Ion transport; Ionic channel; Multigene family;
KW   Phosphorylation; Potassium; Potassium channel; Potassium transport;
KW   Transmembrane; Transport; Voltage-gated channel.
FT   TRANSMEM     92    112       Segment S1 (Potential).
FT   TRANSMEM    123    143       Segment S2 (Potential).
FT   TRANSMEM    167    187       Segment S3 (Potential).
FT   TRANSMEM    198    221       Segment S4 (Potential).
FT   TRANSMEM    232    252       Segment S5 (Potential).
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FT   TRANSMEM     292    312       Segment S6 (Potential).
FT   DOMAIN       265    285       Segment H5 (pore-forming) (Potential).
FT   SITE         277    282       Selectivity filter (By similarity).
FT   MOD_RES       52     52       Phosphoserine (by PKA) (By similarity).
FT   VARSPLIC     310    338       GILGSGFALKVQEQHRPKHFEKRRNPAAG -> VSPAHLPT
FT                                 LEMLGVLEAPHKAWPWPTCEL (in isoform 11).
FT                                 /FTId=VSP_000991.
FT   VARSPLIC     339    759       Missing (in isoform 11).
FT                                 /FTId=VSP_000992.
FT   VARSPLIC     342    349       SAWRFYAT -> GQVRCAGH (in isoform 9).
FT                                 /FTId=VSP_000993.
FT   VARSPLIC     350    759       Missing (in isoform 9).
FT                                 /FTId=VSP_000994.
FT   VARSPLIC     342    347       SAWRFY -> VSLSPC (in isoform 10).
FT                                 /FTId=VSP_000995.
FT   VARSPLIC     348    759       Missing (in isoform 10).
FT                                 /FTId=VSP_000996.
FT   VARSPLIC     372    372       Y -> YSSQTQTYGAS (in isoform 7).
FT                                 /FTId=VSP_000997.
FT   VARSPLIC     406    463       SQKVSLKDRVFSSPRGMAAKGKGSPQAQTVRRSPSADQSLD
FT                                 DSPSKVPKSWSFGDRSR -> RSVPPASSRPGVCCTHLALL
FT                                 SLCIHHVSWGRATMGPCVCFYVQQVTVCPGTPRVTSQL
FT                                 (in isoform 7 and isoform 8).
FT                                 /FTId=VSP_000998.
FT   VARSPLIC     464    759       Missing (in isoform 7 and isoform 8).
FT                                 /FTId=VSP_000999.
FT   VARSPLIC     407    418       Missing (in isoform 3).
FT                                 /FTId=VSP_001000.
FT   VARSPLIC     562    596       IDMIVGPPPPSTPRDKKYPTKGPTAPSRESPQYSP -> QE
FT                                 PLPVQSGHEQGPPGQNQAWHKGHQGLGD (in isoform
FT                                 2).
FT                                 /FTId=VSP_001001.
FT   VARSPLIC     562    597       Missing (in isoform 4).
FT                                 /FTId=VSP_001002.
FT   VARSPLIC     562    570       IDMIVGPPP -> SCDWRGVLA (in isoform 5).
FT                                 /FTId=VSP_001003.
FT   VARSPLIC     571    759       Missing (in isoform 5).
FT                                 /FTId=VSP_001004.
FT   VARSPLIC     562    623       IDMIVGPPPPSTPRDKKYPTKGPTAPSRESPQYSPRVDHIV
FT                                 GRGPTITDKDRTKGPAETELP -> QEPLPVQSGHEQGPPG
FT                                 QNQAWHKGHQGLGDRCAEQGQYQLWRSLPTLLASCCFLLCF
FT                                 HTVCF (in isoform 6).
FT                                 /FTId=VSP_001005.
FT   VARSPLIC     624    759       Missing (in isoform 6).
FT                                 /FTId=VSP_001006.
FT   CONFLICT     125    125       A -> P (in Ref. 1; BAA37161).
FT   CONFLICT     326    326       P -> Q (in Ref. 1; BAA37160/BAA37165).
SQ   SEQUENCE   759 AA;  84450 MW;  C1D12DBFF3979D3F CRC64;

  Query Match           38.6%;  Score 1754;  DB 1;  Length 759;
  Best Local Similarity  51.9%;  Pred. No. 2.1e-89;
  Matches  387;  Conservative   73;  Mismatches  149;  Indels  136;  Gaps   18;

Qy         17 AARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGKPLSYTSSQSCRRNVKYRRV 76
              : |   ||: |: |     |  | : | |  ||     |||          :||  ||::
Db         34 STRDGALLIAGSEAPK---RGSVLSKPRTGGAGA-----GKP---------PKRNAFYRKL 77

Qy         77 QNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVF 136
              ||:||||||||||||||:|||||| ||:||||||| |: | :    | ||| | ||||
Db         78 QNFLYNVLERPRGWAFIYHAYVFLLVFSCLVLSVFSTIKEYEKSSEGALYILEIVTIVVF 137

Qy        137 GLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSAL 196
              |:|: :|||:|||||||||:|||:|||||||||| :||||||||::|  :|||:||||||
Db        138 GVEYFVRIWAAGCCCRYRGWRGRLKFARKPFCVIDIMVLIASIAVLAAGSQGNVFATSAL 197

Qy        197 RSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDA 256
              ||||||||||:|||||||||||||||||||||||:|||||||| || :|||||| ||
Db        198 RSLRFLQILRMIRMDRRGGTWKLLGSVVYAHSKELVTAWYIGFLCLILASFLVYLAEKGE 257

Qy        257 NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFA 316
              |  | ||||||||| |||||||||| | || ||||:| | |:|:|||||||||||||||
Db        258 NDHFDTYADALWWGLITLTTIGYGDKYPQTWNGRLLAATFTLIGVSFFALPAGILGSGFA 317

Qy        317 LKVQEQHRQKHFEKRRNPAANLIQCVWRSYAAD------------EKSVSIATWK--PH 361
              ||||||||| |||||||||||| |||   || || :                |::|::  ::  |
Db        318 LKVQEQHRPKHFEKRRNPAAGLIQSAWRFYATNLSRTDLHSTWQYYERTVTVPMYRLIPP 377

Qy        362 LKALHTC------------------SPTNQKLSFKERVRMASPRGQSIKSRQASVGD-- 400
              |  |                    || :||:| |:||  :|||| : | : :
Db        378 LNQLELLRNLKSKSGLTFRKEPQPEPSP-SQKVSLKDRV-FSSPRGMAAKGKGSPQAQTV 435

Qy        401 RRSPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKG 460
              ||||| | : : ||:|| ||||| ||:| | : |:| : :   :   :  | | | | |
Db        436 RRSPSADQSLDDSPSKVPKSWSFGDRSRTRQAFRIKGAASRQNSEEASLPGEDIVEDNKS 495

Qy        461 CQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRI 520
              | |:   ||||| ||  |||: :|:| |:|||||:|||||| |||||||||||||| ||
Db        496 CNCEFVTEDLTPGLKVSIRAVCVMRFLVSKRKFKESLRPYDVMDVIEQYSAGHLDMLSRI 555

Qy        521 KSLQT-----------------------------------RVDQILGKGQITSDKKSRE 544
              ||||:                                   ||| |:|:|   :| | |
Db        556 KSLQSRIDMIVGPPPPSTPRDKKYPTKGPTAPSRESPQYSPRVDHIVGRGPTITD-KDRT 614

Qy        545 KITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPP 604
              |  || |  :| ||:||: |||||| |:| ||| |: || |  | |           |||
Db        615 KGPAETELPEDPSMMGRLGKVEKQVLSMEKKLDFLVSIYTQ--RMG----------IPP 661

Qy        605 FEC---------EQTSDYQSPVDSKDLSGSAQNSGC---LSRSTSANISRGLQFILTPNE 652
              |         |    | || ||:|    |   ||   : ||||:
Db        662 AETEAYFGAKEPEPAPPYHSPEDSRD---HADKHGCIIKIVRSTSS-------------- 704

Qy        653 FSAQTFYALSPTMHSQATQVPISQS 677
               : |  ||  | :     | | | |
Db        705 -TGQRNYAAPPAI--PPAQCPPSTS 726
```

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RESULT 10
CIQ3_HUMAN
ID   CIQ3_HUMAN     STANDARD;      PRT;   872 AA.
AC   O43525;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Potassium voltage-gated channel subfamily KQT member 3 (Voltage-gated
DE   potassium channel subunit Kv7.3) (Potassium channel alpha subunit
DE   KvLQT3) (KQT-like 3).
GN   Name=KCNQ3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., CHARACTERIZATION OF VARIANT BFNC2 VAL-310, AND
RP   MUTAGENESIS OF GLY-318.
RC   TISSUE=Brain;
RX   MEDLINE=99087323; PubMed=9872318; DOI=10.1038/25367;
RA   Schroeder B.C., Kubisch C., Stein V., Jentsch T.J.;
RT   "Moderate loss of function of cyclic-AMP-modulated KCNQ2/KCNQ3 K+
RT   channels causes epilepsy.";
RL   Nature 396:687-690(1998).
RN   [2]
RP   SEQUENCE OF 48-872 FROM N.A., AND VARIANT BFNC2 VAL-310.
RC   TISSUE=Brain;
RX   MEDLINE=98085869; PubMed=9425900;
RA   Charlier C., Singh N.A., Ryan S.G., Lewis T.B., Reus B.E., Leach R.J.,
RA   Leppert M.;
RT   "A pore mutation in a novel KQT-like potassium channel gene in an
RT   idiopathic epilepsy family.";
RL   Nat. Genet. 18:53-55(1998).
RN   [3]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC   TISSUE=Brain, and Fetal brain;
RX   MEDLINE=98344027; PubMed=9677360; DOI=10.1074/jbc.273.31.19419;
RA   Yang W.-P., Levesque P.C., Little W.A., Conder M.L., Ramakrishnan P.,
RA   Neubauer M.G., Blanar M.A.;
RT   "Functional expression of two KvLQT1-related potassium channels
```

RT responsible for an inherited idiopathic epilepsy.";
RL J. Biol. Chem. 273:19419-19423(1998).
RN [4]
RP INVOLVEMENT IN M-LIKE CURRENT.
RX MEDLINE=99410758; PubMed=10479678;
RA Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Delmas P.,
RA Buckley N.J., London B., Brown D.A.;
RT "Two types of K(+) channel subunit, Erg1 and KCNQ2/3, contribute to
RT the M-like current in a mammalian neuronal cell.";
RL J. Neurosci. 19:7742-7756(1999).
RN [5]
RP ASSOCIATION WITH KCNE2.
RX MEDLINE=20487128; PubMed=11034315; DOI=10.1016/S0014-5793(00)01918-9;
RA Tinel N., Diochot S., Lauritzen I., Barhanin J., Lazdunski M.,
RA Borsotto M.;
RT "M-type KCNQ2-KCNQ3 potassium channels are modulated by the KCNE2
RT subunit.";
RL FEBS Lett. 480:137-141(2000).
RN [6]
RP SURFACE EXPRESSION OF HETEROMERS.
RX MEDLINE=20250883; PubMed=10788442; DOI=10.1074/jbc.275.18.13343;
RA Schwake M., Pusch M., Kharkovets T., Jentsch T.J.;
RT "Surface expression and single channel properties of KCNQ2/KCNQ3, M-
RT type K+ channels involved in epilepsy.";
RL J. Biol. Chem. 275:13343-13348(2000).
RN [7]
RP INHIBITION BY M1 MUSCARINIC RECEPTORS.
RX MEDLINE=20150152; PubMed=10684873;
RA Shapiro M.S., Roche J.P., Kaftan E.J., Cruzblanca H., Mackie K.,
RA Hille B.;
RT "Reconstitution of muscarinic modulation of the KCNQ2/KCNQ3 K(+)
RT channels that underlie the neuronal M current.";
RL J. Neurosci. 20:1710-1721(2000).
RN [8]
RP INHIBITION BY M1 MUSCARINIC RECEPTORS.
RX MEDLINE=20178300; PubMed=10713961;
RA Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Jentsch T.J.,
RA Brown D.A.;
RT "Inhibition of KCNQ1-4 potassium channels expressed in mammalian cells
RT via M1 muscarinic acetylcholine receptors.";
RL J. Physiol. (Lond.) 522:349-355(2000).
RN [9]
RP ACTIVATION BY RETICABINE.
RX MEDLINE=20368587; PubMed=10908292;
RA Main M.J., Cryan J.E., Dupere J.R., Cox B., Clare J.J., Burbidge S.A.;
RT "Modulation of KCNQ2/3 potassium channels by the novel anticonvulsant
RT retigabine.";
RL Mol. Pharmacol. 58:253-262(2000).
RN [10]
RP ACTIVATION BY RETICABINE.
RX MEDLINE=20411474; PubMed=10953053;
RA Wickenden A.D., Yu W., Zou A., Jegla T., Wagoner P.K.;
RT "Retigabine, a novel anti-convulsant, enhances activation of KCNQ2/Q3
RT potassium channels.";
RL Mol. Pharmacol. 58:591-600(2000).
RN [11]
RP ACTIVATION BY RETICABINE.
RX MEDLINE=20180045; PubMed=10713399; DOI=10.1016/S0304-3940(00)00866-1;
RA Rundfeldt C., Netzer R.;
RT "The novel anticonvulsant retigabine activates M-currents in Chinese
RT hamster ovary-cells tranfected with human KCNQ2/3 subunits.";
RL Neurosci. Lett. 282:73-76(2000).
RN [12]
RP CHARACTERIZATION, AND ACTIVATION BY RETICABINE.
RX MEDLINE=21095345; PubMed=11159685;
RA Wickenden A.D., Zou A., Wagoner P.K., Jegla T.;
RT "Characterization of KCNQ5/Q3 potassium channels expressed in
RT mammalian cells.";
RL Br. J. Pharmacol. 132:381-384(2001).
RN [13]
RP VARIANT BFNC2 ARG-309.
RX MEDLINE=20309392; PubMed=10852552;
RX DOI=10.1002/1531-8249(200006)47:6<822::AID-ANA19>3.3.CO;2-O;
RA Hirose S., Zenri F., Akiyoshi H., Fukuma G., Iwata H., Inoue T.,
RA Yonetani M., Tsutsumi M., Muranaka H., Kurokawa T., Hanai T., Wada K.,
RA Kaneko S., Mitsudome A.;
RT "A novel mutation of KCNQ3 (c.925T-->C) in a Japanese family with
RT benign familial neonatal convulsions.";
RL Ann. Neurol. 47:822-826(2000).
CC -!- FUNCTION: Probably important in the regulation of neuronal
CC excitability. Associates with KCNQ2 or KCNQ5 to form a potassium
CC channel with essentially identical properties to the channel
CC underlying the native M-current, a slowly activating and
CC deactivating potassium conductance which plays a critical role in
CC determining the subthreshold electrical excitability of neurons as
CC well as the responsiveness to synaptic inputs.
CC -!- SUBUNIT: Heteromultimer with KCNQ2 or KCNQ5. May associate with
CC KCNE2.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Predominantly expressed in brain.
CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position (By similarity).
CC -!- DISEASE: Defects in KCNQ3 are the cause of benign familial
CC neonatal convulsions type 2 (BFNC2) [MIM:121201]; also known as
CC epilepsy, benign neonatal type 2 (EBN2). BFNC2 is an autosomal
CC dominant form of epilepsy in the newborn that clears spontaneously
CC after a few weeks and is followed by normal psychomotor
CC development.
CC -!- MISCELLANEOUS: Mutagenesis experiments were carried out in Xenopus
CC oocytes by coexpression of either KCNQ3(mut) and KCNQ2 at the
CC ratio of 1:1, or of KCNQ3(mut), KCNQ3(wt) and KCNQ2 at the ratio
CC of 1:1:2, to mimic the situation in a heterozygous patient with
CC BFNC2 disease.
CC -!- SIMILARITY: Belongs to the potassium channel family. KQT
CC subfamily.
CC ---

CC ---
DR EMBL; AF071491; AAC96101.1; -.
DR EMBL; AF071478; AAC96101.1; JOINED.
DR EMBL; AF071479; AAC96101.1; JOINED.
DR EMBL; AF071480; AAC96101.1; JOINED.
DR EMBL; AF071481; AAC96101.1; JOINED.
DR EMBL; AF071482; AAC96101.1; JOINED.
DR EMBL; AF071483; AAC96101.1; JOINED.
DR EMBL; AF071484; AAC96101.1; JOINED.
DR EMBL; AF071485; AAC96101.1; JOINED.
DR EMBL; AF071486; AAC96101.1; JOINED.
DR EMBL; AF071487; AAC96101.1; JOINED.
DR EMBL; AF071488; AAC96101.1; JOINED.
DR EMBL; AF071489; AAC96101.1; JOINED.
DR EMBL; AF071490; AAC96101.1; JOINED.
DR EMBL; AF033347; AAB97314.1; -.
DR HSSP; Q54397; 1JVM.
DR Genew; HGNC:6297; KCNQ3.
DR MIM; 602232; -.
DR MIM; 121201; -.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; TAS.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; TAS.
DR GO; GO:0006813; P:potassium ion transport; TAS.
DR GO; GO:0007268; P:synaptic transmission; TAS.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003937; KCNQ_channel.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF03520; KCNQ_channel; 1.
DR PRINTS; PR00169; KCHANNEL.

```
KW   Disease mutation; Epilepsy; Ion transport; Ionic channel;
KW   Multigene family; Potassium; Potassium channel; Potassium transport;
KW   Transmembrane; Transport; Voltage-gated channel.
FT   TRANSMEM     122     142       Segment S1 (Potential).
FT   TRANSMEM     153     173       Segment S2 (Potential).
FT   TRANSMEM     197     217       Segment S3 (Potential).
FT   TRANSMEM     226     247       Segment S4 (Potential).
FT   TRANSMEM     262     282       Segment S5 (Potential).
FT   TRANSMEM     331     351       Segment S6 (Potential).
FT   DOMAIN       304     324       Segment H5 (pore-forming) (Potential).
FT   DOMAIN        13      24       Poly-Gly.
FT   SITE         316     321       Selectivity filter (By similarity).
FT   VARIANT      309     309       W -> R (in BFNC2).
FT                                  /FTId=VAR_010935.
FT   VARIANT      310     310       G -> V (in BFNC2; about 50% reduction of
FT                                  wild-type heteromeric current; ratio of

  Query Match             34.9%;  Score 1587.5;  DB 1;  Length 872;
  Best Local Similarity   42.8%;  Pred. No. 4.8e-80;
  Matches  386;  Conservative  106;  Mismatches  244;  Indels  165;  Gaps   28;

Qy          3 DVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGK-PLSY 61
              |||       |  | |  || |||          |||     ||  ||  : || | |||
Db         49 DVEQ---VTLALGAGADKDGTLLL--------EGGGRDEGQRRTPQG--IGLLAKTPLSR 95

Qy         62 TSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLA 121
                | | ||||:|  :|: |||||||| :||| |||:| |||||:| :|  |:  ::
Db         96 PVK---RNNAKYRRIQTLIYDALERPRGWALLYHALVFLIVLGCLILAVLTTFKEYETVS 152

Qy        122 SSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAV 181
              ||:||   | :|| || :|||:|||||||:||:|||:||||| |::|  |||||: |
Db        153 GDWLLLLETFAIFIFGAEFALRIWAAGCCCRYKGWRGRLKFARKPLCMLDIFVLIASVPV 212

Qy        182 VSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLV 241
              |:   |||: ||| |||||||||||:|||||||||||||| : ||||||||||||||
Db        213 VAVGNQGNVLATS-LRSLRFLQILRMLRMDRRGGTWKLLGSAICAHSKELITAWYIGFLT 271

Qy        242 LIFSSFLVYLVEKDA----------NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRL 291
              || |||||||||||            :|| ||||||||| ||| |||||||||| || |||
Db        272 LILSSPLVYLVEKDVPEVDAQGEEMKEEFETYADALWWGLITLATIGYGDKTPKTWEGRL 331

Qy        292 LSAGFALLGISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEK 351
              ::| |:|:|:|||||||||||| |||||||||||||||| ||| |||  || || :
Db        332 IAATFSLIGVSFFALPAGILGSGLALKVQEQHRQKHFEKRRKPAAELIQAAWRYYATNPN 391

Qy        352 SVS-IATWK--------PHLKALHTCSPTNQKLSFKERVRMASPRGQSIKSRQASVGDRR 402
               :  :|||:       |  :     : ::|||   :|||:::||| : |      |
Db        392 RIDLVATWRFYESVVSFPFFRKEQLEAASSQKLGLLDRVRLSNPRGSNTK------GKLF 445

Qy        403 SPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRLK------SSQPKPVIDADTALGTDDVY 456
              :|       | ||:|  |    |:: ||| : |:|       ||:     || |    | :
Db        446 TPLNVDAIEESPSKEPKPVGLNNKERFRTAFRMKAYAFWQSSE-----DAGTG---DPMA 497

Qy        457 DEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDM 516
              :::|    |  :||: | ||  |||:||::| : |:|||||||||||||||||||||||
Db        498 EDRGYGNDFPIEDMIPTLKAAIRAVRILQFRLYKKKFKETLRPYDVKDVIEQYSAGHLDM 557

Qy        517 LCRIKSLQTRVDQILGKGQITSDKKSR----------------EKITAEHETT--DDLS 557
              | ||| ||||:| |   |  :: |  :                |    |   |:  :| |
Db        558 LSRIKYLQTRIDMIFTPGPPSTPKHKKSQKGSAFTFPSQQSPRNEPYVARPSTSEIEDQS 617

Qy        558 MLGRVVKVEKQVQSIESKLDCLLDIYQQVLR-----------KGSASALALASFQIPPF 605
              |:|: ||||:||| :  ||| |:|:: | :            ||::|          |
Db        618 MMGKFVKVERQVQDMGKKLDFLVDMHMQHMERLQVQVTEYYPTKGTSS----------PA 667

Qy        606 ECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPNEFSAQTFYALSPTM 665
              | |:  | :   | | :  :|       | :        :| :: |   |:|  |
Db        668 EAEKKEDNRYS-DLKTIICNYSETGPPEPPYSFH-------QVTIDKVSPYGFFAHDP-- 717

Qy        666 HSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLPAIKHLPRPETLHPN 725
                :|        | ||          |  :| | :: |  || :  |    : | :
Db        718 ----VNLPRGGPSSGKVQAT----------PPSSATTYVERPTVLPILTLLDSRVSCH-S 762

Qy        726 PAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETLLSVCPMVPKDLGKS 785
              | ||   ||          :   |         |:|    :| ||:
Db        763 QADLQGPYSD----------RISPRQ---------RRSITRDSDTPLSL---------- 792

Qy        786 LSVQNLIRSTEELNIQLSGSESSGSRGSQDFYP----KWRESKLFITDEEVGPEETETDT 841
              :|| :    |||    ||  |  |   | |     |  | :: :   |  :|:||
Db        793 MSVNH-----EELERSPSGFSISQDRDDYVFGPNGGSSWMREKRYLAE---GETDTDTDP 844

Qy        842 F 842
              |
Db        845 F 845
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RESULT 11
CIQ3_BOVIN
ID   CIQ3_BOVIN   STANDARD;   PRT;   866 AA.
AC   P58126;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Potassium voltage-gated channel subfamily KQT member 3 (Voltage-gated
DE   potassium channel subunit Kv7.3) (Potassium channel alpha subunit
DE   KvLQT3) (KQT-like 3).
GN   Name=KCNQ3;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Rae J.L.;
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Probably important in the regulation of neuronal
CC   excitability. Associates with KCNQ2 to form a potassium channel
CC   with essentially identical properties to the channel underlying
CC   the native M-current, a slowly activating and deactivating
CC   potassium conductance which plays a critical role in determining
CC   the subthreshold electrical excitability of neurons as well as the
CC   responsiveness to synaptic inputs.
CC   -!- SUBUNIT: Heteromultimer with KCNQ2 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC   characterized by a series of positively charged amino acids at
CC   every third position (By similarity).
CC   -!- SIMILARITY: Belongs to the potassium channel family. KQT
CC   subfamily.
CC   ---
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; AF325548; AAK11221.1; -.
DR   HSSP; Q54397; 1JVM.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003091; K_channel.
DR   InterPro; IPR003937; KCNQ_channel.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF03520; KCNQ_channel; 1.
DR   PRINTS; PR00169; KCHANNEL.
KW   Ion transport; Ionic channel; Multigene family; Potassium;
KW   Potassium channel; Potassium transport; Transmembrane; Transport;
KW   Voltage-gated channel.
FT   TRANSMEM   122   142   Segment S1 (Potential).
FT   TRANSMEM   153   173   Segment S2 (Potential).
FT   TRANSMEM   197   217   Segment S3 (Potential).
FT   TRANSMEM   226   247   Segment S4 (Potential).

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FT   TRANSMEM     262    282       Segment S5 (Potential).
FT   TRANSMEM     331    351       Segment S6 (Potential).
FT   DOMAIN       304    324       Segment H5 (pore-forming) (Potential).
FT   DOMAIN        13     24       Poly-Gly.
FT   SITE         316    321       Selectivity filter (By similarity).
SQ   SEQUENCE   866 AA;  95644 MW;  43996161F07A0424 CRC64;

  Query Match             34.2%;  Score 1556.5;  DB 1;  Length 866;
  Best Local Similarity   41.6%;  Pred. No. 2.5e-78;
  Matches  384;  Conservative   99;  Mismatches  258;  Indels  181;  Gaps   29;

Qy          3 DVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGK-PLSY 61
              |||       |   | |  || |||         |||     ||  ||  : || | |||
Db         49 DVEQ---VTLALGAGADKDGTLLL--------EGGGRDEGQRRTPQG--IGLLAKTPLSR 95

Qy         62 TSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLA 121
                 | | ||||:|  :|: |||||||| :||| |||:| |||||:| :|  |:  ::
Db         96 PVK---RNNAKYRRIQTLIYDALERPRGWALLYHALVFLIVLGCLILAVLTTFREYETVS 152

Qy        122 SSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAV 181
               ||:||   | :|| || :|||:|||||||:||:|||:||||| |::|  |||||: |
Db        153 GDWLLLLETFAIFIFGAEFALRIWAAGCCCRYKGWRGRLKFARKPLCMLDIFVLIASVPV 212

Qy        182 VSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLV 241
              |:   |||: ||| |||||||||||:||||||||||||| : ||||||||||||||
Db        213 VAVGNQGNVLATS-LRSLRFLQILRMLRMDRRGGTWKLLGSAICAHSKELITAWYIGFLT 271

Qy        242 LIFSSFLVYLVEKDA----------NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRL 291
              || |||||||||||           :|| ||||||||| ||| |||||||| || |||
Db        272 LILSSFLVYLVEKDVPEVDAQGEEMKEEFETYADALWWGLITLATIGYGDKTPKTWEGRL 331

Qy        292 LSAGFALLGISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEK 351
              ::| |:|:|:|||||||||||||| ||||||||||||||||| ||| |||  || || :
Db        332 IAATFSLIGVSFFALPAGILGSGLALKVQEQHRQKHFEKRRKPAAELIQAAWRYYATNPN 391

Qy        352 SVS-IATWK--------PHLKALHTCSPTNQKLSFKERVRMASPRGQSIKSRQASVGDRR 402
               :  :|||:        |  :       :|||   :|||:::||| : |       |
Db        392 RIDLVATWRFYESVVSFPPFRKEQLDPAASQKLGLLDRVRLSNPRGSNTK------GKLF 445

Qy        403 SPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRLK------SSQPKPVIDADTALGTDDVY 456
              :|      | ||:|  |    |:: ||| : |:|      ||:     || |    |
Db        446 TPLNVDAIEESPSKEPKPVGSNNKERFRTAFRMKAYAFWQSSE-----DAGTG---DPTA 497

Qy        457 DEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDM 516
              :::|   |  :||: | ||  |||:||::| : |:||||||||||||||||||||||
Db        498 EDRGYGNDFLIEDMIPTLKAAIRAVRILQFRLYKKKFKETLRPYDVKDVIEQYSAGHLDM 557

Qy        517 LCRIKSLQTRVDQILGKGQITSDKKSR----------------EKITAEHET--TDDLS 557
              | ||| ||||:| |   |  :: |  :                |   |   |  |:| |
Db        558 LSRIKYLQTRIDMIFTPGPPSTPKHKKSQRGAAFTYPSQQSPRNEPYVARPSTSETEDQS 617

Qy        558 MLGRVVKVEKQVQSIESKLDCLLDIYQQVLR------------KGSASALALASFQIPPF 605
              |:|: ||||:||  :  ||| |:|:: | :             ||::|         |
Db        618 MMGKFVKVERQVHDMGKKLDFLVDMHLQHMERLQVHVAGFSPSKGASS----------PA 667

Qy        606 ECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFILTPNEFSAQTFYALSPTM 665
              | ||  | :  | | :  :  :|                              :|
Db        668 EAEQKED-RRDADLKTIICNYSETG------------------------------APDA 695

Qy        666 HSQATQVPISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLPAIKHLPRPETLHPN 725
                  |||: :     |      |:          | |    ||       |      |
Db        696 PYSFHQVPVDK-----VGPYGFFAHD---------PVNL----PLGG----PSSGKGHAT 733

Qy        726 PAGLQESISDVTTCLVA-SKENVQVAQSNLTKDR---SMRKSFDMGGETLLSVCPMVPKD 781
              |   : ::  : | | :      ||      ||      |:|     :| ||:
Db        734 PYAERPTVLPILTLLDSRGSYRSQVELHGPCSDRVSPRQRRSITRDSDTPLSL------- 786

Qy        782 LGKSLSVQNLIRSTEELNIQLSGSESSGSRGSQDFYP----KWRESKLFITDEEVGPEET 837
              :|| :     |||    ||   |  |    | |     |   | :: :      ||
Db        787 ----MSVNH-----EELERSPSGFSISQDRDDYAFGPSGGSSWMREKRYLAE-----GET 832

Qy        838 ETDTFDAAPQPAREAAFASDSL 859
              :|||    |  :   :   | :
Db        833 DTDTEPFTPSGSLPLSSTGDGI 854


RESULT 12
Q8K3F6
ID   Q8K3F6      PRELIMINARY;      PRT;   873 AA.
AC   Q8K3F6;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Potassium voltage-gated channel subfamily Q member 3.
GN   Name=Kcnq3;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Isbrandt D., Peters H.C., Pongs O.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY118171; AAM81579.1; -.
DR   HSSP; Q54397; 1J95.
DR   MGD; MGI:1336181; Kcnq3.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR   GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006813; P:potassium ion transport; IEA.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003948; KCNQ3_channel.
DR   InterPro; IPR003937; KCNQ_channel.
DR   InterPro; IPR003091; K_channel.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF03520; KCNQ_channel; 1.
DR   PRINTS; PR00169; KCHANNEL.
DR   PRINTS; PR01462; KCNQ3CHANNEL.
DR   PRINTS; PR01459; KCNQCHANNEL.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
SQ   SEQUENCE   873 AA;  96796 MW;  B216709DA8CCFE9E CRC64;

  Query Match             34.2%;  Score 1556.5;  DB 2;  Length 873;
  Best Local Similarity   42.1%;  Pred. No. 2.6e-78;
  Matches  376;  Conservative  107;  Mismatches  261;  Indels  149;  Gaps   25;

Qy          3 DVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGK-PLSY 61
              |||       |   | |  || |||         |||     ||  ||  : || | |||
Db         50 DVEQ---VTLALGAGADKDGTLLL--------EGGGREEGQRRTPQG--IGLLAKTPLSR 96

Qy         62 TSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLA 121
                 | | ||||:|  :|: |||||||| :||| |||:| |||||:| :|  |:  ::
Db         97 PVK---RNNAKYRRIQTLIYDALERPRGWALLYHALVFLIVLGCLILAVLTTFKEYETVS 153

Qy        122 SSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAV 181
               ||:||   | :|| || :|||:|||||||:||:|||:||||| |::|  |||||: |
Db        154 GDWLLLLETFAIFIFGAEFALRIWAAGCCCRYKGWRGRLKFARKPLCMLDIFVLIASVPV 213

Qy        182 VSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLV 241
              |:   |||: ||| |||||||||||:||||||||||||| : ||||||||||||||
Db        214 VAVGNQGNVLATS-LRSLRFLQILRMLRMDRRGGTWKLLGSAICAHSKELITAWYIGFLT 272

Qy        242 LIFSSFLVYLVEKDA----------NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRL 291
              || |||||||||||           :|| ||||||||| ||| |||||||| || |||
Db        273 LILSSFLVYLVEKDVPEMDAQGEEMKEEFETYADALWWGLITLATIGYGDKTPKTWEGRL 332

Qy        292 LSAGFALLGISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEK 351
              ::| |:|:|:|||||||||||||| ||||||||||||||||| ||| |||  || || :
Db        333 IAATFSLIGVSFFALPAGILGSGLALKVQEQHRQKHFEKRRKPAAELIQAAWRYYATNPN 392

Qy        352 SVS-IATWK--------PHLKALHTCSPTNQKLSFKERVRMASPRGQSIKSRQASVGDRR 402
               :  :|||:        |  :       :  :|||   :|||:::||| : |       |
```

```
Db        393 RLDLVATWRFYESVVSFPFFRKEQLEAAASQKLGLLDRVRLSNPRGSNTK------GKLF 446

Qy        403 SPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRLK------SSQPKPVIDADTALGTDDVY 456

Db        447 TPLNVDAIEESPSKEPKPVGLNNKERFRTAFRMKAYAFWQSSE-----DAGTG---DPMA 498

Qy        457 DEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDM 516

Db        499 EDRGYGNDFLIEDMIPTLKAAIRAVRILQFRLYKKKFKETLRPYDVKDVIEQYSAGHLDM 558

Qy        517 LCRIKSLQTRVDQILGKGQITSDKKSREK------------------ITAEHETTDDLS 557

Db        559 LSRIKYLQTRIDMIFTPGPPSTPKHKKSQKGSAFTYPSQQSPRNEPYVARAATSETEDQS 618

Qy        558 MLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPPECEQTSDYQSPV 617

Db        619 MMGKFVKVERQVHDMGKKLDFLVDMHMQHMER----------LQVHVTEYYPTKGASSPA 668

Qy        618 D---SKDLSGSAQNSGCLSRSTSANISRGLQFILTP-NEFSAQTFYALSPTMHSQATQVP 673

Db        669 EGEKKEDNRYSDLKTIICNYSETGPPDPPYSFHQVPIDRVGPYGFFAHDP--------VK 720

Qy        674 ISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLPAIKHLPRPETLHPNPAGLQESI 733

Db        721 LTRGGPSSTKAQANLPS--------SGSTYAERPTVLPILTLLDSCVSYH---------- 762

Qy        734 SDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETLLSVCPMVPKDLGKSLSVQNLIR 793

Db        763 ---------SQTELQGPYSDHISPR-QRRSITRDSDTPLSL----------MSVNH--- 798

Qy        794 STEELNIQLSGSESSGSRGSQDFYP----KWRESKLFITDEEVGPEETETDTF 842

Db        799 --EELERSPSGFSISQDRDDYVFGPSGGSSWMREKRYLAE---GETDTDTDPF 846
```

```
RESULT 13
CIQ3_RAT
ID   CIQ3_RAT       STANDARD;      PRT;   873 AA.
AC   O88944; Q9Z240;
DT   16-OCT-2001 (Rel. 40, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Potassium voltage-gated channel subfamily KQT member 3 (Voltage-gated
DE   potassium channel subunit Kv7.3) (Potassium channel alpha subunit
DE   KvLQT3) (KQT-like 3).
GN   Name=Kcnq3;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Brain;
RA   Derst C., Preisig-Mueller R., Hennighausen A., Daut J.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Brain;
RX   MEDLINE=99055398; PubMed=9836639; DOI=10.1126/science.282.5395.1890;
RA   Wang H.-S., Pan Z., Shi W., Brown B.S., Wymore R.S., Cohen I.S.,
RA   Dixon J.E., McKinnon D.;
RT   "KCNQ2 and KCNQ3 potassium channel subunits: molecular correlates of
RT   the M-channel.";
RL   Science 282:1890-1893(1998).
CC   -!- FUNCTION: Probably important in the regulation of neuronal
CC       excitability. Associates with KCNQ2 to form a potassium channel
CC       with essentially identical properties to the channel underlying
CC       the native M-current, a slowly activating and deactivating
CC       potassium conductance which plays a critical role in determining
CC       the subthreshold electrical excitability of neurons as well as the
CC       responsiveness to synaptic inputs.
CC   -!- SUBUNIT: Heteromultimer with KCNQ2.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=O88944-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=O88944-2; Sequence=VSP_001012;
CC         Note=No experimental confirmation available;
CC   -!- TISSUE SPECIFICITY: Expressed in brain and sympathetic ganglia. In
CC       brain, expressed in cortex, hippocampus and at much lower levels
CC       in cerebellum. In sympathetic ganglia, expressed at approximately
CC       equal levels in both superior cervical ganglia and prevertebral
CC       ganglia.
CC   -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC       characterized by a series of positively charged amino acids at
CC       every third position (By similarity).
CC   -!- SIMILARITY: Belongs to the potassium channel family. KQT
CC       subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF087454; AAC36723.2; -.
DR   EMBL; AF091247; AAC79846.1; -.
DR   HSSP; Q54397; 1JVM.
DR   RGD; 69222; Kcnq3.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003091; K_channel.
DR   InterPro; IPR003937; KCNQ_channel.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF03520; KCNQ_channel; 1.
DR   PRINTS; PR00169; KCHANNEL.
KW   Alternative splicing; Ion transport; Ionic channel; Multigene family;
KW   Potassium; Potassium channel; Potassium transport; Transmembrane;
KW   Transport; Voltage-gated channel.
FT   TRANSMEM    123    143       Segment S1 (Potential).
FT   TRANSMEM    154    174       Segment S2 (Potential).
FT   TRANSMEM    198    218       Segment S3 (Potential).
FT   TRANSMEM    227    248       Segment S4 (Potential).
FT   TRANSMEM    263    283       Segment S5 (Potential).
FT   TRANSMEM    332    352       Segment S6 (Potential).
FT   DOMAIN      305    325       Segment H5 (pore-forming) (Potential).
FT   DOMAIN       13     25       Poly-Gly.
FT   SITE        317    322       Selectivity filter (By similarity).
FT   VARSPLIC      1     83       MGLKARRAAGAAGGGGGEGGGGGGGAANPAGGDSAVAGDEE
FT                                RKVGLAPGDVEQVTLALGTGADKDGTLLLEGGGREEGQRRT
FT                                P -> MALEFPGLQPPPPPRPRTPSAPSSRSSSGEGEAPSG
FT                                GEADGAQGS (in isoform 2).
FT                                /FTId=VSP_001012.
FT   CONFLICT    654    654       H -> R (in Ref. 2).
SQ   SEQUENCE   873 AA;  96897 MW;  D77AF88088051E15 CRC64;

  Query Match             34.2%;  Score 1555.5;  DB 1;  Length 873;
  Best Local Similarity   42.1%;  Pred. No. 2.9e-78;
  Matches  376;  Conservative  106;  Mismatches  262;  Indels  149;  Gaps   25;

Qy          3 DVESGRGRVLLNSAAARGDGLLLLGTRAATLGGGGGGLRESRRGKQGARMSLLGK-PLSY 61

Db         50 DVEQ---VTLALGTGADKDGTLLL--------EGGGREEGQRRTPQG--IGLLAKTPLSR 96

Qy         62 TSSQSCRRNVKYRRVQNYLYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLA 121

Db         97 PVK---RNNAKYRRIQTLIYDALERPRGWALLYHALVFLIVLGCLILAVLTTFKEYETVS 153

Qy        122 SSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAV 181

Db        154 GDWLLLLETFAIFIFGAEFALRIWAAGCCCRYKGWRGRLKFARKPLCMLDIFVLIASVPV 213
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Qy        182 VSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLV 241
Db        214 VAVGNQGNVLATS-LRSLRFLQILRMLRMDRRGGTWKLLGSAICAHSKELITAWYIGFLT 272

Qy        242 LIFSSFLVYLVEKDA----------NKEFSTYADALWWGTITLTTIGYGDKTPLTWLGRL 291
Db        273 LILSSFLVYLVEKDVPEMDAQGEEMKEEFETYADALWWGLITLATIGYGDKTPKTWEGRL 332

Qy        292 LSAGFALLGISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAADEK 351
Db        333 IAATFSLIGVSFFALPAGILGSGLALKVQEQHRQKHFEKRRKPAAELIQAAWRYYATNPN 392

Qy        352 SVS-IATWK--------PHLKALHTCSPTNQKLSFKERVRMASPRGQSIKSRQASVGDRR 402
Db        393 RLDLVATWRFYESVVSFPFFRKEQLEAAASQKLGLLDRVRLSNPRGSNTK------GKLF 446

Qy        403 SPSTDITAEGSPTKVQKSWSFNDRTRFRPSLRLK------SSQPKPVIDADTALGTDDVY 456
Db        447 TPLNVDAIEESPSKEPKPVGLNNKERFRTAFRMKAYAFWQSSE-----DAGTG---DPMT 498

Qy        457 DEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDM 516
Db        499 EDRGYGNDFLIEDMIPTLKAAIRAVRILQFRLYKKKFKETLRPYDVKDVIEQYSAGHLDM 558

Qy        517 LCRIKSLQTRVDQILGKGQITSDKKSREK------------------ITAEHETTDDLS 557
Db        559 LSRIKYLQTRIDMIFTPGPPSTPKHKKSQKGSAFTYPSQQSPRNEPYVARAATSETEDQS 618

Qy        558 MLGRVVKVEKQVQSIESKLDCLLDIYQQVLRKGSASALALASFQIPPPECEQTSDYQSPV 617
Db        619 MMGKFVKVERQVHDMGKKLDFLVDMHMQHMER----------LQVHVTEYYPTKGASSPA 668

Qy        618 D---SKDLSGSAQNSGCLSRSTSANISRGLQFILTP-NEFSAQTFYALSPTMHSQATQVP 673
Db        669 EGEKKEDNRYSDLKTIICNYSESGPPDPPYSFHQVPIDRVGPYGFFAHDP--------VK 720

Qy        674 ISQSDGSAVAATNTIANQINTAPKPAAPTTLQIPPPLPAIKHLPRPETLHPNPAGLQESI 733
Db        721 LTRGGPSSTKAQANLPS--------SGSTYAERPTVLPILTLLDSCVSYH---------- 762

Qy        734 SDVTTCLVASKENVQVAQSNLTKDRSMRKSFDMGGETLLSVCPMVPKDLGKSLSVQNLIR 793
Db        763 ---------SQTELQGPYSDHISPR-QRRSITRDSDTPLSL----------MSVNH--- 798

Qy        794 STEELNIQLSGSESSGSRGSQDFYP----KWRESKLFITDEEVGPEETETDTF 842
Db        799 --EELERSPSGFSISQDRDDYVFGPSGGSSWMREKRYLAE---GETDTDTDPF 846
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RESULT 14
Q8C9Y6
ID   Q8C9Y6      PRELIMINARY;      PRT;   523 AA.
AC   Q8C9Y6;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched
DE   library, clone:A430075J21 product:potassium voltage-gated channel,
DE   subfamily Q, member 4, full insert sequence. (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK040190; BAC30534.1; -.
DR   HSSP; Q54397; 1J95.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR   GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006813; P:potassium ion transport; IEA.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003937; KCNQ_channel.
DR   InterPro; IPR003091; K_channel.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 1.
DR   PRINTS; PR00169; KCHANNEL.
DR   PRINTS; PR01459; KCNQCHANNEL.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER       1      1
FT   NON_TER     523    523
SQ   SEQUENCE   523 AA;  58016 MW;  A9D3C67024F84C18 CRC64;

  Query Match             33.5%;  Score 1525.5;  DB 2;  Length 523;
  Best Local Similarity   58.3%;  Pred. No. 7.1e-77;
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  Matches  308;  Conservative   59;  Mismatches   70;  Indels   91;  Gaps    9;

Qy         35 GGGGGLRESRRGKQGARMSLLGKPL---------------SYTSSQSCRRNVKYRRVQNY 79
              ||||  |          |: ||| ||               :    :|     :|||:||:
Db         14 GGGGSPR---------RLGLLGSPLPPGAPLPGPGSGSGSACGGQRSSAAQKRYRRLQNW 64

Qy         80 LYNVLERPRGWAFIYHAFVFLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIVVFGLE 139
              :|||||||||||:|| |:|||| ||:||| ||| || :||: |||||||||||||||||
Db         65 VYNVLERPRGWAFVYHVFIFLLVFSCLVLSVLSTIQEHQELANECLLILEFVMIVVFGLE 124

Qy        140 FIIRIWSAGCCCRYRGWQGRLRFARKPFCVIDTIVLIASIAVVSAKTQGNIFATSALRSL 199
              :|||:|||||||||||||| |||||||||| || :||:||::| ||||||||||||:
Db        125 YIIRVWSAGCCCRYRGWQGRFRFARKPFCVIDFIVFVASVAVIAAGTQGNIFATSALRSM 184

Qy        200 RFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKE 259
              |||||||||||||||||||||||||||||||||||||||||||:|||||| ||||| :
Db        185 RFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFASFLVYLAEKDANSD 244

Qy        260 FSTYADALWWGTITLTTIGYGDKTPLTWLGRLLSAGFALLGISFFALPAGILGSGFALKV 319
              ||:|||:|||||||||||||||| |||||:|:|||||||||||||||||||||||||||
Db        245 FSSYADSLWWGTITLTTIGYGDKTPHTWLGRVLAAGFALLGISFFALPAGILGSGFALKV 304

Qy        320 QEQHRQKHFEKRRNPAANLIQCVWRSYAAD-EKSVSIATW-------------------- 358
              |||||||||||||| |||||||  || |: |  ::   |||
Db        305 QEQHRQKHFEKRRMPAANLIQAAWRLYSTDTSRAYLTATWYYYDSILPSFRELALLFEHI 364

Qy        359 -------------------------KPHLKALHT------CSPTNQKLSFKERVRMASPR 387
                                      | :   |      |   : ::  |:|:|::| :
Db        365 QRARNGGLRPLEVRRAPVPDGAPSRYPPVATCHRPGSASFCPGESSRMGIKDRIRISSSQ 424

Qy        388 GQSIKSRQ--ASVGDRRSPSTDITAE-GSPTKVQKSWSFNDRTRFRPSLRLK---SSQPK 441
               ::  |:|  |      |||::   |  ||:|||||||||||||| |||||   |::
Db        425 KRTGPSKQHLAPPPIPTSPSSEQVGEASSPSKVQKSWSFNDRTRFRASLRLKPRCSAEEG 484

Qy        442 PVIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKFHVA 489
              |        :::| :||  ||:::|:|: | :|:|||::||:|| ||
Db        485 P---------SEEVAEEKSYQCELTVDDVMPAVKSVIRSVRILKPLVA 523


RESULT 15
Q8IGU8
ID   Q8IGU8      PRELIMINARY;      PRT;   840 AA.
AC   Q8IGU8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   RE26469p (Fragment).
GN   Name=KCNQ;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA   George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA   Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA   Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA   Celniker S.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BT001588; AAN71343.1; -.
DR   HSSP; Q54397; 1BL8.
DR   FlyBase; FBgn0033494; KCNQ.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR   GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006813; P:potassium ion transport; IEA.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003937; KCNQ_channel.
DR   InterPro; IPR003091; K_channel.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF03520; KCNQ_channel; 1.
DR   PRINTS; PR00169; KCHANNEL.
DR   PRINTS; PR01459; KCNQCHANNEL.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER       1       1
SQ   SEQUENCE   840 AA;  95154 MW;  C1813B33F528588A CRC64;

  Query Match             30.0%;  Score 1364.5;  DB 2;  Length 840;
  Best Local Similarity   38.9%;  Pred. No. 1.2e-67;
  Matches  333;  Conservative  112;  Mismatches  247;  Indels  165;  Gaps   23;

Qy         51 RMSLLGKPLSYTSSQSCRRNVKYRRVQNYLYNVLERPRG-WAFIYHAFVFLLVFGCLILS 109
              |||||||||:|  ::  ||:|:|||:|: ||| ||||||  |  ||  |||:|| || ||
Db         66 RMSLLGKPLNY--NRGTRRDVRYRRLQSRLYNPLERPRGLHAIFYHVMVFLMVFTCLALS 123

Qy        110 VFSTIPEHTKLASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGWQGRLRFARKPFCV 169
              ||||| |: : |   |  :| :::: | :||  |:||:||  ||:|  |||:| ::|||:
Db        124 VFSTIKEYEEDAVYILFRMEILVVIWFTMEFGARLWSSGCRSRYQGCLGRLKFVKRPFCI 183

Qy        170 IDTIVLIASIAVVSAKTQGNIFATSALRSLRFLQILRMVRMDRRGGTWKLLGSVVYAHSK 229
              || : ::||| |:   | | :||||||| ||| |||||||||||||||||||||||| :
Db        184 IDIVTILASIVVLGMGTSGQVFATSALRGLRFFQILRMVRMDRRGGTWKLLGSVVYAHRQ 243

Qy        230 ELITAWYIGFLVLIFSSFLVYLVEKDANKEFSTYADALWWGTITLTTIGYGDKTPLTWLG 289
              ||||  ||||| |||:|||||: ||| | :|| :| ||||| ||| |:||||  |:|| |
Db        244 ELITTMYIGFLGLIFASFLVYMWEKDVNDKFSNFAQALWWGVITLCTVGYGDMVPITWQG 303

Qy        290 RLLSAGFALLGISFFALPAGILGSGFALKVQEQHRQKHFEKRRNPAANLIQCVWRSYAAD 349
              :|::: |||||||||||||||||||||:| ||||  :|| ||| ||| ||| ||||
Db        304 KLIASCCALLGISFFALPAGILGSGFALKVQQQQRQKHMIRRRQPAATLIQAVWRCYAAD 363

Qy        350 EKSVSIATWKPHLKALHTCSPTNQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDIT 409
              | |||:|||  |  || :   :    |||           |  :|  ::   :| :
Db        364 EHSVSVATWNIHRVALPSPPASRASSSFKHNT--------SFVARLPTIRRHKSQTIQTP 415

Qy        410 AEGSPTKVQK-SWSFNDRTRFRPSLRLKSSQPKPVIDADTALGTDDVYDEKGCQCDVSVE 468
              |   | |  |    ||:  ::|         | : ::   |  ||  |
Db        416 GGGDGGGVSKPPGSSSRASTRYTRTIR----------DINASVENLDEEDEPRC------T 459

Qy        469 DLTPPLKTVIRAIRIMKFHVAKRKFKETLRPYDVKDVIEQYSAGHLDMLCRIKSLQTRVD 528
              ||   || || || :|: ||:||||| |:|||||||:|||:|||:|:| |:|  |  |:|
Db        460 QLTNRHKTAIRFIRKLKYFVARRKFKEALKPYDVKDVMEQYAAGHVDLLGRVKMLHLRLD 519

Qy        529 QILGKGQITSDKKSREKITAEHETTDDLSMLGRVVKVEKQVQSIESKLDCLLDIYQQVLR 588
              |||||       |:::   ::      :|:  ||||||:||  || ||| |:  |
Db        520 QILGK----QGSKAKDVYASK------ISLASRVVKVERQVADIEEKLDILIKAY----- 564

Qy        589 KGSASALALASFQIPPFECEQTSDYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLQFIL 648
                                      :: :|                      :|:
Db        565 ----------------------------MEDRD----------------------RFLA 573

Qy        649 TPNEFSAQTFYALSPTMHS-QATQVPISQSDGSAV-------AATNTIANQINTAP--KP 698
              |           | :||   :  |:  :   |:          || :    |: | |  |
Db        574 LP--------LPAKPKIHSISPSHKPLHHAHNLAMIDVWKRTAALSVHPEQVTTTPLLNP 625

Qy        699 AAP--------TTLQIP-----------PPLPAIKHL---PRPETLHPNPAGLQ-ESISD 735
              :||        |  | |           |  | ::|      :   |:    | : :  :|
Db        626 SAPDSSELRSLTATQTPTTTTDAIATQTPMPPHVQHTATNTKSSVLNSYQLGSEKQQHND 685

Qy        736 VTTCLVASKENVQVAQSNLTKDRSMRKSF----------DMGGETLLSVCPMVPKDLGKS 785
              |    :   ||    :  |:  ||  : :          | | ::| |     | |
Db        686 V---FMTELENRTKKRVTLSLHRSTSEPYSKQEQRIIIPDEGADSLDSSAKPTPPDSSII 742

Qy        786 LSVQNLIRSTEELNIQLSGSESSGSRGSQDFYPKWRESKLFITDEEVGPE-ETETDTFDA 844
              |  :      |:|| :          | | :| |           | ::| | : : |
Db        743 LIDEYEDFEEEDLNCE----------GEMDHFPTWE------IDSDIGVEVDVDADADGD 786

Qy        845 APQPAREAAFASDSLRT 861
                :   : |    : ||
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Db 787 CDESTEDTALLQCATRT 803

Search completed: April 8, 2005, 16:41:54
Job time : 192 secs